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listing and declared, that it includes no new matter.

(54) Genomic DNA sequences of *Ashbya gossypii* and uses thereof

(57) The present invention relates to the terminal sequencing of random genomic fragments performed with the filamentous fungus *A. gossypii*, to the sequences obtained therewith and the use of the sequences for forensic identification, to characterize genes and gene organization of this ascomycete by inter-genomic comparison, to identify biosynthetic genes that can be used as selection markers, to isolate promoters and terminators

for application in a homologous as well as heterologous context, to find putative centromere containing clones, chromosome mapping, chromosome identifying, general information about chromosome organization and in addition to identify ORF containing SRS sequences with no homology to *S. cerevisiae* or any other organism which allows the identification of *A. gossypii* specific genes.

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Description

The present invention relates to genomic DNA sequences obtained from terminal sequencing of random genomic fragments of the filamentous fungus *Ashbya gossypii* and uses thereof.

The phytopathogenic fungus *Ashbya gossypii* is a filamentously growing ascomycete that was first isolated as a plant pathogen in tropical and sub-tropical regions. It infects the seed capsule of cotton plants (Ashby S.F. and Nowell W. (1926) Ann. Botany 40: 69-84) and has also been isolated from tomatoes and citrus fruits (Phaff H.J. and Starmer W.T. (1987) In "The Yeasts", Vol. I Rose A.H., Harrison, J.S. (eds), Academic Press, London, 123 ff; Dammer K.H. and Ravelo H.G. (1990). Arch. Phytopathol. Pflanzenschutz, Berlin 26: 71-78 Dammer and Ravelo, 1990). The infection of the seed capsule is caused by transmission of *A. gossypii* mycelium pieces or spores by stinging-sucking insects and causes a disease called stigmatomycosis.

Studies characterising the karyotype of *A. gossypii* have been performed (Wright, 1990; Wendland, 1993; Gaudenz, 1994, "The small genome of the filamentous fungus *Ashbya gossypii*. Assessment of the karyotype", Diploma Thesis, Department of Applied Microbiology, Biocenter, University Basel). It has been found using yeast chromosomes of precisely known length as size markers that the genome of *A. gossypii* has a total nuclear genome size of 8.85 Mb.

A. gossypii is systematically grouped to the endomycetales belonging to the family of sperophthoraceae (Lodder J (1970) General classification of the yeasts. In: "The Yeasts", Lodder J. (ed.), North Holland Publishing Company, Amsterdam-London, 1ff Lodder, 1970). This classification is based on the observation that the spores that develop in hyphal compartments called sporangia look like ascospores, which are defined as endproducts of meiosis (Muller E. und Löffler W. (1971) Mykologie. Grundriß der Pilzkunde. DTV-Thieme, Stuttgart, 37 ff). However, in several respects, *A. gossypii* more closely resembles the budding yeast *Saccharomyces cerevisiae* than other filamentous fungi. For example, homologous recombination has been found to be the main mode of integration of transforming DNA (Steiner S. (1991). Diplomarbeit, Institut für Mikro- und Molekularbiologie der Justus Liebig Universität Gießen Steiner *et al.*, 1995), which is in contrast to findings made in many other filamentous fungi (reviewed by Fincham J.R.S (1989) Transformation in fungi. Microbiol. Rev. 53 (1): 148-170).

Additionally, sequence analysis of the *A. gossypii* *TEF*, *LEU2* and *THR4* genes (Altmann-Jöhl and Philippsen, 1996; Mohr, May 1997; Steiner and Philippsen, 1994) has identified high sequence homology to their functional homologues in *S. cerevisiae*. In addition, for the latter genes, syntenic (positionally conserved) arrangement of adjacent homologous ORF's has been found. The growing number of completely sequenced reference genomes, such as for example *S. cerevisiae*, offers new prospects for rapid comparative gene and genome analysis of so far less characterized organisms, such as *A. gossypii*, in parallel or even before the application of genetic techniques.

In view of the above, the present invention provides genomic DNA sequences obtained from terminal sequencing of random genomic fragments of *Ashbya gossypii*. The present invention particularly relates to genomic *A. gossypii* DNA sequences that are obtainable from the series of clones listed in Table 1 and presented in the attached Sequence Listing. Some of these *A. gossypii* sequences are homologous to *S. cerevisiae* sequences and to sequences from other filamentous fungi, e.g. ORF's specifically required for growth in filamentous fungi. Others of these *A. gossypii* sequences, such as those set forth in Table 2, have no homology to *S. cerevisiae* sequences, including sequences which have no homology to known sequences from any other fungus. The sequences of the invention find particular use in forensic identification, chromosome mapping, chromosome identification, and tagging of genes of known and useful function. Procedures such as these can easily be carried out by those of ordinary skill in the art.

The present invention also concerns chimeric genes comprising the sequences of the invention, recombinant vectors comprising such chimeric genes, wherein the vectors are capable of being stably transformed into hosts, as well as hosts stably transformed with such vectors. Preferred hosts are fungi such as *A. gossypii* as well as bacteria.

Furthermore, the present invention relates to the identification and characterization of *A. gossypii* ORF's based on the high homology of primary structures in *A. gossypii* and *S. cerevisiae* and the sequences obtained therewith. The present invention also relates to the use of the *A. gossypii* sequences provided in the Sequence Listing to characterize genes and gene organization of this ascomycete by inter-genomic comparison, to identify biosynthetic genes that can be used as selection markers, to isolate promoters and terminators for application in a homologous as well as heterologous context, to find putative centromere containing clones, general information about genome organization and in addition to identify ORF's containing single read sequences (SRS) with no homology to *S. cerevisiae* or any other organism, which allows the identification of *A. gossypii*-specific genes.

Encompassed by the present invention is a method of sequencing the termini of randomly picked *A. gossypii* shotgun clones to obtain linked pairs of genomic sequences. Said linked pairs of genomic sequences can be used for identification of open reading frames (ORFs) showing or lacking homology to functionally characterized or uncharacterized genes from *S. cerevisiae*, other fungi or other organisms. The sequence information provided herein in the attached Sequence Listing is sufficient to generate gene deletions in *Ashbya* by using, for example, by PCR-based gene targeting methods as described herein.

One of the main prerequisites for success in such an analysis is a relatively compact, organized genome. This is

required to obtain a maximum of information from the limited length of single read sequence (SRS) analysis. *A. gossypii* represents such a compact genome. The presence within the *Ashbya* genome of short intergenic regions and rare occurrence of introns increases the probability of finding matches to open reading frames (ORF's) in the majority of SRS's.

Thus one embodiment of the present invention is a method to identify and characterize *A. gossypii* ORF's by sequence comparison of their *S. cerevisiae* homologues without the requirement of complete sequence information for the *A. gossypii* ORF's.

Further encompassed by the invention is a method for characterization of an *Ashbya* gene, the knockout of which leads to a non-growth phenotype.

In a specific embodiment of the invention a method for characterization and validation of an *Ashbya* gene is provided comprising

- (a) inserting into *Ashbya* sequences of genomic pAG clones as provided herein in the attached Sequence Listing a chimeric gene construct comprising a selectable marker plus adjacent multiple cloning regions from a suitable cloning vector;
- (b) selecting clones carrying *Ashbya* sequences disrupted by the selection marker gene in a suitable host system;
- (c) transforming *Ashbya* with a disruption cassette according to (a);
- (d) revealing the disrupted open reading frame by DNA sequence analysis around the site of integration of the selection marker module and determining the orientation of the selection marker module;
- (e) determining whether deletion/insertion at the disruption site results in any phenotypic alterations.

A further embodiment of the invention relates to a method for characterization and validation of an *Ashbya* gene comprising

- (a) designing cassette for gene targeting comprising terminal Short Flanking Homology regions encompassing a selectable marker module;
- (b) transfecting the gene targeting cassette of (a) into *A. gossypii* and selecting transformants;
- (c) verifying correct gene targeting by applying suitable testing procedures;
- (e) determining whether deletion/insertion at the disruption site results in any phenotypic alterations.

Further comprised by the present invention is a method for characterization and validation of an *Ashbya* gene involving a triple selection marker module which method comprises

- (a) inserting of a reporter, a selectable marker and a strong promoter, which is preferably a regulatable promoter, in front of the start codon of a coding sequence of interest (promoter exchange mutant) within the *Ashbya* genome
- (b) applying potential antifungal agents for growth to the promoter exchange mutant of (a) and to a wild-type strain, respectively;
- (c) identifying a growth or non-growth phenotype of the strong promoter exchange mutant.

Within this novel process any DNA encoding a selectable marker can be used that, upon transformation, is capable of conferring a resistance phenotype to *A. gossypii* or any other advantage based on which the transformant can be separated from non-transformed clones such as, for example, ScLEU2, kanMX, kanSC or GEN3.

Promoters that can be suitably used as part of the triple selection marker module are those that are capable of functioning in *Ashbya* and in heterologous systems such as, for example, *S. cerevisiae* or *K. lactis*. Preferred within this invention is a heterologous promoter from *S. cerevisiae* or *K. lactis*, which is not only to be qualified as a strong promoter also within the *Ashbya* system but is also well regulatable in *Ashbya*.

A reporter that can be suitably used within the triple selection marker module is one that is easily detectable such as, for example, the green fluorescent protein.

If the activity or expression of the gene product is inhibited by one or more agents, the inhibitory effect for growth will be overcome in the strain overexpressing the gene product. If the reporter expression, controlled by the wild-type promoter, is not changed one can conclude that the agent inactivates the gene product and not a transcription factor or signaling factor for expression of the gene product. If the reporter expression is much lower, the agent most likely affects the expression of the gene product and not the gene product itself.

The present invention further relates to a DNA molecule comprising a DNA sequence selected from the attached Sequence Listing which molecule is validated as a potential target in a pesticide screen based on the use of said molecule in a gene disruption method as described herein.

Further encompassed by the present invention is the use of sequences selected from the attached Sequence Listing to identify substances having antifungal activity; the use of sequences selected from the attached Sequence

Listing to identify substances having pesticidal activity; the use of sequences selected from the attached Sequence Listing to identify biosynthetic genes that can be used as selection markers; the use of sequences selected from the attached Sequence Listing to identify promoter and terminator regions including downstream non-translated regions and up-stream nontranslated regions, respectively; the use of sequences selected from the attached Sequence Listing to identify putative centromere-containing clones; the use of sequences selected from the attached Sequence Listing to identify ORFs containing SRS sequences with no homology to *S. cerevisiae*; the use of sequences selected from the attached Sequence Listing to identify ORF's containing SRS sequences with no homology to any other organism, which allows the identification of *A. gossypii*-specific genes; the use of sequences selected from the attached Sequence Listing to characterize genes and gene organization of this ascomycete by inter-genomic comparison; and the use of sequences selected from the attached Sequence Listing to identify and characterize the genome organization of *Ashbya gossypii*.

In particular, the present invention encompasses the use of a DNA sequence selected from the Sequence Listing to identify *Ashbya gossypii* promoter and terminator regions including downstream non-translated regions and up-stream nontranslated regions, respectively.

The invention further relates to the use of a DNA sequence selected from the Sequence Listing wherein a putative promoter region is identified by sequence alignments and the ORF of a genetic selection marker plus start codon and terminator is placed downstream of said putative promoter region.

Further comprised is the use of an a DNA sequence selected from the Sequence Listing and variants thereof in a screening method for identifying compounds capable of inducing broad spectrum disease resistance in plants.

The suitability of the DNA sequence to be used in such a screening assay is determined in gene disruptions in the *Ashbya* genome. For that purpose a disruption cassette may be used comprising a selectable marker plus adjacent multiple cloning regions from a suitable cloning vector.

In a further embodiment of the invention a DNA sequence selected from the Sequence Listing or parts thereof is used within a gene targeting procedure involving short target sequence homologies added to both ends of a DNA molecule encoding a selectable marker.

In a further embodiment according to the invention a DNA sequence selected from the Sequence Listing may also be used for distinguishing among different species of plant pathogenic fungi and for distinguishing fungal pathogens from other pathogens such as bacteria.

It is one embodiment of the present invention to use sequences selected from the attached Sequence Listing to identify promoter and terminator regions including downstream non-translated regions and up-stream nontranslated regions, respectively. In many cases, the attached sequences allow to locate the precise boundaries between open reading frames and promoter or terminator regions either from the first single read or after additional sequencing. The promoter and terminator regions so obtained are also part of the present invention.

In particular, sequence alignments can reveal 5' ends of open reading frames plus adjacent sequences of their putative promoter regions. By placing the ORF of a genetic selection marker plus start codon and terminator downstream of this putative promoter sequence, one can identify and use novel *Ashbya gossypii* promoters.

The promoter and terminator regions so obtained are also part of the present invention.

The DNA sequences provided in this application are especially suitable to be used in gene disruptions in the *Ashbya* genome. This can be performed, for example, using classical procedures involving gene disruption cassettes.

Said gene disruption cassettes essentially consists of a selectable marker plus adjacent multiple cloning regions from a suitable cloning vector. This transformation selection module upon expression of the selection marker gene preferably leads to resistance in yeast and filamentous fungi and also in bacteria such as, for example, *E. coli*. This module is inserted into *Ashbya* sequences of genomic pAG clones as provided herein in the attached Sequence Listing. To this purpose the selectable marker is released from the cloning vector by cleavage with a suitable restriction enzyme such as, for example, BamHI, Sall or XhoI. It is ligated into cloned *Ashbya* DNA cleaved with a corresponding restriction enzyme that is, for example either BglII, XhoI (partial) or Sall (partial), respectively. Clones carrying *Ashbya* sequences disrupted by the selection marker gene are selected in a suitable host system such as, for example, *E. coli*. DNA sequence analysis around the site of integration of the selection marker module (i1 and i2sequences in the attached *Ashbya* data base) reveal the disrupted open reading frame and determine the orientation of the selection marker module.

A selection marker that is especially suited to be used within the scope of the present invention is kanMX0 expressing G418 resistance in yeast and filamentous fungi and kanamycin resistance in *E. coli* (International Patent Application No PCT/EP 91/01116; Steiner *et al*, 1995).

Especially preferred within the scope of the present invention is a new PCR-based *Ashbya* gene targeting procedure provided herein. Gene targeting in *Ashbya* relies on homologous recombination in this fungus (Steiner *et. al.*, (1995) Genetics (in press 1995)). Short target sequence homologies added to both ends of a DNA molecule encoding a selectable marker are sufficient to mediate sequence specific gene targeting in *Ashbya*. The length of the target sequence homologies is preferably in the range of between about 20 to 80 nt, more preferably between 35 and 60 nt,

and most preferably is about 45 nt. Within this novel process any DNA encoding a selectable marker can be used that, upon transformation, is capable of conferring a resistance phenotype to *A. gossypii* or any other advantage based on which the transformant can be separated from non-transformed clones.

The fragment designed for gene targeting thus carries terminal Short Flanking Homology regions encompassing the selectable marker module. These fragments are transfected into *A. gossypii* by a suitable method such as, for example, electroporation and transformants are selected. Verification of correct gene targeting is achieved by suitable testing procedures such as, for example, PCR testing the presence of the new junctions between target DNA and integrated marker using specific verification primers. Verification of the gene targeting can also be performed by DNA-hybridization experiments.

In using verification primers it proved advantageous to use specific primer pair combinations. One pair of verification primers, for example, may be derived from the open reading frame of the selectable marker gene. Whereas a second pair of primer sequences can be derived from the single read sequence and correspond to regions upstream and downstream, respectively, of the homology regions used for the targeting process. Using this PCR-based targeting approach sequences can be manipulated that are app. 150 nt in length. A criterium matched by all single read sequences of the attached *Ashbya* database. This is of major advantage considering classical methods of gene disruption that are laborious and require cloning steps to incorporate a selectable marker within rather large flanks of surrounding target sequence homology.

After clonal purification (spore isolation) it can be easily determined whether deletion/insertion at the targeted locus results in any phenotypic alterations such as, for example, a reduction or abolition of fungal growth, decrease or loss of viability, etc. Once such a phenotypic alteration can be established for one of the *Ashbya* disruption or knockout mutants it is further examined whether said mutant qualifies as a target to be used in a pesticide screen, preferably a fungicide screen.

Owing to the provision within the scope of this invention of a novel and powerful gene disruption process, there is no longer a need to know the exact biological function of the protein product encoded by a gene comprising or, in the alternative, being flanked by one of the *A. gossypii* DNA sequences provided herein.

Those sequences that have no homology neither to *S. cerevisiae* nor to any other organism and are thus *A. gossypii* specific are especially useful, as they are promising candidates to be used in a pesticide screen for identifying substances which have pesticidal and, preferably, fungicidal activity, but are non-toxic to other organisms especially mammals. Though nothing is known about the exact biological function of the genes comprising said DNA sequences or being flanked by said DNA sequences, they are nevertheless especially valuable owing to their being unique to the fungal pathogen. Thus, any pesticidally active substance being identified in a pesticide screen involving one or more of those sequences have a high potential of exhibiting a biological activity that only affects *A. gossypii* and possibly other pathogenic fungi having (yet unidentified) homologous sequences, but do not interfere with any vital functions in other organisms such as, for example, mammals.

It is thus a further embodiment of the present invention to identify genes within the *A. gossypii* genome which are potential targets for the action of pesticidally active compounds, but especially fungicidally active compounds, by using those *Ashbya* sequences identified in the Sequence Listing corresponding to ORF's with 100 and more codons showing less than 20% homology to a yeast gene classified as 3 or as "none".

ABBREVIATIONS

LIPS Linked Pairs of Sequences
MCS Multi Cloning Site
ORF Open Reading Frame
SRS Single Read Sequence
RP Reversed Primer
UP Universal Primer

DESCRIPTION OF TABLE 1 AND THE SEQUENCE LISTING

The sequences in the Sequence Listing correspond to the PAG names in Table 1. Thus, Table 1 describes each sequence in the Sequence Listing in six columns: "PAG name", "Yeast", "Gene Name", "Brief Description", "Homology Class", and "Additional Comments", the details of which are as follows:

PAG Name: Number of *Ashbya gossypii* plasmid clone (e.g. PAG1001) followed by RP (sequence obtained using the reverse primer) or by UP (sequence obtained using the universal primer) or 11 or 12 (internal sequences obtained after insertion of kanMX0 in the *Ashbya* DNA at a BglII, XhoI or BamHI site and sequencing in both directions from these sites using sequencing primers binding to the 5' and 3' region of kanMX0). CRP and CUP mark sequences from rare chimeric genomic clones, the ends of which map to different genomic regions. For a few clones, only RP or UP

sequences are listed. 5% of the plasmid clones carry ribosomal DNA sequences, as concluded from high sequence homologies of their RP and UP sequences to ribosomal DNA of *S. cerevisiae*. These overlapping clones representing tandem copies of the 8.2 Kb *Ashbya* ribosomal DNA repeat are not listed in the *Ashbya* genome data base. The PAG name is set out above each individual sequence in the Sequence Listing.

Yeast name: Systematic name of *S. cerevisiae* gene with highest homology to the *Ashbya* sequence, as determined by the search algorithm. For some *Ashbya* sequences, two systematic names are listed because they carry information from two *Ashbya* ORF's with homology to *S. cerevisiae* genes. Sequences of high (significant) homology are distinguished from those with low (insignificant) homology by the classification in column 5 (Homology Class). If no systematic gene name is listed, the *Ashbya* sequence shows either no homology to *S. cerevisiae* genomic DNA or it is mitochondrial DNA (around 80% AT base pairs and homology to genes coded by the mitochondrial genome).

Gene name: *S. cerevisiae* gene name used in the literature.

Brief Description: Brief description of the *S. cerevisiae* gene showing highest homology to the *Ashbya* sequence.

Homology Class (HC): Significant homologies to *S. cerevisiae* genes are classified as 1. Intermediate homologies (about one quarter to one third identity on the amino acid level) are classified as 2. ORFs with 100 and more codons showing less than 20% homology to a yeast gene are classified as 3. *Ashbya* sequences lacking ORF's of 100 and more codons and showing less than 20% sequence homology to *S. cerevisiae* are classified as 4.

Additional Comments: Useful comments concerning (a) presence of promoter or terminator sequences as judged by the presence of 5' ends (N-terminus) and/or 3' ends (C-terminus) of ORF's and adjacent DNA, (b) identification of novel *Ashbya* ORFs (minimum size in nucleotides (nt) as only ORF in frames +1 to +3 or -1 to -3 and lacking significant homology to yeast and fungi, (c) syntenic, (d) reason for changes of ORF classification, (e) matches to tRNA genes, (f) presence of intron, judged from interruption of regions of high level of protein homology and confirmed, in addition, by applying the *S. cerevisiae* intron-recognition rules, (g) high CAI (codon adaptation index) marking a well expressed gene and with that a strong promoter. Further abbreviations are explained in the MIPS yeast data base.

EXAMPLES

Example 1: Construction of a Genomic Library

A.) Preparation of Partially Digested DNA

Genomic DNA of *A. gossypii* (strain ATCC10895) was partially digested with *Sau3A* and separated on a low melting agarose gel. Two regions were cut out off the gel: A first the gel piece containing DNA fragments in the range of 3.5-6 kb in length and the second gel piece from containing DNA fragments in the range of 5-8 kb in length.

B.) Ligation and Cloning (standard procedures and media as described in Sambrook et al Cold Spring Harbor Press, 1989)

Sau3A fragments of different sizes, derived from the partial digestion of the genomic DNA, were cloned into the yeast shuttle vector pRS416 (Sikorski and Hieter, 1989, Genetics 122: 19-27). For this purpose pRS416 was cut with *Bam*HI. The 5'-phosphate group of the linearized vector (4.8 kb) was removed with Calf Intestinal Phosphatase to minimize the recircularization of the vector during ligation. DNA of the two size fractions, one with fragments in the range of 3.5-6 kb and the other with fragments in the range of 5-8 kb were cloned separately into the vector. The ligation samples were separately transformed into the *E. coli* strain XL1-blue yielding together approximately 21,500 colonies on 55 plates. 80 % of the colonies (17,000) were white indicating insertion of a *A. gossypii* DNA. The 21,500 colonies derived from the two size fractions were combined by washing each plate with 2 ml full medium (2*YT). Approximately 120 ml cell suspension were obtained. 100 ml of the cell suspension were used to inoculate once a 1 litre culture for the isolation of plasmid DNA. The remaining 20 ml cell suspension were mixed with 5 ml glycerol and stored divided into two aliquots at -70 °C. The ratio of white to blue colonies stayed stable after growth in selective full medium ON. The isolated plasmid DNA was purified over a caesium chloride density gradient and separated on agarose gel. The total yield of plasmid DNA isolated from the 1 litre culture was approximately 5 mg.

All plasmids of the genomic library had a common structure based on plasmid pRS416. The average insert length was approximately 4 kb. The genomic library with 17,000 recombinant clones carrying an insert therefore covers 8 times the 9.7 Mb *A. gossypii* genome (Gaudenz, 1994).

Example 2: Sequence determination

A.) Sequencing the partial Sau3A fragments at both ends

Approximately 350 to 450 ng of plasmid DNA was taken for cycle sequencing (T3 and KS primer or similarly binding primers) with the Peikin Elmer AmpliTaq FS PRISM™ Ready Reaction Dye Terminator Cycle Sequencing kit using the protocol of the manufacturer (addition of 1% DMSO to the sequencing reaction, 95 °C denaturing temperature) and the 373A automated sequencing system (Perkin Elmer) for electrophoresis and fragment detection. SRS's were named with the plasmid name and the suffix UP or RP was added to mark the side of the insert from which the sequence was derived regardless, of which primer present at this side of the multiple cloning site was actually used.

B.) Sequence processing

Concerning the pAG1001 to pAG1000 and 1201 to 1700 series of clones, the vector part of the sequences was removed, obvious base-calling errors were edited and, depending on the quality of the sequence, an individual end point was determined. SRS of the pAG1001 to pAG1100 and 1201 to 1700 series were not further edited and were taken as provided. All sequences were transferred on a VAX system and put into GCG format. Query sequences were translated in all six reading frames and run in a BLAST search (Altschul *et al.*, 1990) against MIPS data base at <http://www.mips.biochem.mpg.de/mips/yeast/>

Alignment of sequences from mitochondrial or rDNA clones was performed with the SeqMan module of the Lasergene software package (DNASTAR, Ltd., London, UK) on a Macintosh Power PC.

Example 3: Classification of the BLAST search results

In the evaluation of the BLAST results, four different categories of homology class (HC) were used. HC 1 and 2 represent SRS's showing a significant hit to an *S. cerevisiae* ORF. The border between category 1 and 2 was made at approximately 40 % identity in the aligned protein sequences. SRS's showing no convincing homology (around 20 % identity and lower) but with an possible open reading frame (with or without ATG) of at least 300 nt length were assigned to HC 3. All SRS's with no significant homology and no possible open reading frame of at least 300 nt were put into HC 4. However, the described values for classification were not applied as strict rules. Factors such as length of homologous block, in cases of several blocks the overall homology, relation of scoring hit to possible open reading frames, position of homologous block within the *S. cerevisiae* protein sequence (for example very N- or C-terminus), a biased sequence, etc. were taken into account for classification.

Almost 30% of the clones listed in the attached Sequence Listing show synteny with *S. cerevisiae*. Thus, *Ashbya* genes of interest for antifungal screening assays (e.g. homologues of essential fungal or yeast genes) can be found due to positional conservations (synteny) when RP and/or UP sequences match adjacent *S. cerevisiae* homologues. Applying the rules of ancient synteny, the frequency of such predictions increases by a factor of 2 or even more.

Over 5% of RP and UP sequences identified open reading frames of 100 and more codons with no apparent homology to sequences in data bases. In Table 1, they are marked as class 3 or 4. These sequences are therefore candidates for novel lead target genes. Fungal pathogens (e.g. *Candida albicans* or phytopathogenic fungi) carrying homologues of these genes can be treated by compounds which were developed based on assays using the *Ashbya* I ad target.

Example 4: Use of the *Ashbya gossypii* sequences for isolation of *Ashbya gossypii* promoters

Sequence alignments can reveal 5' ends of open reading frames plus adjacent sequences of their promoter regions. By placing the ORF of a genetic selection marker plus start codon and terminator downstream of this promoter sequence, one can identify and use novel *Ashbya gossypii* promoters. For example, an ORF of 67 amino acids was identified on the SRS of pAG1245rp. This ORF shows 98 % homology to the *S. cerevisiae* Ribosomal Protein S28.e. 12 in a BLAST search (Altschul *et al.* (1990) J. Mol. Biol. 215: 403-410). The ORF (AgRPS33B) for the putative *A. gossypii* Ribosomal Protein is located from 195 to 395 on the SRS with 700bp, leaving 300bp for the promoter. Based on these findings plasmid pAG1245 may be used for isolation of a novel promoter using the AgLEU2 marker in PCR-targeted gene exchange in *S. cerevisiae*.

A.) PCR synthesis of a DNA fragment carrying the AgLEU2 marker

Two primers, RP5 and RP3, are selected for the amplification of the AgLEU2 gene. Both primers are 60 mers showing beside 20 bp homology to AgLEU2 in addition to 40 bp homology to pAG1245.

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Primer RP5: 5'TTT TAC TAG ATA TTT TAT ATC CAA GAA GCA ATA GAT CAA AAT GGC TGC GGT AAA GAG AAT 3'. The 40 bp at the 5'end of RP5 are homologous to 40 nucleotides in front of the ATG start codon of AgRPS33B. The 20 bp at the 3' end of RP5 are homologous to the first 20 nucleotides of the AgLEU2 ORF, including the ATG start codon.

5 Primer RP3: 5' CTG GAG CTC CAC CGC GGT GGC GGC CGC TCT AGA ACT AGT GCG CCA ACG TTG CGA GAT ATA 3', The 40 bp at the 5' end of RP3 are homologous to 40 nucleotides in the pBlISK+ multiple cloning site (Alting-Mess M. A. and Short J.M. (1989) Nuc. acids Res. 17(22): 9494) of pAG1245 covering the SacI, SacII, NotI, EagI, XbaI and SpeI restriction sites. The 20 bp at the 3'end of RP3 are homologous to 20 nucleotides in the AgLEU2 terminator region (1261-1281).

10 Sequence carrying the AgLEU2 coding region and the AgLEU2 terminator sequence (the ATG start codon of AgLEU2 is written in bold letters and the stop codon (1117-1119) is underlined):

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25

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35

45

50

55

(1) ATGGCT GCGGTAAGA GAATTGTGGT GCTTCGGGGC
 GACCACATCG GCCGCGAGGT CGTGGAGGAG GCGGTGAAGG TGCTTGGCGC CGTGGAGCAG AGCCTGTCCG ACGTGCACCTT
 TGACTTCCAG TACCACCTGG TCGGCGGGGC GGCCATCGAC GCCACGGGT CCGCGCTGCC GGACGAGGCG CTGGGGCGCG
 CGAAGGAGGC GGACGCGGTA CTGCTGGGG CAGTTGGCGG ACCGAAGTGG CAGGGCGGCG CCGTCAGGCC GGAGCAGGGC
 CTGCTGAAC TGAGACAGGA GTTGGGCGTG TACGGAACC TGCGTCCCCTG CAACTTTGCG GCGGACTCGC TGCTCGAGCT
 GTCGCCGTG CGCCCCGAGA TTGCCCGGA TACCGATATT ATGGTGTGTC GGGAGCTGCT GGGCGGGAGC TACTTCGGCG
 AGCGCCACGA GGACGAGGGC GACGGAGTGC CGTGGGACAC CGACAAGTAC ACCGTGAAGG AGGTGCAGCG CATCGCGCGC
 ATGGCGGGGT TCCTGGCTCT GCAGCAGGAC CCGCCGCTAC CTGTGTGGTC GCTGGACAAG GCGAACGTCC TGGCCAGCTC
 CCGCCTGTG CGCAAGACCG TGGAGGAAAC CTTCCAGAGT GAGTTCCCA ACGTGCAATT GCAACACCAG TTGATAGATT
 CAGCTGCAAT GATTTTGGTC AAGAACCCGC GGGCGTTCAA CGGGGTGCTG GTGACGAGCA ACATGTTCCG GGACATTATC
 TCTGACGAAG CGTCGGTGAT CCCAGGGTCC CTAGGGTTGC TGCCATCGGC CTCGCTCGCG TCTTTGCCCG ATAGCAAGAG
 CGCCTTTGGC CTCACGAGC CCTGCCACGG CTCTGCCGCC GATCTGCCCG CCGGGAAGGC GAACCCGATC GGATGCATCC
 TCTCTGCTGC CATGATGCTG AAGTTGTCGT TGAACATGGT TGCTGCCGGC GAGGCGGTG AGCAGGCAGT GCAGGAGGTG
 TTGGACTCGG GAGTCAGAAC GGGCGACCTG CTCGGCTCGA GCTCCACTTC GGAGGTGGC GACGCCATTG CGCTTGCACT
 TAAGGAAGCC TTGCGCAGGC AATCCGCAGC TGGTCTGAGC TAGCCTCGAG GACCCTTCTC TTTAGACTAT TCTACTCTTA
 TGCACGTAAA AAATCTAGG AAATAATGAT TAACTAGGAG TAAATAACC GGCTAGTGGC ATTCATATAG CCGTCTGTCT
 ACATCTACAT CACACATTC GAGTGTATAT CTCGCAACGT TGGCG (1281)

The PCR reaction is performed in a Thermocycler from ams Biotechnology. As a template, the isolated 3.1 kb BamHI/Sall fragment from plasmid pAG150 (Mohr Ch. (1997) Ph.D. Thesis, Institute of Applied Microbiology, University

of Basel) carrying the AgLEU2 gene is used. 100 ng template are added for a 50µl reaction volume supplemented with 0.2mM of dATP, dCTP, dGTP and dTTP. 5µl of 10*Thermo Pol Buffer (Biolabs). The concentration of primer RP5 and primer RP3 in the reaction is 1µM. After the hot start, 1µl enzyme mixture (Taq Polymerase (Pharmacia) and Vent Polymerase (Biolabs) 5:1) is added. PCR is executed under the following conditions: hot start 2 min at 94 °C, 30 cycles of 30 sec at 94°C, 30 sec at 55°C and 2 min at 72°C and finally 4 min at 72°C.

Analysis of the PCR reaction on a 1% agarose gel shows a concentration of 100ng/µl for the 1.36 kb PCR product, which can be used to transform *S. cerevisiae*.

Example 4.2: Transformation of *S. cerevisiae*

For the direct exchange of the ORF of AgRPS33B on plasmid pAG1245 in *S. cerevisiae* with the AgLEU2 marker via homologous recombination a cotransformation is carried out. As a recipient strain, YP98 with the phenotype a, ura3-52, lys2-801^{amber}, ade2-101^{ochre}, trp1-Δ1, leu2-Δ1 (Sikorski R.S. and Hieter P. (1989) Genetics 122: 19-27) is used. Transformation is performed according to Gietz et al. (1992) Nuc. Acid Res. 20 (6): 1425.

2µg plasmid DNA of pAG1245 and 2µg PCR product are cotransformed into strain YP98. Plasmid pAG1245 carries the CEN6/ARSH4 cassette and the URA3 gene providing replication and selection in strain YP98. Recombination between the 40 bp at the ends of the PCR product, which are homologous to parts of the pAG1245rp SRS, leads to excision of the AgRPS33B open reading frame and integration of the AgLEU2 marker gene. Transformants are double selected for URA⁺ and LEU⁺ on SD-minimal medium supplemented with lysine, adenine, tryptophan and lacking uracil and leucine (Sikorski R.S. and Hieter P. (1989) Genetics 122: 19-27). As a positive control, 2µg plasmid DNA of pRS415 and pRS416 (Sikorski R.S. and Hieter P. (1989) Genetics 122: 19-27) were cotransformed. Plasmid pRS416 carries the CEN6/ARSH4 cassette and the URA3 gene, and pRS415 carries the CEN6/ARSH4 cassette and the LEU2 gene for replication and selection. Transformants are also selected on SD-minimal medium supplemented with lysine, adenine, tryptophan and lacking uracil and leucine. As a negative control, 2µg PCR product are transformed to exclude the possibility of genomic integration of the AgLEU2 marker gene. Selection for the negative control is carried out on SD-minimal medium plates supplemented with lysine, adenine, tryptophan, uracil and lacking leucine. After 2-3 days of incubation, the first transformants appear, and after 5 days the transformation efficiency is calculated. The negative control, only transformed PCR product; has no transformants. The positive control, pRS415 and pRS416, has a transformation efficiency of 300 transformants/µg DNA. The cotransformation of pAG1245 and the PCR product shows a transformation efficiency of 10 transformants/µg DNA. For verification of the integration of the AgLEU2 marker gene into pAG1245, the new plasmid, which is named pAG1245-1, is isolated from the transformants and further investigated.

C.) Verification of the integration of the AgLEU2 marker into pAG1245

Genomic DNA from several independent *S. cerevisiae* transformants harboring the newly generated plasmid pAG1245 is isolated according to Philippsen P. et al., (1991) Methods in Enzymology 194: 169-182, Guide to Yeast Genetics and Molecular Biology, Academic Press.

The genomic DNA is transformed into the *E. coli* strain XL1-blue (Bullock W.O. et al., (1987) Bio Techniques 5 (4): 376-378) using the protocol described by Dower J.W., (1988) Nuc. Acids Res. 16: 6127-6145). Plasmid DNA of pAG1245-1 is isolated and integration of the AgLEU2 marker gene is verified via analytical PCR. A primer pair with one primer located in the multiple cloning site and one primer in the promoter region of AgRPS33B indicates excision of the ORF of AgRPS33B and integration of the AgLEU2 marker gene. For this purpose, two primers RP1 and RP2 are selected. RP1 (5'CAT GAT TAC GCC AAG CGC GC 3') is homologous to 20 nucleotides in the pBlISk+ multiple cloning site (Altling-Mess M. A. and Short J.M. (1989) Nuc. acids Res. 17(22): 9494) in pAG1245 adjacent to the Reverse Primer binding site. RP2 (5'CCA AGC ACA TTT CAC CTG CG 3') is homologous to 20 nucleotides to the pAG1245 SRS from 521-540. With this primer combination, the expected PCR product is 0.6kb for pAG1245 and 1.5kb for pAG1245-1. PCR reactions were performed using plasmid DNA from pAG1245 and from pAG1245-1, originated from two independent *S. cerevisiae* transformants, as templates. 100 ng template are added for a 50µl reaction volume supplemented with 0.2mM of dATP, dCTP, dGTP and dTTP. 5µl of 10*Thermo Pol Buffer (Biolabs). The concentrations of primer RP1 and primer RP2 in the reaction is 1µM. After the hot start, 1 µl enzyme mixture (Taq Polymerase (Pharmacia) and Vent Polymerase (Biolabs) 5:1) is added. PCR is executed under the following conditions: hot start 2 min at 94 °C, 30 cycles of 30 sec at 94°C, 30 sec at 55°C and 2 min at 72°C and finally 4 min at 72°C.

Analysis of the PCR reaction on a 1% agarose gel shows a band at 0.6 kb for pAG1245 and a band at 1.5 kb for pAG1245-1. This result demonstrates the right integration of the AgLEU2 marker gene in pAG1245.

Example 5: Isolation of new fungal DNA elements based on synteny of linked sequence pairs

With the initial bi-terminal SRS's of the DNA insert of plasmid PAG1489 (PAG1489RP and PAG1489UP), synteny

is discovered to the centromeric region of *S. cerevisiae* CEN2. This synteny reveals homology to the yeast genes YBL003c and YBR001c. The complete double stranded insert sequence shows synteny to the yeast genes YBL003c (97% identity), YBL002w (94% identity), YBL001c (69% identity), and YBR001c (73% identity) as determined by BLAST searches to the Yeast Genome Database (Altschul, Stephen F., Gish, Warren, Miller, Webb, Myers, Eugene W., and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-410). In yeast, the centromere of chromosome II is placed between YBL001 c and YBR001c. Homologous sequences to the yeast centromere II are found in the *A. gossypii*. DNA sequence of PAG1489 between positions 2900 to 3200. This homology comprises the essential Centromere DNA Elements CDEI, CDEII, and CDEIII. Making use of the synteny of RP and UP sequences of a single pAG-plasmid to a reference genome, the detection of potential antifungal drug targets can be inferred in the same way as the centromere on PAG1489. In addition, using *Ashbya gossypii* as a reference genome, potential antifungal drug targets of other pathogenic fungi can be isolated.

Sequence of pAG1489 insert DNA :

GATCGTAACATTGCCCAATAGCTTGTTTAGCTCGTCATCGTTTCTGATGGCTAGCTGTAGATGTCTT
 GGGATGATTCTGGTCTTCTTGTGTCTCTGGCGGCGTTACCGGCCAACTCTAGGATTTTCGGCGGCCA
 AGTATTCTAGCACAGCGGTTAGGTACACAGGCGCGCCCGACCCGATTCTCTGTGCGTAGTTGCCCTT
 TCTGAGCAATCTGTGGACTCTACCGACAGGGAAAGTCAAACCGGCCTTAGCCGATCTCGACTGCGAA
 GCCTTGGCGGCAGAACCAGCTTTACCTCCTTTACCAGACATTATTTGTGTTGTGTGTGTGTGTGTGT
 GTTTAGTGTGAACTGCGTGTGCTATGAGAAAACACTACGCTGAAACTGCTAAATAATCCAGACAGGT
 CCCCCACCGCAAAGGATCCACGCTATACTTCTCTCTACATATTTATACTTGTCTTTTGCCTTCTA

ATCCTCGATCGTACGCGTCTGACGCTTCAACAGACGCTTCACCTAGACGCTCGACCTGTGCGGCCTG
GTTTTTTCGCATGACATGTCCGTGCTGGTTTTTTCGCGCTGAAAAGGAAAGCGCGTGGCTCCCAGCA
5 CCAGAGCCGTACTAGCTCTTTCGCGTGCTGTCCTATGTGCACGCGAAATTTTCATACTGTAGAGTGT
GCCATCAGCTTCACAGAGTACAAACGGTAGGCGAGTGGATACGCGTCTTGTAGCCGGACGTGAATGG
CAGAACTTTTTTGGCAGTCGCGTAATCTTAGATTGAAAGTATTTAAGTGGAACGTATAAAACAAAAGT
TCGGGCTGAAGAGGACCTCTTTTGGCGSTCTGCTACTTCCCAGTTATCTGTTGGATACTAAGCATAT
10 CGAACTCTAATTGCAATTCTAAAGATGGCACCAAAGGCTGAGAAGAAACCTGCTTCCAAGGCCCCAG
CGGCAAAGAAGACCACTGCTTCTACCGACGCTTCTAAGAAGCGGACGAAGACTAGAAAGGAGACCTA
CTCCTCTTACATTTACAAGGTTCTTAAGCAGACTCACCCAGATACTGGTATCTCGCAGAAGTCTATG
TCCATTTTGAAGTCGTTTGTGAACGATATCTTTGAGAGAATCGCGTCTGAGGCATCCAAGCTTGCGG
15 CCTACAACAAGAAGTCTACGATCTCTGCTAGAGAAATCCAGACTGCTGTCAGATTGATCTTGCCCCG
TGAGCTAGCCAAGCACGCCGTGCTGAGGGTACCAGAGCTGTTACCAAGTACTCGTCTTCTACCCAA
GCCTGAATGGAACCTCATTCTTAGAATGAAAGAACTTCCTTCAAGAAGGTTCTCGTCAGCTAGTGCTT
20 GTGGGACCCGCCCTCTTATTCAGAGCAGCTGCGGCAGAGCGGTATGTGGTACGTTCCGTTTCATCAT
TTTGTATTATTAGTACATGTAGAAATAGGGTTTTCTGGTTTCATAATTCCGGTATAAATTCCAACGTA
ATGTATATTAGATAAGTTTTAACTAGTAATCGGAGAGCTTCTTTTCAACCACGTCTACCTTGCTT
GCGCAGTCTGCTGTTTGTCTGTTCTAGTTCGAGCCTCATTTCGGTGTGGATTCTAACGTATCCCAA
25 TTCGTGGCTGTATTTCGTGCAACTGGCCGATGAGGCTCATGACCTCGTCCCAAGGGCCCTCAATCGTC
GTTCCAAAGCTGTGCATAGTGCTTTTCAAGTGACTCTCCCTAATTGTTTTCTCAATCTTGGTGACAT
AGTCTGAGACACTTGGTGAGCTAGTACCTAGCTATGATTCAAAGTTTAGTATATTGTTTTATATAT
GCAGCTGGAGATGTGAACATACCGGCACCATGCAAATGTCCACTAATGTGTGCAGCTTCGACATTTT
30 GATTTCTACCTTCAGAGTATTGGAATATGTTCTTGATGTAACGTCTACTAATTTTCTGGTTTATAT
CGCTGATCTTAAGGGAGATAATTTGTTTACCCATCACACAGAAGTTTTAAGTACAAAACCTTGTCCTC
CAGATATAGCAAGTCATCAATTCAGGTATAATTTGGTGTGCATGCTAATTTGAAGGGCTGTTATATAG
35 TTGAAGTTGTTCTTTTGGCATTGAGCCAAATTTGGATTCTATTTCAGTAGTATTGAACATCAAGTCTC
CAAAGCTGAAGTCTGAAGCAAAACATCTCAATAGCTATAGAACTCTAGCAAACAACAGACCAGAGCT
TATATCATGACACATTATAAGCTCAGCTATTACTCTGAGTGATAGAGTGACCTCAATTAGTTGGTT
CATTTTATATATAAAAAATATAAACTATAGCTATTTCAAATGACTACTAATAATACGAGAGAAGAA
40 AACAAATTAAACACGATGGTCTACAGATAGCTTGAAAGAGACACTAAGAGAAATTTCAAGGAAACAGT
TCAGAAAATAGCCATTCAGCTCTACAGCTCTCTTTATTATCAAGAGTACAGTTTCTTTTCACTAATAT
CGCTTAATTAATTATATTTCTTGCCATTAAATGCGACGGTGACGGGATAACAATTTTGGCAATTCT
TCATATTTTGATTTAAAAAACAATTTACCAGAATTAGACGAAATAGTCGCTTACTACAAACAG
45 GTTCAGCCACTGGATAAATCTCATAGTTTAAAATATTGAGTTACAGAAATTGGCTTACAGAAAGCAC
TAGCGATTAGGCCATTTGCCATTGATTTAAACATGAACCTAACGAACCTCCATGAATTACAATAACCA
CAAATTTAACCGGACAATTAATTTTATGTAGCAGGCTCTGCCATGGGAATAGCTTTACGTGAACAGG
50 ATATTTAACGTATATCCTTGTTATGATAAAGACTTTGATAGGTGCTTATACTTGCAAGTTCATATTT
TACAGTTAAATATCTAAATTTAATATATTACGCAGTTCACGCAATGTAGCACGTGACATAAATATGA
AATTTACTATGTGCTTGCTTTATTTAAATAAGTTTATAAAGTTAGTAAAAATATCAGAGTATATAT
ATTTAATTAAATAATATCCTAAAATATACTAATAACAATTTATCAATTAAGCTTTATACACTTTATAA
55 ATAGTTATAATTATAGATGTGTATACGATTTCCGAAACATAAAAATATTTCACTGCTTTTCGTGAAAA

ATAATTTTTTTATTATAAAACAATCCCTAATATAGTATTACCTCCAATTATGAGTCTATCGTAATAT
 ATGAAGTACTACCAAATTTACCACTGATTTTTCAAAAAAAAAACACCATTTTTCAAAAATATTTTA
 5 TTAAGTGAATTTTTTATAATTAATTTTTTATATCTATATAGAATATCTATTATACGCAAGAAAAAC
 CAAAAGTACCCTATAAGTAGGTACCGCTTGTCACATTATAATAAAAAAGTGAAGTACTCATCAA
 TACTTTTTATTTAGGATACCTGCAGTCTAATATCCCTTCACGTAAGTTACTTAGTGCACAATATTCAC
 10 AGTGAGTTAGTAACCCGGTTCAGATCAAGGCATACCGAGCTTCTCTTCTGGCTTCATATGCTTAAA
 GAAATATCAGGGACGGTGCAGTTAGCTAAAGCTCTCTTAGCATAAGTATTCATAAATTTCAAACCT
 AAGATATAACTGGAATTGACCCAGCCAAATCCCTTCAGTAGCAACACCTTTAAAGTCTGCACCTTGGT
 TACCATATTCGGCATCAACTCTATGAGGATCTGTGCCTCTGGTAACGTCGTATTTCTCTACTACGAT
 15 ACCATTGTAGTCGACAAATGCCCTGGTCATTAAAAATAACCACCTATAGGCCAACCTTCTTGCAACT
 CCTGTAAATCCGTAATTATCTAACCCTGTCAGCAAGCATTTGATGAGGGGCCCAACCATAAGGGT
 AATCCCATTTGCCCTGCTTGGTCTATTCAATTGTTATCTCACCCGAGACTCCTCAGTACAGGCAACCAG
 GCCTCCTAGCATTTCAAGCCTTGGCAATGCCCTTCTCGACCATAGCGTTGGCTTGTTCTCTGGGTTGCC
 20 AAGCCTGCCCACATGGCCCAAAATGTTGTTGCAGAATCGTAAGATGTTCTCTTTCCAATATGGACAT
 TGTAGTCATAGAAAAAGCCTGTTTCTCGTCCCACAAATATTTTCGTGATTCTTTTGCTTACGAATGTC
 TGCAAGTGCCTCCCAATGAGAAGAAGTGGTGGTTTCACCAGCATAATCAGTAATACTATCATCGAAG
 25 TACTTGGAACACATATGCAATATCTTTTCGTACTTGTATAGTAACGAATTCAAATCAATCGTCG
 CTAAGTAAGCACAGACGTTCTCTAGACGGTAAGAGGTGTCATGTCCACTCTCACGTACAGCACGATC
 ATGCAAAAAGAACTCATCTAGTTCGGGCTCGTGTAATTCGCCGGCATCGTACATGCACCTGAACTCC
 GGAATCGTTACATTGTGCTTTTCCGCAAAATTTCCGGCAAAATGCGTCAAAGTGGTCAGGCTCGGTTT
 30 CTGGTGGGAAACCGATACCATCTGGATGATAACATGAAAGACCCGTGGTTTTGTCTGACCGCGGTTT
 TGCCATCCATACACTCTTGATTTCTTAATGGCTGCGATGAATGCTCTTTTCAAGAAATCCACAGCG
 GTAGGATTTTGGTCAACACCGAACTTTTTCAAGACCTTCAAAGCCATGTCGGTTAGGAACGGGGTT
 GTGACCGACAGAGGTAGTAGCTCCTATTGGCGTTCAATATTTTACCGTAATGCTCTATCTCAAAGAT
 35 GAAATGCTCAACCATCCACGTGCTATGTCCACTTTGTTACAGTCTAGAAGACCCAAAGCCATTAGG
 TATGAGTCCCAGCCGTAAAGTTCATTAAAAACGACCGCCCGGAACAACGTAGGGAAAACCAACCAATG
 TACTCTACCGGTAATTGGGTCCCTGTGACTCTCCATCGCCAAAGCAAGCAACCCCGGGCTTTTCGTT
 40 CAATGATTGCACGTGCTCCGGCGTGATC

Example 6: Identification of antifungal drug targets represented in the attached *Ashbya gossypii* database

A.) Principle of gene disruption using Short Flanking Homology (SFH)-PCR mediated transformation of *Ashbya gossypii*

Gene disruptions in the *Ashbya* genome represented by sequences provided in the Sequence Listing are performed using a new PCR-based *Ashbya* gene targeting procedure. Gene targeting in *Ashbya* relies on homologous recombination in this fungus (Steiner et. al., 1995). It has been found that short (approximately 45 bp) target sequence homologies added by PCR to both ends of a selectable marker (e.g. GEN3) are sufficient to mediate sequence-specific gene targeting in *Ashbya*. The PCR fragment for gene targeting thus carries terminal Short Flanking Homology regions encompassing the selectable marker module. These PCR fragments are transfected into *A. gossypii* (e.g. by electroporation) and transformants are selected for G418 resistance. Verification of correct gene targeting is achieved by PCR-testing the presence of the new junctions between target DNA and integrated marker using verification primer pairs G1-G2 and G3-G4 as described by Wach et al. (1997) P. Yeast 13: 1065-1075. Also, verification of the gene targeting can be performed by DNA-hybridization experiments. The verification primers (G2: 5' GTTTAGTCTGAC-CATCTCATCTG 3' and G3: 5' TCGCAGACCGATACCAGGATC 3') are derived from the open reading frame of the selectable marker gene GEN3. G1 and G4 primer sequences are derived from the single read sequence and correspond to regions upstream and downstream, respectively, of the homology regions used for PCR-based targeting. Using this

PCR-based targeting approach, sequences can be manipulated that are approximately 150 nt in length, a criterium matched by all single read sequences of the attached *Ashbya* database. This is of major advantage considering classical methods of gene disruption that are laborious and require cloning steps to incorporate a selectable marker within rather large flanks of surrounding target sequence homology.

After clonal purification (spore isolation) it is determined whether deletion/insertion at the targeted locus results in any phenotypic alterations (e.g. decrease or loss of viability) identifying a potential target for antifungal drugs.

B.) Protocol for Short Flanking Homology (SFH)-PCR mediated transformation of *Ashbya gossypii*

1.) Selection of S1 and S2 primers is done in order to link app. 45 nt specific of the target locus sequence to 20 nt homologous to pGEN3 in order to allow amplification of the selection marker *GEN3*. The standard sequence on the 5' side of *GEN3* corresponds to 5' GCTAGGGATAACAGGGTAAT 3', which includes the recognition site of the rare cutting endonuclease I-SCE1 to the PCR fragment. This restriction site is not found in the nuclear genome of *A. gossypii* and can be used to physically map the position of the *A. gossypii* insert DNA to a chromosomal location. The sequence on the 3' side of *GEN3* corresponds to 5' AGGCATGCAAGCTTAGATCT 3'. Put together, the S1 and S2 primers comprise a total of app 65 nt. Selection of verification primers G1 and G4 which are neither part nor overlap with S1 and S2 primer sequences is dependent on the target locus sequence.

2.) Generation of SFH-PCR fragment is achieved by using the S1 and S2 primers to amplify *GEN3* to an amount of approximately 10mg from linearized pGEN3 cleaved by the restriction endonucleases *EcoRI* and *BamHI* (Biolabs). To increase the fidelity of the PCR-product a mixture of Taq DNA Polymerase (Pharmacia) and Vent DNA Polymerase (Biolabs) is used in a ratio of 10: 1-2 units.

Standard PCR conditions are:

Step 1: Initial denaturation	at 96°C for 2min.
Step2: Denaturation	at 96°C for 30s.
Step3: Primer annealing	at 50°C for 30s.
Step4: Elongation period	at 72°C for 2.5min.

Steps 2-4 are repeated for 25-35 times.

Step5: Terminal elongation period:	at 72°C for 5min.
Step6: Storage at 4°C (optional).	

3.) Transfection of the SFH-PCR product into *A. gossypii* is done by electroporation (Steiner et al., 1995 with modifications):

- 1.) Inoculate 100-200ml YPD or AFM (YPD: 2% casein peptone, 2% glucose, 1% yeast extract; AFM: 1% casein peptone, 2% glucose, 1% yeast extract, 0.1% myo-inositol) with a spore suspension of app. 10^7 spores.
- 2.) Incubate at 30°C for a max. of 18h under rotation of 200rpm.
- 3.) Collect the mycelium by filtration and wash once with sterile H₂O.
- 4.) Resuspend 1g of wet weight mycelium in 40ml of 50mM potassium phosphate buffer, pH 7.5 containing 25mM DTT and incubate at 30°C for 30min with gentle shaking.
- 5.) Collect the mycelium by filtration and wash once with 50ml cold STM buffer (STM: 275mM sucrose, 10 mM Tris-HCl, pH 7.5, 2mM MgCl₂.)
- 6.) Resuspend to a densely packed mixture of mycelium in STM buffer.
- 7.) Mix app. 150ml of mycelium with max. 50 ml of SFH-PCR product in an Eppendorf tube and transfer the mixture into an electroporation cuvette (BioRad 4mm).
- 8.) Apply an electric field pulse of 1.5kV, 100%, 25 mF which will result in a pulse length of app 2.3ms. Add 1 ml of YPD or AFM and spread equal amounts onto 3 pre-dried AFM plates.
- 9.) Incubate at 30°C for a min. of 4h.
- 10.) Overlay with 8ml 0.5% agarose top layer containing Geneticin/G418 at a final concentration of 200 mg/ml.
- 11.) Incubate at 30°C for a max. of 4 days.

C.) Examples of gene disruptions revealing potential antifungal drug targets using Short Flanking Homology (SFH)-PCR.

1.) Disruption of PAG1025RP

The amino-terminal part of the *RHO 3* gene is located on PAG1025RP. The location of the homology region to the target locus of the four primers (S1, S2, G1, and G4) necessary to construct and verify the SFH-PCR transformants are indicated in section E.) below. Using the S1 and S2 primers (including the 20 nt homologous to pGEN3 at the 3' end of the homology region to the target locus as indicated in A) together with pGEN3, the plasmid carrying the selectable marker gene *GEN3*, (linearized by cutting with *EcoRI* and *BamHI* restriction nucleases [Biolabs]), a PCR fragment is generated that carries terminal Short Flanking Homology regions encompassing the selectable marker module. Primary transformants, which are heterokaryotic with respect to transformed and untransformed nuclei, are clonally purified by spore isolation using a micromanipulator. Germination of spores deleted for *RHO 3* on selective medium is only obtained by adding osmotic stabilizers such as 1 M sorbitol. Verification of the set deletion is performed by PCR using the verification primers G1 and G4 that are unique to the target locus and are not used in the initial transformation event, as well as the primers G2 and G3 that are specific to the selectable marker. PCR products indicative of a homologous gene targeting event can be obtained by using the verification primers in the combination G1-G4 (which amplifies the entire locus in which integration of *GEN3* is targeted), G1-G2 (which amplifies the 5' novel joint that is created by insertion of *GEN3*) and G3-G4 (which amplifies the 3' novel joint that is created by insertion of *GEN3*).

2.) Disruption of PAG1634RP

The amino-terminal part of the *BAL 1* gene is located on PAG1634RP. The location of the homology region to the target locus of the four primers (S1, S2, G1, and G4) necessary to construct and verify the SFH-PCR transformants are indicated in section E.) below. Using the S1 and S2 primers (including the 20 nt homologous to pGEN3 at the 3' end of the homology region to the target locus as indicated in A) together with pGEN3, the plasmid carrying the selectable marker gene *GEN3*, (linearized by cutting with *EcoRI* and *BamHI* restriction nucleases [Biolabs]), a PCR fragment is generated that carries terminal Short Flanking Homology regions encompassing the selectable marker module. Primary transformants, which are heterokaryotic with respect to transformed and untransformed nuclei, are clonally purified by spore isolation using a micromanipulator. Germination of spores deleted for *BAL1* on selective medium is only obtained by adding osmotic stabilizers such as 1 M sorbitol. Verification of the gene targeting event is done as described in C.1)

3.) Disruption of PAG1486RP

The aminoterminal part of the *BUB1* open reading frame is located on PAG1486RP. The location of the homology region to the target locus of the four primers (S1, S2, G1, and G4) necessary to construct and verify the SFH-PCR transformants are indicated in section E.) below. Using the S1 and S2 primers (including the 20 nt homologous to pGEN3 at the 3' end of the homology region to the target locus as indicated in A) together with pGEN3, the plasmid carrying the selectable marker gene *GEN3*, (linearized by cutting with *EcoRI* and *BamHI* restriction nucleases [Biolabs]), a PCR fragment is generated that carries terminal Short Flanking Homology regions encompassing the selectable marker module. Primary transformants, which are heterokaryotic with respect to transformed and untransformed nuclei, are clonally purified by spore isolation using a micromanipulator. Germination of spores, deleted for *BUB 1* cannot be obtained indicating that this gene is essential in *A. gossypii*. Verification of the gene targeting event is done as described in C.1)

SFH-PCR mediated marker integration into the *A. gossypii* DNA can be applied to all RP and/or UP sequences of the attached data base. Further applications of SFH-PCR mediated gene targeting in *A. gossypii* are:

- 1.) Generation of antisense transcripts.
- 2.) Overproduction of mRNA and presumably overexpression of a protein.
- 3.) Addition of reporter genes to a target sequence (e.g. GFP, lacZ).
- 4.) Introduction of longer deletions using RP and UP sequences.

D.) Examples of gene disruptions revealing potential antifungal drug targets by classical procedures

1.) Construction of disruption cassettes

As a selectable marker, kanMX0 is used. This is a transformation selection module expressing G418 resistance in yeast and filamentous fungi and kanamycin resistance in *E. coli* (International Patent Application No PCT/EP 91/01116). This module is inserted into *Ashbya* sequences of genomic pAG clones. The module is a chimeric kanamycin gene plus adjacent multiple cloning regions from the cloning vector pAG-231 (Steiner, Wendland, Wright, and Philippsen, Genetics 1995: 140, 973-987). To this purpose the selectable marker is released from the cloning vector pAG-231 (by cleavage with either BamHI, Sall or XhoI. It is ligated into cloned *Ashbya* DNA cleaved with either BglII, XhoI (partial) or Sall (partial), respectively. Clones carrying *Ashbya* sequences disrupted by kanMX0 are selected in *E. coli* by kanamycin resistance. DNA sequence analysis around the site of integration of the kanMX0 module (i1 and i2 sequences in the attached *Ashbya* data base) reveal the disrupted open reading frame and determine the orientation of the kanMX0 module.

2.) Disruption of PAG1010i1/i2, PAG1017i1/i2, PAG1021i1/i2, and PAG1044i1/i2

Disruption cassettes are released from the plasmids leaving several hundred base pairs of *Ashbya* DNA flanking kanMX0 (e.g. by cleavage with NotI and KpnI in the multicloning region). Transformation of *Ashbya* with the disruption cassettes induces homologous recombination into the target locus (Steiner et al., 1995). Primary transformants are selected on G418 containing plates and analyzed by DNA hybridization experiments or by PCR, followed by clonal purification (spore isolation). Chromosomal mapping of the target loci is achieved by I-SceI endonuclease mapping of chromosomal DNA separated by pulsed-field gel electrophoresis.

Primary transformants are heterokaryotic, carrying nuclei with a wild type allele and nuclei with a disrupted allele. Spores with single haploid nuclei develop in the older mycelium and allow clonal purification of transformants (e.g. by single spore isolation with a micromanipulator, Steiner et al., 1995). Spore isolation is followed by a growth assay. The disruption of *Ashbya* ORF's identified for example in sequences PAG1010i1/i2, PAG1017i1/i2, PAG1021i1/i2, and PAG1044i1/i2 do not grow on reveals no growth of spores on G418 medium thereby classifying the products of these ORF's as essential for growth (novel antifungal targets).

One advantage of using *Ashbya*, a fungus with a small genome and apparently very few gene duplications, for novel drug target identification is demonstrated by the fact that the ORF represented by PAG1017i1/i2 is essential in *Ashbya* but the highly homologous ORF Yer082c of *S. cerevisiae* is not (Smith, Chou, Lashkari, Botstein, and Brown Science 1996: 274, 2069-2074).

Clonally purified disruptions of several other ORF's do grow on G418 medium, sometimes identifying mutants that display slow growth phenotypes (e.g. disruption of AgDHC1).

E.) Construction of pGEN3

The GEN3 selection module is designed specifically to allow homologous recombination in *Ashbya gossypii* using short flanks of DNA sequence homology to the desired target locus. GEN3 consists of the open reading frame of the kan^R-gene which is under the transcriptional control of the *S. cerevisiae* TEF2 promoter and terminator. GEN3, which confers resistance to the antibiotic drug geneticin, bears no sequence homology to the *A. gossypii* genome.

To construct pGEN3, the ORF of the kan-gene is amplified from pFA-kanMX4 (Wach, A., Brachat, A., Poehlmann, R., and Philippsen, P. (1994). New heterologous modules for classical or PCR-based gene disruptions in *Saccharomyces cerevisiae*. Yeast 10:1793-1808) using primers PTEF2-kan and TTEF2-kan (table 1) that contain an additional 40 bp of short flanks of homology to the *S. cerevisiae* TEF2 gene. The diploid yeast strain FY1679 is transformed with this SFH-PCR product (Wach et al., 1994). Genomic DNA of transformants resistant to G418 is checked for integration of the PCR product at the TEF2 locus by analytical PCR using primers TEF2-150RPG and TEF2-BglII. Because of the diploid background a wild-type band 2.26 kb and a replacement band of 1.7 kb is generated. This 1.7 kb fragment contains the kan-ORF flanked by 609 bp of the TEF2-promoter region and 274 bp including the TEF2-terminator. This gene is termed GEN3. The fragment is extracted out of an agarose gel and ligated as an BglII-fragment into the BglII site of pAF100 (Thierry A., Fairhead, C., and Dujon, B. (1990). The complete sequence of the 8.2 kb segment left of MAT on chromosome III reveals five ORF's, including a gene for a yeast ribokinase. Yeast 6:521-534) yielding pGEN3. The usefulness of GEN3 as a marker gene in *A. gossypii* is corroborated by recloning of the gene in an ARS containing vector (Sikorski, R.S. and Hieter, P. (1989). A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in *Saccharomyces cerevisiae*. Genetics 122:19-27.) that allows free replication upon transformation in *A. gossypii*.

Oligonucleotide primers ¹⁾

PTEF2-kan GTTTTTAGAAATATACGGTCAACGAACTATAATTAACATAACatccgctaagcaaaaagacica
 TTEF2-kan GGTATATAAAAATATTATATGGAAGCAATAATTATTACTCttagaaaaaactcatcaaca
 TEF2-150RPG gcgagatctGGTGTATTACCAATAAT
 TEF2-BglII gcgagatctGATGAGGCCGTCTTTTGTG

¹⁾ Upper case letters correspond to *S. cerevisiae* DNA used as homology regions. Lower case letters correspond to homologies to pGEN3, pFA-kanMX4 (double underlined), or represent additional nucleotides containing the restriction site BglII (bold) used in the cloning of pGEN3.

Example 7: Forensic identification using PCR-based diagnostic techniques

The DNA sequences of the present invention are also useful for distinguishing among different species of plant pathogenic fungi and for distinguishing fungal pathogens from other pathogens such as bacteria. Particularly, the DNA sequences of the invention can be used as primers in PCR-based analysis for fungal identification, as well as primers derived from these DNA sequences. DNA sequences that vary among different pathogens can be used to identify and distinguish among those specific specific pathogens. For example, the presence of *Gaumannomyces graminis* in infected wheat has been detected using PCR of sequences specific to the pathogen mitochondrial genome (Schlesser *et al.*, 1991; *Applied and Environ. Microbiol.* 57: 553-556), and random amplified polymorphic DNA (*i.e.* RAPD) markers have been able to distinguish numerous races of *Gremmeniella abietina*, the causal agent of scleroderris canker in conifers. U.S. Patent No. 5,585,238 describes primers derived from the ITS sequences of the ribosomal RNA gene region of strains of *Septoria*, *Pseudocercospora*, and *Mycosphaerella* and their use in the identification of these fungal isolates using PCR-based techniques.

Methods for the use of DNA sequences in PCR analysis are well known in the art. See, for example, see U.S. Patent Nos. 4,683,195 and 4,683,202, as well as Schlesser *et al.* (1991) *Applied and Environ. Microbiol.* 57:553-556. See also, Nazar *et al.* (1991; *Physiol. and Molec. Plant Pathol.* 39: 1-11), which used PCR amplification to exploit differences in the ITS regions of *Verticillium albo-atrum* and *Verticillium dahliae* and therefore distinguish between the two species; and Johanson and Jeger (1993; *Mycol. Res.* 97: 670-674), who used similar techniques to distinguish the banana pathogens *Mycosphaerella fijiensis* and *Mycosphaerella musicola*. Similarly, the sequences of the present invention set forth in the Sequence Listing can be adapted for use in such PCR analysis.

Table 1: Description of *Ashbya gossypii* genomic fragments in the Sequence Listing

<u>pAG name</u>	<u>Yeast Name</u>	<u>Gene Name</u>	<u>Brief Description</u>	<u>HC</u>	<u>Additional Comments</u>
PAG1001RP	YNR030w		weak similarity to SMP3 protein	1	
PAG1001UP	YCR069w	SCC3	peptidyl-prolyl cis-trans isomerase precursor	1	
PAG100211	YIL014w		similarity to Mnn1p (alpha-1,3-mannosyltransferase)	2	homology due to PAG100212-hit
PAG100212	YIL014w		similarity to Mnn1p (alpha-1,3-mannosyltransferase)	2	
PAG1002RP	YIL105c		similarity to hypothetical protein YNL047c	3	open frame > 450 nt in -2
PAG1002UP	YBL009w		homology to DNA damage responsive ALK1 protein	4	
PAG1003RP	YCR053w	THR4	threonine synthase (o-p-homoserine p-lyase)	1	Terminator, Syntenie, see PAG1003UP
PAG1003UP	YCR057c	PWP2	periodic tryptophan protein	1	Syntenie, see PAG1003RP
PAG1004RP	YLR102c		hypothetical protein	2	Syntenie, see PAG1004UP
PAG1004UP	YLR100w		hypothetical protein	1	Syntenie, see PAG1004RP
PAG1005RP	YBR216c		homology to hypothetical protein (chromosome VII)	3	open frame > 350 nt in -1
PAG1005UP	YNL068c	FKH2	homolog of <i>Drosophila</i> forkhead protein	3	open frame 300 nt in -3
PAG1006RP	YDR432w	NPL3	nucleolar protein	3	open frame > 450 nt in -3
PAG1006UP	YOR290c	SNF2	component of SWI/SNF global transcription activator complex	3	open frame > 350 nt in -1
PAG1007RP	YER091c	MET6	5-methyltetrahydropteroyl triglutamate-homocysteine methytransferase	1	Syntenie, see PAG1007UP

PAG1007UP	YER093c		1	weak similarity to <i>Staphylococcus epidermidis</i> PepB protein	Syntenie, see PAG1007RP
PAG1008I1	YHR196w		1	hypothetical protein	does not fit in Syntenie of PAG1008RP, UP and I2
PAG1008I2	YJR133w		1	similarity to hypothetical D9509.18p	Promotor + Terminator (the latter according to PAG1008I1), 279 nt.Syntenie, see PAG1008RP and UP
PAG1008RP	YJR132w	NMD5	2	putative Upt1p-interacting protein	Terminator, Syntenie, see PAG1008I2 and UP
PAG1008UP	YJR134c		1	unclear similarity to paramyosin, myosin	Terminator, Syntenie, see PAG1008I2 and RP
PAG1009RP	YNL218w		1	homology to <i>C.burnetii</i> trxB, spolIIE and serS genes	Syntenie, see PAG1109UP
PAG1009UP	YNL219c		2	probably membrane protein	Syntenie, see PAG1109RP
PAG1010I1	YLR337w	VRP1	3	proline-rich protein verprolin	open frame 350 nt in +3 and -2
PAG1010I2	YLR332w	MID2		serine-rich protein, multicopy suppressor of temperature sensitivity of <i>hir1</i> null mutant. Open frame whole length in +3 and -3	
PAG1010RP	YOR240w		1	weak similarity to unknown <i>S.pombe</i> protein	
PAG1010UP	YGR115c		1	questionable ORF	
PAG1011I1	YLR374c		4	questionable ORF	

PAG1011I2	YKR054c	DYN1	dynein heavy chain, cytosolic	1	additional Hit see PAG1011RP and PAG1219RP
PAG1011RP	YKR054c	DYN1	dynein heavy chain, cytosolic	1	additional Hit see PAG1011I2 an PAG1219RP
PAG1011UP	YJL133w	MRS3	splicing protein and member of the mitochondrial carrier family	1	Terminator
PAG1012RP	YER074w	RP50A	ribosomal protein S24.e	1	Terminator, cannot be checked for Intron, not on sequence of PAG1012RP
PAG1012UP	YIL068c	SEC6	component of a multiprotein complex involved in fusion of post-golgi vesicles to plasma membrane	1	
PAG1013I1	YLR344w	RPL33	ribosomal protein	1	Promotor, Syntenie, see PAG1013UP, RP and I2 2nd Hit, Intron in A.g. at the same position like in S.c. (CAI S.c. 0.63)
PAG1013I2	YLR344w	RPL33	ribosomal protein	1	Terminator, Syntenie, PAG1013UP, RP and I1
PAG1013RP	YLR345w		similarity to 6-phosphofructo-2-kinase (EC 2.7.1.105)	1	Syntenie, see PAG1013UP, I1 and I2 2nd Hit
PAG1013UP	YLR343w		homology to Candida albicans pH responsive	1	Syntenie, see PAG1013RP,

	PAG1014RP	YDR376w	ARH1	protein similarity to human adrenodoxin reductase	1	I1 and I2 2nd Hit
	PAG1014UP	YDR375c	BCS1	MT protein of the CDC48/PAS1/SEC18 (AAA) family of ATPases	1	Syntenie, see PAG1014UP Terminator, Syntenie, see PAG1014RP
	PAG1016RP	YIR002c		similarity to ATP-dependent RNA helicases	1	
	PAG1016UP	YJR078w		indoleamine 2,3-dioxygenase homolog	1	
	PAG1017I1	YER082c		hypothetical protein	1	
	PAG1017I2	YER082c		hypothetical protein	1	
	PAG1017RP	YIL075c	SEN3	tRNA processing	1	
	PAG1017UP	YKL216w	URA1	dihydroorotate dehydrogenase (EC 1.3.99.11)	2	
	PAG1018RP	YKL018w		hypothetical protein	1	
	PAG1018UP	YIR019c	STA1	extracellular glucoamylase	3	open frame whole length in +1 and -3
	PAG1019RP	YKR084c	HBS1	elongation factor 1 alpha-like protein	2	
	PAG1019UP	YKR092c	SRP40	weak suppressor of a mutant of the subunit AC40 of DNA dependent RNA POL I and III	3	open frame whole length in +1
	PAG1020RP	YOL130w		strong homology to YFL050c (ALR2,aluminium resistance protein)	1	
	PAG1020UP	YNL310c		hypothetical protein	1	
	PAG1021I1	YIL019w		hypothetical protein	1	Terminator, Syntenie
	PAG1021I2	YIL019w		hypothetical protein	1	syntenie
	PAG1021RP	YIL022w	TIM44	MT inner membrane protein required in transport across the inner membrane	1	syntenie
	PAG1021UP	YIL019w		hypothetical protein	1	syntenie

PAG1022RP			3	open frame whole length in -1
PAG1022UP	YDR331w	weak similarity to S.japonicum hemoglobinase	3	open frame > 350 in +1
PAG1023I1	YCR092c	DNA-repair protein	2	
PAG1023I2	YCR092c	DNA-repair protein	1	
PAG1023RP	YCR092c	DNA-repair protein	1	
PAG1023UP	YNR047w	similarity to microtubule-associated serine/threonine protein kinases	1	
PAG1024RP	YBR119w	U1 snRNP-specific A protein (snRNA- associated protein)	2	most likely intron, no ATG in correct frame found slightly different position compared to S.c. open frame whole length in +3 and -2
PAG1024UP	YER105c	nuclear pore protein (nucleoporin)	3	
PAG1025RP	YIL118w	similarity to RAS proteins; belongs to RHO sub- family	1	
PAG1025UP	YNL061w	homolog to human proliferation-associated nuclear antigen, p120	1	
PAG1026RP	YIL096c	hypothetical protein	1	Terminator
PAG1026UP	YNL039w	transcription factor TFIIB, B" component of RNA polymerase III	2	
PAG1027RP	YOL122c	suppressor of mitochondrial matrix protease (MAS1) mutant	1	
PAG1027UP	YOR359w	hypothetical protein	4	

PAG1028RP	YNL308c	similarity to unknown protein on S.pombe CHR I cosmid c22G7	1	Syntenie, see PAG1028UP
PAG1028UP	YNL309w	Sin3p-binding protein (transcription regulatory protein)	2	Syntenie, see PAG1028RP, (classification in Hom_Class 2 according to Syntenie)
PAG1029RP	YOR205c	hypothetical protein	2	
PAG1029UP	YGL141w	similarity with hypothetical protein 1 - human (A38919)	2	
PAG1030RP	YHR205w	cAMP-dependent protein kinase homolog	1	Syntenie, see PAG1030UP
PAG1030UP	YHR204w	similarity to alpha-mannosidases	1	Syntenie, see PAG1030RP
PAG1031RP	YKL012w	similarity to C.elegans hypothetical protein ZK1098.1 and to Myo2p	1	Promotor, Syntenie, see PAG1031UP
PAG1031UP	YKL011c	cruciform-cutting endonuclease 1	2	Syntenie, see PAG1031RP, (classification in Hom_Class 2 according to Syntenie)
PAG1032RP	YKL209c	ABC transporter responsible for export of A factor mating pheromone	4	
PAG1032UP	YDL133w	putative membrane protein	1	Terminator
PAG1033RP	YBR274w	probable serine/threonine-specific protein kinase (EC 2.7.1.-)	1	
PAG1033UP	YDL037c	putative glucan 1,4-alpha-glucosidase (EC 3.2.1.3)	3	open frame whole length in -2

PAG1034RP	YGL114W	hypothetical protein	1	
PAG1034UP	YOR246c	similarity to reductases	4	
PAG1035I1	YLR337W	proline-rich protein verprolin	3	open frame 300 nt in -3
PAG1035I2	YNL281W	hypothetical protein	3	open frame > 350 nt in -1
PAG1035RP	YJR090c	required for glucose repression and for glucose and cation transport	3	open frames > 350 nt in -1
PAG1035UP	YBL079W	nuclear pore (nucleoporin)	1	see PAG1035UP for additional Hit to YBL079W
PAG1036RP	YLR266c	similarity to transcription factors	3	open frames 350 nt in -3, 300 nt in +2
PAG1036UP	YDR370c	hypothetical protein	2	
PAG1037RP	YLR430W	positive effector of tRNA-splicing endonuclease	1	
PAG1038RP	YNL068c	homolog of Drosophila forkhead protein	3	open frame whole length in -3
PAG1038UP	YLR389c	protease involved in a-factor processing	1	
PAG1039RP	YDR443c	component of RNA-POL holoenzyme and komberg's mediator (SRB) subcomplex	1	nearly whole gene on clone
PAG1039UP	YDR443c	component of ma polymerase holoenzyme and komberg's mediator (SRB) subcomplex	1	Promotor, nearly whole gene on clone
PAG1040RP	YAL040c	G1/S-specific cyclin	4	tRNA (Val1), pos. 134 - 207, perfect match to S.c. tRNA(Val1A), 1 mismatch to tRNA(Val1B), no intron
PAG1040UP	YPR097W	hypothetical protein	2	

PAG1041RP	YJL054w	hypothetical protein	2	
PAG1041UP	YLR337w	proline-rich protein verprolin	4	
PAG1042RP	YGL035c	transcriptional repressor involved in glucose-repression	3	open frame > 300 nt in -2
PAG1042UP	YKR075c	weak similarity to negative regulator Sm1p/Hex2p	3	open frame 300 nt in +1
PAG1043RP	YDR456w	similarity to NA ⁺ -H ⁺ antiporters	2	
PAG1043UP	YML029w	putative membrane protein	2	
PAG1044I1	YDL076c			
PAG1044I2	YDL076c			
PAG1044RP	YDL077c	hypothetical protein	2	syntenie
PAG1044UP	YDL075w	ribosomal protein L31.e.c12	1	Promotor; Intron, in A.g. at same position compared to S.c. (CAI S.c. 0.60);syntenie
PAG1045RP	YBL096c	hypothetical protein	4	
PAG1045UP	YDL195w	component of the COPII coat of ER-golgi vesicles	4	
PAG1046RP	YHR132c	carboxypeptidase homolog	1	
PAG1046UP	YBR149w		3	open frame 350 nt in +1
PAG1047RP	YLR377c	fructose-1,6-bisphosphatase, gluconeogenic enzyme	1	Syntenie, see PAG1047UP
PAG1047UP	YLR378c	member of the protein permease family of the major		

Accession	Gene	Protein	Length	Notes
PAG1048RP	YBL023c	member of the Mcm2p,Mcm3p,Cdc46p family	1	facilitator superfamily (MFS)
PAG1048UP	YER139c	similarity to YD9609.20 (similarity to amino acid permeases)	1	questionable ORF
PAG1049RP	YLR050c	similarity to human MAC30 C-terminus	1?	has STOP in Hom_Reg
PAG1049UP	YFL018c	dihydrolipoamide dehydrogenase precursor	1	
PAG1050RP	YGL139w	similarity with hypothetical protein (chromosome XVI) YPL221w	1	
PAG1050UP	YIL090w	hypothetical protein	1	
PAG1052I1	YPL221w	homology to hypothetical protein (CHR VII) and probable membrane protein YAL053w	2	
PAG1052I2	YPL221w	homology to hypothetical protein (CHR VII) and probable membrane protein YAL053w	1	
PAG1052RP	YGL139w	similarity with hypothetical protein (chromosome XVI) YPL221w	1	Syntenie, see PAG1052UP
PAG1052UP	YGL137w	coatomer complex beta chain (beta'-cop) of secretory pathway vesicles	1	Promotor, Syntenie, see PAG1052RP, I1 and I2 (match all to YGL139w),

PAG1053RP	YJL197w	UBP12	ubiquitin specific protease	3	Intron possible, same position like in S.c. (CAI S.c. 0.21)
PAG1053UP	YGR255c		hypothetical protein	1	Terminator
PAG1054RP	YBL023c	MCM2	contains N-term down to codon 106, Member of the CDC46p/ MCM2p/MCM3p family that acts as a complex at ARS's to initiate replication	1	former class III
PAG1054UP	YDL120w		hypothetical protein	3	open frame 350 nt in +3, +2, and -2
PAG1055RP	YBL023c	MCM2	member of the Mcm2p,Mcm3p,Cdc46p family	2	
PAG1055UP	YDR065w		hypothetical protein	3	open frame 350nt in +3 and -2
PAG1056RP	YBR290w	BSD2	metal homeostasis protein and probable metal ion transporter	1	
PAG1056UP	YNL228w		questionable ORF	4	
PAG1057RP	YDR143c	SAN1	protein that may antagonize the function of Cdc68p (general chromatin factor) and Sir4p	2	
PAG1057UP	YIL169c		homology to glucan 1,4-alpha-glucosidase	3	open frame 400 nt in +3
PAG1058I1	YDR151c	CTH1	protein of the inducible CCCH zinc-finger family	1	Syntenie, see PAG1058UP
PAG1058I2	YOR306c		similarity to human X-linked PEST-containing transporter	4	
PAG1058RP	YDR150w	NUM1	nuclear migration protein	4	

PAG1058UP	YDR152w		1	1	hypothetical protein	involved in recognition of signal peptides	SEC72	YLR292c	YLR292c	1	Terminator + Promotor (300 nt, for Terminator see PAG1059UP 2nd Hit), Syntenie
PAG1059RP	YLR289w	GUF1	1	1	similarity to E. coli elongation factor-type GTP-binding protein lepa					1	Syntenie, see PAG105811
PAG1059UP	YLR291c	GCD7	1	1	translation initiation factor eif2b, 43 KD (beta) subunit					1	Terminator + Promotor (300 nt, for Terminator see PAG1059UP 2nd Hit), Syntenie
PAG1060RP	YER157w		1	1	unknown function					1	Terminator + Promotor (300 nt, for Terminator see PAG1059UP 1st Hit), Syntenie
PAG1060UP	YER155c	BEM2	1	1	GTPase-activating protein					1	same as PAG1637
PAG1061RP	YGR276c		1	1	weak similarity with GOR protein - Pan troglodytes					1	same as PAG1112
PAG1062RP	YMR297w	PRC1	1	1	carboxypeptidase y (CPY) (YSCY), serine-type protease					1	
PAG1062UP			3	3	ORF not regarded, homolog to Gly-X carboxypeptidase, pseudogene in S288C, three ORF's are separated by two in-frame STOP-codons					3	open frame 300 nt in -1, many stops in other frames
PAG1063RP	YPL004c		1	1	homology to hypothetical protein (chromosome VII)					1	

PAG1063UP	YFL002c	SPB4	putative ATP-dependent RNA helicase	1	
PAG1064RP	YBR180w		similarity to drug resistance proteins	1	
PAG1064UP	YNL185c		similarity to ribosomal protein L11	4	
PAG1065RP	YPL040c	ISM1	mitochondrial isoleucine--tRNA ligase (EC 6.1.1.5)	2	Syntenie, see PAG1065UP
PAG1065UP	YPL037c	EGD1	protein with a negative role in gal gene expression	1	Terminator, Syntenie, see PAG1065RP
PAG1069RP	YPL265w	DIP5	dicarboxylic amino acid permease	1	former class III
PAG1069UP	YGR211w		hypothetical protein	1	
PAG1071CRP	YLR405w		similarity to <i>Azospirillum brasilense</i> nifR3 protein	3	(Chimera or) repated region, hybridizes to A.g. chr. II and III open frame> 350 nt in +2 and -3
PAG1071CUP	YDL164c	CDC9	DNA ligase	3	(Chimera or) repated region (see pG1071CRP), hybridizes to A.g. chr. II and III , open frame whole length in -3
PAG1073RP					Mito
PAG1073UP					Mito
PAG1074RP					Mito
PAG1074UP					Mito
PAG1075RP					Mito
PAG1075UP					Mito

PAG1076RP						Mito	
PAG1076UP						Mito	
PAG1077RP						Mito	
PAG1077UP						Mito	
PAG1078I1	YJL024c	YKS7	sigma-2 adaptin homolog		1	Intron possible, 5' splice site not found	
PAG1078I2	YJL024c	YKS7	sigma-2 adaptin homolog		1	Terminator, for Intron see PAG1089I1	
PAG1078RP	YCR081w	SRB8	component of RNA polymerase holoenzyme and SRB subcomplex		4		
PAG1078UP	YGR175c	ERG1	squalene monooxygenase		1	Terminator	
PAG1079RP	YNL133c		hypothetical protein		2	tRNA (Phe), pos. 446 - 538, Syntenie of YNL133c and tRNA (Phe), 18 nt Intron in S.c., anticodon (gene)=GAA, same as PAG1200	
PAG1079UP	YHR069c		homology to unknown S.pombe and human proteins		1	same as PAG1200	
PAG1080UP	YLL009c	COX17	interacts genetically with SCO1 and SCO2 in cytochrome oxidase assembly		1	Promotor, whole gene on clone, (CAI S.c. 0.09))	
PAG1081RP	YOR378w		homology to aminotriazole resistance protein		3	open frame whole length in +3	
PAG1081UP	YCR075c	ERS1	Intracellular protein transport		2		

PAG1082RP	YGR055w	MUP1	high affinity methionine permease	1	
PAG1082UP	YLR357w		similarity to hypothetical protein (chromosome VII)	2	
PAG1083RP	YNL283c		similarity to mammalian mucin and yeast chitinase	3	open frame whole lenght in -2, many stops in other frames
PAG1083UP	YDR158w	HOM2	aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	1	Promotor (CAI S.c. 0.43)
PAG1201RP	YDL140c	RPO21	RNA polymerase II, largest subunit (B220)	1	Promotor (CAI S.c. 0.21)
PAG1201UP	YLR218c		hypothetical protein	2	
PAG1202RP	YPR003c		hypothetical protein	2	
PAG1202UP	YPL108w		hypothetical protein	1	
PAG1203RP	YMR076c		similarity to E. nidulans bimD protein, includes C-term + terminator	1	two genes covered by RP-SRS;syntenie
PAG1203UP	YMR075w		promoter terminator combination,		
	YMR076c		similarity to Emericella nidulans bimD protein	1	syntenie;covers codons 170-372
PAG1204RP	YGR282c	BGL2	endo-beta-1,3-glucanase of the cell wall	1	Promotor, Syntenie, see PAG1204UP
PAG1204UP	YGR284c		similarity with mouse Surf-4 protein	1	Syntenie, see PAG1204RP
PAG1205RP	YJR104c	SOD1	superoxide dismutase (EC 1.15.1.1) (Cu-Zn)	1	divergent Terminator (123 nt)
	YBL039c	URA7	CTP synthase 1;last step in pyrimidine biosynthesis pathway	1	divergent Terminator (123 nt)

PAG1205UP	YHR150w	unknown function	1	former class III
PAG1206RP	YDR353w	putative thioredoxin reductase (NADPH)	1	Promotor
PAG1206UP	YHR103w	homology to hypothetical protein D9476.7	1	
PAG1207RP	YPL072w	hypothetical protein	2	Syntenie, see PAG1107UP.Classification in Hom_Class 2 according to Syntenie
PAG1207UP	YPL074w	probable regulatory subunit of 26S proteasome complex	1	Syntenie, see PAG1107RP
PAG1208RP				Mito
PAG1208UP				Mito
PAG1209RP	YDL073w	putative mitochondrial protein	2	
PAG1210RP	YLR094c	hypothetical protein	1	Terminator, Syntenie, see PAG1210UP
PAG1210UP	YLR095c	hypothetical protein	2	Syntenie, see PAG1210RP
PAG1211RP	YHR072w	lanosterol synthase (EC 5.4.99.7)	1	
PAG1211UP	YDR317w	hypothetical protein	2	
PAG1212RP	YBR180w	similarity to drug resistance proteins	1	
PAG1212UP	YDL202w	hypothetical protein	2	
PAG1213RP	YJR005w	clathrin-associated protein complex beta chain, large subunit	2	
PAG1213UP	YLR007w	hypothetical protein	1	open frames whole length in +1 and -3,former class III
PAG1214RP	YIR008c	DNA polymerase alpha subunit 48KD (DNA	3	open frame whole length in
	PRI1			

PAG1214UP	YLL031c	primase)	-2
PAG1215RP	YIR035c	similarity to YJL062p	4
		similarity to YIR036p and YIL124p	1
			Promotor, "Syntenie", see PAG1215UP.
	YIR036c	similarity to short-chain alcohol dehydrogenase	1
		family, YIR035p and YIL124p	PAG1215UP
PAG1215UP	YIR035c	similarity to YIR036p and YIL124p	1
			Promotor, "Syntenie", see PAG1215RP.
	YIR036c	similarity to short-chain alcohol dehydrogenase	
		family	
		YIR035p and YIL124p	1
			Promotor, "Syntenie", see PAG1215RP
PAG1216RP	YIL047c	protein for which truncation and overexpression	3
		can suppress \$ lethality of G-alpha protein	
		deficiency	
PAG1216UP	YJR032w	peptidylprolyl isomerase homolog	4
PAG1218RP	YAL053w	homology to hypothetical proteins on	1
		chromosomes VII, XV and XVI	
PAG1218UP	YOR367w	homology to human SM22 homolog	2
PAG1219RP	YKR054c	dynein heavy chain, cytosolic	2
			Syntenie, see PAG1219UP, additional hit see PAG1011I2 and RP
PAG1219UP	YKR056w	endo-exonuclease	1
PAG1220RP	YBR082c	unknown function	2
			Syntenie, see PAG1219RP

PAG1220UP	YDR044w	HEM13	coproporphyrinogen III oxidase	1	
PAG1221RP	YGL227w		hypothetical protein	2	Terminator
PAG1221UP	YER043c	SAH1	S-adenosyl-L-homocysteine hydrolase	1	
PAG1222RP	YLR403w	SFP1	involved in nuclear protein localization	1	Terminator, Syntenie, see PAG1222UP
PAG1222UP	YLR401c		hypothetical protein	1	Syntenie, see PAG1222RP
PAG1223RP	YGR002c		hypothetical protein	1	syntenie
PAG1223UP	YGL003c		unknown function, has MT-energy transfer proteins signature,		
			has cytochrome c oxidase subunit I, copper B binding region signature	1	former class III.SYNTENIE
PAG1224RP	YML127w		hypothetical protein	1	
PAG1224UP	YLL067c		homology to other subtelomeric encoded proteins	3	open frame > 300 nt in -1
PAG1225RP	YNL087w		probably membrane protein	1	
PAG1225UP	YKR092c	SRP40	weak suppressor of a mutant of the subunit AC40 of DNA dependent RNA polymerase I and III	3	open frames > 500 nt in +2 (S-rich) and >450 nt in -1
PAG1226RP	YOR181w	LAS17	proline-rich protein	3	open frame whole length in +2
PAG1226UP	YFL049w		weak similarity to Npl6p (nuclear protein localization factor)	2	
PAG1227RP	YDR262w		hypothetical protein	2	
PAG1227UP	YGR160w		questionable ORF	4	

Accession	Gene	Protein	Function	Length (aa)	Notes
PAG1228RP	YFL008w	SMC1	chromosome segregation protein	1	Promotor (CAI S.c. 0.16)
PAG1228UP	YAL017w	FUN31	probable serine/threonine protein kinase	1	
PAG1230RP	YNL317w		similarity to Arabidopsis thaliana PRL1 protein	1	
PAG1230UP	YOL138c		hypothetical protein	1	
PAG1231RP	YMR176w		hypothetical protein	3	open frame > 350 nt in -1
PAG1231UP	YPL027w		hypothetical protein	3	open frame > 400 nt in +1
PAG1232RP	YGL027c	CWH41	Involved in beta-1,6-glucan assembly	1	open frame 300 nt in +1
PAG1232UP	YBL014c	RRN6	component of a multiprotein complex essential for		
			initiation of RNA-POL I	2	
PAG1233RP	YKR092c	SRP40	weak suppressor of a mutant of the subunit AC40 of DNA dependent RNA polymerase I and III	3	open frame whole length in +2 and nearly whole length in -3
PAG1233UP	YML102w		similarity to human chromatin assembly factor I p60 chain	2	
PAG1235RP	YDL122w	UBP1	ubiquitin-specific protease	1	
PAG1235UP	YGL156w	AMS1	alpha-mannosidase	1	
PAG1236RP	YDR373w		homology to human BDR-1 protein and other calcium binding proteins	1	Promotor
PAG1236UP	YOR124c	UBP2	ubiquitin-specific proteinase (EC 3.4.-.-)	1	
PAG1238RP	YPL195w	YKS4	putative alpha/gamma adaptin	1	
PAG1238UP	YGL080w		similarity with R07E5.13 protein (clone R07E5) - C. elegans	1	Promotor
PAG1240RP					Mito

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PAG1249RP	YOR244w	similarity to SAS2 protein (involved in silencing at HMR)	1	Syntenie, see PAG1249UP
PAG1249UP	YOR243c	hypothetical protein	1	Syntenie, see PAG1249RP
PAG1250RP				Mito
PAG1250UP				Mito
PAG1251RP	YCR076c	glycine-rich	3	open frames > 450 nt in +1 and > 400 nt in -3
PAG1251UP	YMR259c	hypothetical protein	2	Terminator
PAG1252RP	YFR015c	UDP glucose--starch glucosyltransferase 1	1	
PAG1252UP	YFR014c	Ca2+/calmodulin-dependent serine/threonine protein kinase type I	1	
PAG1253RP	YGL122c	nuclear poly(A)-binding protein	3	open frame > 500 nt in +2
PAG1253UP	YIL130w	similarity to probable membrane protein YJL206c and Put3p	1	
PAG1254RP	YJR016c	dihydroxy-acid dehydratase (EC 4.2.1.9)	1	Terminator
PAG1254UP	M_D113	hypothetical protein	4	
PAG1255RP	YDR300c	glutamate 5-kinase	1	
PAG1256RP	YGL195w	component of a protein complex required for activation of Gcn2p protein kinase	1	Syntenie, see PAG1256UP
PAG1256UP	YGL194c	high similarity with RPD3 protein (transcription modifier protein)	1	Syntenie, see PAG1256RP
PAG1257RP	YGL147c	ribosomal protein RPL9	1	Terminator
PAG1257UP	YDL117w	hypothetical protein	2	Terminator
PAG1258RP	YOL023w	mitochondrial translation initiation factor 2	1	

PAG1258UP	YPL115c	BEM3	GTPase-activating protein for Cdc42p and Rho1p	1	
PAG1259RP	YBR087w	RFC5	replication factor C subunit 5 (40kDa)	1	Promotor (CAI S.c. 0.15)
PAG1259UP	YBL036c		similarity to Caenorhabditis elegans cosmid F09E5	1	
PAG1260RP	YDR306c		hypothetical protein	2	Promotor, Syntenie, see PAG1260UP, next to tRNA (Val) in S.c.
PAG1260UP	YDR304c	CPR5	cyclophilin of the ER	1	Promotor, Syntenie, see PAG1260RP
PAG1261RP	YLR333c	RPS31B	ribosomal protein S25.e.c12	1	Terminator
PAG1261UP	YLR336c		hypothetical protein	2	Terminator
PAG1262RP	YER069w	ARG5,6	acetylglutamate kinase	1	Syntenie, see PAG1262UP
PAG1262UP	YER068w	MOT2	transcriptional repressor	1	Promotor, Syntenie, see PAG1262RP
PAG1263RP	YJR090c	GRR1	required for glucose repression and for glucose and cation transport	1	
PAG1263UP	YIR019c	STA1	extracellular glucosylase	3	open frame > 400 nt in -1
PAG1264RP	YBL051c		similarity to Schizosaccharomyces pombe protein Z66568_C	4	
PAG1264UP	YHR202w		hypothetical protein	1	
PAG1265RP	YHR143w		similarity to a-agglutinin core protein AGA1	3	open frame 450 nt in -1, same as PAG1176
PAG1265UP	YNL083w		hypothetical protein	1	same as PAG1176

PAG1266RP	YGL163c	RAD54	DNA-dependent ATPase of the Snt2p family	1	
PAG1266UP	YNL066w	SUN4	homology to Candida wickerhamii beta-glucosidase (EC 3.2.1.21)	3	open frame > 400 nt in +3, check Hom_Class, better 2 (25%/95 aa)
PAG1267RP	YLL040c		hypothetical protein	4	
PAG1267UP	YGR054w		hypothetical protein	3	open frame nearly whole length in +1
PAG1268RP	YGL142c		hypothetical protein	1	
PAG1268UP	YDL108w	KIN28	cyclin-dependentSER/THR protein kinase component		
			of transcription initiation factor TFIIF	1	Terminator + Promotor (177 nt, see 2nd Hit for Promotor), Syntenie
	YDL107w	MSS2	serine/threonine protein kinase	2	Terminator + Promotor (177 nt, see 1st Hit for Terminator), ATG not Inframe Syntenie
PAG1269RP	YCL057w	PRD1	saccharolysin;proteinase yscD	2	Terminator
PAG1269UP	YPL101w		hypothetical protein	1	
PAG1270RP	YLR106c		putative membrane protein	2	longest yeast gene, only 1 gene on clone
PAG1270UP	YLR106c		putative membrane protein	1	longest yeast gene, only 1 gene on clone
PAG1271RP					Mito

Accession	Gene	Protein	Function	Notes
PAG1271UP				Mito
PAG1272RP	YDR083w		hypothetical protein	1 Terminator
PAG1272UP	YIR019c	STA1	extracellular glucoamylase	3 open frame whole length in +3 (?)
PAG1273RP	YCR098c		similarity to Pho84p, Itr1p, Itr2p (myo-inositol transporter) and to E. coli citrate transport protein	1
PAG1273UP	YGR160w		questionable ORF	4
PAG1274RP	YOR338w		similarity to FUN19 protein	4
PAG1274UP	YOR347c		similarity to pyruvate kinase Pyk1p	1 Terminator
PAG1275RP	YKL079w	SMY1	member of the kinesin family that can interact with or substitute for Myo2p	3 open frame whole length in -3
PAG1275UP	YKL081w	TEF4	elongation factor eEF-1 gamma chain	2 Intron possible, same position like in S.c., unusual 5'-splice site
PAG1277RP	YKR043c		similarity to phosphoglycerate mutase (EC 5.4.2.1)	1
PAG1277UP	YNR044w	AGA1	A-agglutinin anchor subunit	3 open frame > 500 nt in -1
PAG1278RP	YDL042c	SIR2	protein involved in maintenance of silencing of HMR, HML and telomeres	2 Terminator
PAG1278UP	YOL067c	RTG1	basic helix-loop-helix (BHLH) transcription factor see 2nd Hit (CAI S.c. 0.12)	1 Divergent Promotor of 215 nt, for 2nd Promotor
	YDL007w	YTA5	similarity to human S4 component of 26S	2 divergent Promotor of 215

Gene	Accession	Protein	Function	Notes
PAG1279RP	YCR032w	protease	probable acetic acid export pump	Hit
PAG1279UP	YCR032w		probable acetic acid export pump	only 1 gene on clone
PAG1280RP	YBR156c		weak similarity to myosins	Terminator, only 1 gene on clone
PAG1280UP	YPR026w		required for vacuolar acid trehalase activity	open frame whole length in -2, two separated short blocks with high homology
PAG1281RP	YER172c		RNA helicase-related protein	1
PAG1281UP	YER171w		DNA helicase/ATPase	Syntenie, see PAG1281UP
PAG1282RP	YBL019w		hypothetical protein	1
PAG1282UP	YBL022c		serine protease required for intramitochondrial proteolysis	Syntenie, see PAG1282UP
PAG1283RP	YPL217c		hypothetical protein	2
PAG1283UP	YPL219w		similarity to hypothetical protein (chromosome VII)	1
PAG1284RP	YDL126c		microsomal protein of CDC48/PAS1/SEC18 (AAA) family of ATPases	1
PAG1284UP	YOR348c		proline and gamma-aminobutyrate permease	1
PAG1285RP	YGR068c		with sim to ROD1 (which is a protein that mediates resistance to o-dinitrobenzene)	1
PAG1285UP	YMR137c		DNA repair protein for interstrand crosslinks	former class III
PAG1286RP	YAL056c		hypothetical protein	2
PAG1286UP	YAL056c		hypothetical protein	Terminator

PAG1286RP	YBR204c	similarity to peroxisomal serine-active lipase	3	open frame > 400 nt in -3,
PAG1286UP	YIR019c	extracellular glucoamylase	3	open frames > 500 nt in +1 and -3
PAG1287RP	YBL004w	hypothetical protein	1	
PAG1287UP	YDL003w	similarity to S.pombe rad21	2	
PAG1289UP	YKR072c	stimulates G1 cyclin expression	1	
PAG1289RP	YGR061c	5'-phosphoribosylformyl glycine synthetase	4	
PAG1291UP	YKL211c	contains anthranilate synthase (EC 4.1.3.27); glutamine amidotrans- ferase (EC 2.6.1.-); indole-3-glycerol-phosphate synthase(EC4.1.1.48)	1	
PAG1292RP				Mito
PAG1292UP				Mito
PAG1293RP	YGL062w	pyruvate carboxylase 1	1	
PAG1293UP	YPL187w	MFalpha1;mating pheromone alpha-1 precursor	3	open frames 300 nt in +2 and > 400 nt in +1, check Hom_Class: mating pheromone in S.c. is processed a lot
PAG1294RP	YLR147c	snRNA-associated protein of the SM class required for pre-mRNA splicing, snRNP D3 homolog	1	open frame > 300 nt in +3,former class III
PAG1294UP	YDR167w	similarity to human TBD-associated factor 30	1	Promotor + Terminator (171

	PAG	YDR	CDC	Description	Number	Hlt, Syntenie 0.10)	nnt) , for Promotor see 2nd Hlt, Syntenie (CAI S.c.
PAG1295RP	YJL172w	CPS1	Gly-X carboxypeptidase (EC 3.4.17.4) precursor	2			Pormotor + Terminator (171 nt), for Terminator see 1st Hlt, Syntenie
PAG1295UP	YMR298w		hypothetical protein	2			
PAG1296RP	YGL246c		hypothetical protein	1			
PAG1296UP	YFR050c	PRE4	proteasome subunit	1			
PAG1297RP	YGL123w	SUP44	ribosomal protein SUP44/RP54	1			Promotor (CAI S.c. 0.80)
PAG1297UP	YMR136w		hypothetical protein	2			
PAG1299RP	YLR223c	IFH1	controlling pre-rRNA processing machinery in conjunction with Fhl'p	3			open frame > 350 nt In -1
PAG1299UP	YAL017w	FUN31	probable serine/threonine protein kinase	1			
PAG1300RP	YOR104w		hypothetical protein	3			open frames > 350 nt In +1 and -2
PAG1300UP	YNL097c		similarity to YHR090p (similarity to human zinc finger/leucine zipper protein) and YM9916.14 (Chr. XV)	1			
PAG1301RP	YCL064c	CHA1	L-serine/L-threonine deaminase	1			Syntenic, see PAG1301UP
PAG1301UP	YCL061c		partial identity to hypothetical protein 1 (URK1 5' region)	2			Syntenic, see PAG1301RP
PAG1302RP	YGR058w		weak similarity with calcium-binding protein	1			

[illegible]

YLL035w	hypothetical protein	2	divergent Terminator (100 nt), for 1st Terminator see 1st Hlt, Syntenie, see PAG1308RP 1st Hlt	2	divergent Terminator (100 nt), for 1st Terminator see 1st Hlt, Syntenie, see PAG1309UP, see PAG1165UP for additional Hit to YDR270w
PAG1308UP	single-stranded zinc-finger DNA binding protein required for replication in mitochondria	2		2	Homology due to zinc-finger?
PAG1309RP	copper-transporting P-type ATPase of the cation transport (E1-E2) ATPase family	1	CCC2	1	Syntenie, see PAG1309UP, see PAG1165UP for additional Hit to YDR270w
PAG1309UP	mitochondrial tryptophanyl-tRNA synthetase	1	MSW1	1	divergent Terminator (40 nt) -> see PAG1309UP 3rd Hlt, Syntenie -> see PAG1309RP
YOR038c	histone transcription regulator	1	HIR2	1	divergent Terminator (40 nt) -> see PAG1309UP 1st Hlt
PAG1310UP	homology to cytidine deaminases (EC 3.5.4.5)	1		1	
PAG1311RP	unknown function	1		1	former class III
PAG1311UP	probable transcription factor, suppressor of Ty transcription	1	SPT7	1	open frame 500 nt in -2, former class III
PAG1312RP	Ser/Thr protein kinase; limited homology only	2		2	
PAG1312UP	phosphatidylinositol 3-kinase required for G1 progression	3	TOR2	3	open frame whole length in +1
PAG1313RP	hypothetical protein	1		1	
PAG1313UP	weak similarity to human BRCA2 early onset	1		1	former class III

PAG1314RP	YGR023w	breast cancer gene	3	open frame > 350 nt in -3
PAG1314UP	YJR151c	similarity with Mid2p and Kai1p	4	
PAG1315RP	YPR181c	similar to proteins of the Srp1p/Tip1p family	1	Syntenie, see PAG1315UP
PAG1315UP	YPR184w	component of COPII coat of ER-golgi vesicles	1	Promotor, Syntenie, see PAG1315RP
		protein with strong similarity to glycogen debranching enzyme (4-alpha- glucanotransferase)	2	
PAG1316RP	YLR440c	hypothetical protein	1	Promotor
PAG1316UP	YLR441c	ribosomal protein S3a.e	1	Syntenie, see PAG1317up
PAG1317RP	YJL085w	hypothetical protein	1	Syntenie, see PAG1317RP
PAG1317UP	YJL087c	tRNA ligase (EC 6.1.1.-)	3	open frames > 300 nt in -2
PAG1318RP	YIL159w	similarity to BNI1 protein	3	open frames > 450 nt in -3 and > 600 nt in +2
PAG1318UP	YER073w	probable aldehyde dehydrogenase (NAD+)	1	Syntenie, see PAG1319UP
PAG1319RP	YMR277w	hypothetical protein	1	Syntenie, see PAG1319RP
PAG1319UP	YMR276w	ubiquitin-like protein	1	
PAG1320RP	YOR207c	DNA-directed RNA polymerase (EC 2.7.7.6) III	1	
		second-largest chain	4	
PAG1320UP	YMR147w	hypothetical protein	1	Syntenie, see PAG1321UP
PAG1321RP	YBL020w	involved in nuclear division	1	1st and 2nd Hit
PAG1321UP	YBL018c	hypothetical protein	1	divergent Terminator (38 nt), Syntenie, see PAG1321RP and

[illegible]

PAG1327RP	YER011w	TIR1	cold-shock induced protein of the Tir1p, Tip1p family	4	
PAG1327UP	YLR337w	VRP1	proline-rich protein verprolin	4	
PAG1328RP	YNL201c		involved in regulation of carbon metabolism	2	Syntenie, see PAG1328UP, Classification in Hom_Class 2 according to Syntenie
PAG1328UP	YNL200c		hypothetical protein	1	Syntenie, see PAG1328RP
PAG1330RP	YLL039c	UBI4	ubiquitin precursor	1	100 % Identity on AA-level, 78.3% on DNA, Syntenie, see PAG1330UP
PAG1330UP	YLL036c	PRP19	non-snRNP spliceosome component	1	Most probable Intron in A.g. but NOT in S.c. Syntenie, see PAG1330RP
PAG1331RP	YDR150w	NUM1	nuclear migration protein	2	open frame > 450 nt in -2, 30% ident./140 aa, check Hom_Class: better 3?
PAG1331UP	YNR044w	AGA1	A-agglutinin anchor subunit	3	open frames > 400 nt in +2> 350 nt in +3 and > 350 nt in +3
PAG1332RP	YKL014c		hypothetical protein	3	open frame nearly whole length in +1
PAG1332UP	YJL194w	CDC6	involved in initiation of DNA replication and spindle function	2	Terminator

PAG1334RP	YHR217c	similarity to hypothetical protein (chromosome IV)	3	open frame whole length in -2 and +2
PAG1334UP	YMR038c	homocitrate dehydrogenase	1	
PAG1335RP	YKL129c	myosin type I	3	open frames whole length in -2 and 300 nt in +3
PAG1335UP	YOR008c	similarity to N0583	4	
PAG1336RP	YJR092w	required for formation of axial but not bipolar budding pattern	1	Terminator, Syntenie, see PAG1336UP
PAG1336UP	YJR095w	protein of the mitochondrial carrier (MCF) family	1	Promotor, Syntenie, see PAG1336RP
PAG1337RP				Mito
PAG1337UP				Mito
PAG1338RP	M_A394	hypothetical transmembrane protein	4	
PAG1338UP	YCR065w	transcription factor	2	
PAG1339RP	YDL244w	nearly identical to Thi5p (involved in pyrimidine biosynthesis pathway), YJR156p, and YNL332w (nmt1 homolog to fission yeast and Aspergillus parasiticus)	1	Promotor, YNL332w near telomere
PAG1339UP	YKL213c	protein involved in ubiquitin proteolysis	1	Terminator
PAG1340RP	YMR004w	required for sorting proteins to the vacuole	1	Terminator, Syntenie (?), see PAG1340UP
PAG1340UP	YMR003w	hypothetical protein	2	Terminator, Syntenie (?), see PAG1340RP
PAG1341RP	YPL242c	hypothetical protein	4	

PAG1341UP	YFL036w	RPO41	mitochondrial DNA-directed RNA polymerase	1	
PAG1342RP	YNR030w		weak similarity to SMP3 protein (functions in the protein kinase C pathway)	2	
PAG1342UP	YPR088c	SRP54	signal recognition particle 54K protein homolog	1	
PAG1343RP	YKL134c	(MIP1)	mitochondrial intermediate peptidase (EC 3.4.24.-) precursor	1	
PAG1343UP	YLR109w		similarity to Candida boldinii peroxisomal membrane protein 20K A	4	UGG tRNA (Pro), pos. 434-545, intron pos.470-509 (40 nt), intron in S.c. 32nt, w/o intron only 1 difference
PAG1344RP					Mito
PAG1344UP					Mito
PAG1345RP	YPL042c	SSN3	cyclin-dependent serine/threonine protein kinase of the RNA polymerase II holoenzyme complex and kornberg's mediator (SRB) subcomplex		
PAG1345UP	YPL040c	ISM1	mitochondrial isoleucine--tRNA ligase (EC 6.1.1.5)	1	Syntenie, see PAG1345UP
PAG1347RP	YBR221c	PDB1	pyruvate dehydrogenase (lipoamide) beta chain precursor	1	Syntenie, see PAG1345RP
PAG1347UP	YGL126w	SCS3	probably involved in the synthesis of inositol phospholipids	2	Promotor (CAI S.c. 0.34)

PAG1349RP	YEL011w	GLC3	1,4-glucan branching enzyme (glycogen branching enzyme)	1	Promotor (CAI S.c. 0.13)
PAG1349UP	YCR017c		putative membrane protein	1	
PAG1350RP	YPR105c		hypothetical protein	2	Promotor, Syntenie, see PAG1350UP
PAG1350UP	YPR106w		similarity to protein kinases Gcn2p, galactosyltransferase-associated protein kinase P58/GTAP, and the raf proto-oncogene	2	Syntenie, see PAG1350RP
PAG1351RP					Mito
PAG1351UP					Mito
PAG1352RP	YFL033c		similarity with to S.pombe CEK1 serine/threonine protein kinase	2	
PAG1353RP	YDR456w		similarity to NA ⁺ -H ⁺ antiporters	2	Terminator
	YML031w	NDC1	component of the nuclear envelope	2	Terminator, Syntenie, see PAG1335UP 1st Hit
PAG1353UP	YML029w		putative membrane protein	2	Terminator, Syntenie, see PAG1353RP 2nd Hit
PAG1354UP	YOR017w	PET127	probable mitochondrial translation factor	2	
PAG1355RP	YCR092c	MSH3	DNA-repair protein	2	Syntenie, see PAG1355UP, order wrong
PAG1355UP	YCR094w		homology to hypothetical protein YNL323w and EST from rice	2	Syntenie, see PAG1355RP, order wrong
PAG1356RP	YKR092c	SRP40	weak suppressor of a mutant of the subunit	3	open frame whole length in

			AC40 of DNA dependent RNA polymerase I and III	-3
PAG1356UP			SP entry: UAPC_EMENI purine permease	2
PAG1357RP	YPL158c		hypothetical protein	3 open frame whole length in -2
PAG1357UP	YPL155c	KIP2	kinesin-related protein	1
PAG1359RP	YIL130w		similarity to probable membrane protein YJL206c (probable regulatory zinc-finger protein) and Put3p (positive activator of the proline utilization pathway)	4
PAG1359UP	YER163c		hypothetical protein	1
PAG1360RP	YCR057c	PWP2	periodic tryptophan protein	1
PAG1360UP	YLR342w	GLS1	component of beta-1,3-glucan synthase	1
PAG1362RP	YOR340c	RPA43	essential subunit of RNA polymerase I	1 Terminator
PAG1362UP	YCR065w	HCM1	transcription factor	3 open frames > 350 nt in +3 and > 300 nt in -3
PAG1363RP	YLR454w		similarity to hypothetical protein YPR117w	1
PAG1363UP	YDL037c		putative glucan 1,4-alpha-glucosidase (EC 3.2.1.3)	3 open frame whole length in +2
PAG1364RP	YDL108w	KIN28	cyclin-dependent serine/threonine protein kinase component of transcription initiation factor TFIIF	1 Terminator, cannot be checked for Intron, not on

sequence of PAG1363RP

PAG1364UP	YGL142c	1	hypothetical protein	1	open frame whole length in
PAG1365RP	YIL011w		similarity to YIL176p, YIR041p and other members of the Srp1p/Tip1p family		+3 (?)
PAG1365UP	YHR144c	1	deoxycytidylate deaminase (EC 3.5.4.12)	1	open frame whole length in
PAG1366RP	YLR413w	3	homology to hypothetical protein YKL187c	3	+2
PAG1366UP	YKL188c	1	similarity to human adrenoleukodystrophy (ALD) protein and yeast peroxisomal protein Pal1p	1	
PAG1367RP	YHR089c	1	associated with snoRNA and involved in 35S rRNA processing	1	
PAG1367UP	YBR115c	1	L-aminoacidipate-semialdehyde dehydrogenase	1	
PAG1368RP	YDL171c	1	putative glutamate synthase	1	
PAG1368UP	YNR012w	1	uridine kinase	1	
PAG1369RP	YPR175w	1	DNA-directed DNA polymerase II chain B	1	Terminator, Syntenie, see PAG1369UP, same as PAG1144
PAG1369UP	YPR179c	1	hypothetical protein	1	Syntenie, see PAG1369RP, same as PAG1144

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PAG	YAL	PYK	pyruvate kinase, activity is regulated by glucose levels, inducer:glucose	1	Mito
PAG1381UP					
PAG1382RP	YAL038w	PYK1		1	CDC19
PAG1382UP	YOR346w	REV1	similarity with E. coli mutagenic repair protein umuC	1	
PAG1384RP	YAL042w	FUN9	similarity to hypothetical S.pombe protein	1	Syntenie, see PAG1384UP
PAG1384UP	YAL043c	PTA1	pre-tRNA processing protein	1	Syntenie, see PAG1384RP
PAG1385RP	YGR207c	ETF-b	electron-transferring flavoprotein, beta chain	2	Terminator, Syntenie, see PAG1385UP
PAG1385UP	YGR205w		hypothetical protein	1	Terminator, Syntenie, see PAG1385RP
PAG1386RP	YIL093c		hypothetical protein	1	
PAG1386UP	YNL023c		similarity to Drosophila melanogaster shuttle craft protein probable transcription factor, has something to do with prolyl-isomerase?	1	
PAG1387RP	YDR371w		similarity to chitinases	2	
PAG1387UP	YPL150w		probable serine/threonine kinase	3	open frames > 450 nt int -3, >350 nt in +1 and +2
PAG1388RP	YFL013c		hypothetical protein	4	
PAG1388UP	YPR160w	GPH1	glycogen phosphorylase (EC 2.4.1.1)	1	Terminator
PAG1389RP	YDR327w		homology to hypothetical protein YHR080c	1	Syntenie, see PAG1389UP
PAG1389UP	YDR328c	SKP1	kinetochore protein complex CBF3, subunit D	1	Terminator, Syntenie, see

[illegible]

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Strain	Gene	Protein	Phenotype	Chimeric Plasmid
PAG1406RP	YHR007C	ERG11	Cytochrome P450 L1 (14DM) (Lanosterol 14-alpha-demethylase)	1
PAG1406UP	YPL026c	SHA3	Ser/Thr-protein kinase, suppressor of Hta1p mutations that cause aberrant transcription	1
PAG1408RP	MITO-DNA			
PAG1408UP	YBR072w	HSP26	YEAST HEAT SHOCK PROTEIN 26 expressed during entry to stationary phase and induced by osmostress	1
PAG1409RP	YPR154W		YPR153W:unknown function, gene may be spliced; YPR154w:protein with sim to several SH3 domain-containing proteins including myosin ID and IC heavy chains, human growth factor receptor-bound grb2 protein, C.elegans sex muscle abnormal protein 5	1
PAG1409UP	YPR153W YPR156c		member of the major facilitator superfamily (MFS) multidrug resistance proteins family 1	1
PAG1410RP	YOR116c		YOR116c: RPO31: RNA-POLIII largest subunit	1

PAG1410UP	YOR117w:	YOR117w: YTA1: Syntenie: subunit of 26S proteasome complex	1	syntenie
PAG1412RP	YJR153w	and member of the ATPase family	1	
PAG1412UP		sim to polygalacturonases	4	
PAG1413RP	YDR150w	NUM1 nuclear migration	1	syntenie ;should contain the N-term of NUM1
PAG1413UP	YDR152w	unknown function	1	Syntenie
				YDR151c:CTH1:protein of the mammalian growth factor induced proteins, len 325 aa
PAG1414RP	YLR272c	unknown function	1	
PAG1414UP			4	
PAG1415RP	YGR271w	seems to be an RNA-helicase related protein;	1	just one gene on this plasmid
PAG1415UP	YGR271w	has sim to Yer172p; has A(P-loop)	1	UP-SRS covers 1917aa to 1676aa
PAG1416RP	YLR430w	SEN1 positive effector of tRNA-splicing endonuclease, required for intron cleavage for all ten precursor tRNA families	1	codons1790 up to 1971:C-term including terminator should be on this plasmid;syntenie
PAG1416UP	YLR432w	protein highly similar to to PUR5p and inosine-	1	syntenie

5'-monophosphate of human and E.coli, has
sim to YML056c (which was actually hit no 1)

PAG1417RP	YPR183W	Dolichol-phosphate mannosyltransferase	1	syntenie.SMX3:YPR182W: SnRNA associated protein
PAG1417UP	YPR181C	Protein transport protein	1	syntenie
PAG1418RP	YCL060C	protein with sim to SDL1 L-serine dehydratase	1	syntenie
PAG1418UP	YCL061C	unknown function	1	syntenie
PAG1419RP	YLR219W		2	
PAG1419UP			4	
PAG1420RP	YJR107W	sim to acylglycerol lipase	1	
PAG1420UP	YJR014W	YJR014w: unknown function YGR198w: unknown function	1	two genes covered by UP- SRS
PAG1421RP	YNL075W	unknown function	1	
PAG1421UP		only sim with Ser/Thr rich sequences	4	
PAG1422RP	YGL091C	NBP35: nucleotide binding protein (ATP/GTP)	1	syntenie
	YGL092W	nuclear pore protein (nucleoporin)	1	
PAG1422UP	YGL092W		1	Hit no 1 to YGL172w corresponds to NUP48 and was disregarded due to syntenie
PAG1423RP	YDR189W:	SLY1: YDR189w: member of the SEC1-family,		

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5							1	same gene sequenced with RP-SRS	
10							1	syntenie, whole gene on plasmid	
15							1	start of gene, syntenie. Two genes covered by UP-SRS	
20							1	syntenie. Two genes covered by UP-SRS; identical to YLR388w	
25							4		
30							1	protein with weak sim to human bcr (break point cluster) protein	
35								YLR213C : unknown fnction, has WAP-type 'four disulfide core'	
40								domain signature	
45								unknown function	
50								YDL145c: RET1: N-Term has 4 WD-beta transducin repeats.	
55								Coatomer complex alpha chain	
							1	protein with sim to transcription factors, has Zn(2)-Cys(6) fungal-type binuclear cluster domain in the N-terminal	

Accession	Gene	Protein	Function	Notes
PAG1431UP	YMR270C	RRN9	component of the upstream activation factor (UAF)-complex, involved in activation of RNA polymerase I promoter; non-essential	1
PAG1432RP			sim to proline rich sequences	4
PAG1432UP	YDR330W		Small region of similarity near C-terminus to Undulin extracellular matrix glycoprotein	1
PAG1433RP	YBR141c		unknown function	1 involved in maintenance of M dsRNA killer plasmid
PAG1433UP	YBR143c	SUP45	SUP45:recessive omnipotent suppressor, translational release factor eRF1	1 syntenic
PAG1434RP				4
PAG1434UP	YCR065W	HCM1	HCM1 hom to forkhead. Has a transcriptional activation domain of Drosophila fkh homeotic gene	1
PAG1435UP				4
PAG1436RP	YCR093W	CDC39	nuclear protein that negatively affects basal transcription from many promoters, mutants activate the pheromone response pathway at the level of the G-proteins	1 N-term up to aa570 on plasmid
PAG1436UP	YKL215c		protein with sim to Pseudomonas	1

PAG1437RP	YOR224C	RPB8	hydanoinases hyuA-hyuB RPB8: Shared subunit of RNA-POL I, II, III, essential protein with sim to nitrogen fixation proteins	1	syntenie. Two genes with RP-SRS Hit no3 was YPL135w: LPI10: protein with sim to H. influenza nitrogen fixation protein HIU32721-12 which was equally good as hit no 2. Taken this we reach syntenie to PAG1437UP
PAG1437UP	YPL133c	LPI12	protein with sim to transcription factors, has Zn(2)-Cys(6) fungal type binuclear cluster domain in the N-terminal region	1	syntenie
PAG1438RP	YJR132w	NMD5	Nam7p/Upf1p interacting protein. Nam7p: protein involved in decay of mRNA containing nonsense codons	1	
PAG1438UP	YBR079c		protein homologous to surface antigens from trophoblast endothelial activated lymphocytes and P.falciparum	1	
PAG1439RP	YGR276c		unknown function	1	
PAG1440RP	YGL137w	SEC27	Coatomer complex beta chain of secretory pathway vesicles required for transport from ER	1	syntenie. Two genes with RP-SRS. C-term must be

Accession	Protein Name	Function	Notes
PAG1440UP	YGL136c YGL134w	protein with sim to E.coli ftsJ protein unknown function	1 1
PAG1442RP	YLR149c	unknown function	1
PAG1442UP	YLR150w	MPT4: protein with specific affinity for guanine rich quadruplex nucleic acids and multipcopy suppressor of pop2;G4 quadruplex nucleic acid binding protein; multicopy suppressor of tom1 and pop2 mutations	1 1
PAG1443RP	YGL141w	unknown function	2
PAG1443UP	YMR171c	ALD2 Aldehyde dehydrogenase2	1
PAG1444RP	YFR042W	unknown function	1
PAG1444UP	YGL232w	protein with sim to dihydropteroate synthase	1
PAG1445RP			4
PAG1445UP	YOR281c	protein with weak sim to phosducins	1
PAG1446RP	YHR077C	NMD2 protein involved in decay of mRNA containing nonsense codons	1

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PAG1449RP	YPL041c	unknown function	1	syntenie; YPL040c:ISM1:Isoleucyl- tRNA synthetase of mitochondria; YPL042c: SSN3: cyclin dependent Ser/Thr protein kinase of the RNA Pol II holoenzyme
PAG1449UP	YPL043w	nucleolar protein required for ribosome biogenesis	1	syntenie
PAG1450RP	YMR109w	protein with sim to myosin heavy chain homolog YKL 129 (76% id over 1090 AA)	1	syntenie
PAG1450UP	YMR108w	ILV2 Acetolactate synthase, first step in the valine and isoleucine biosynthesis pathway	1	
PAG1452RP	YBR269c	unknown function	1	syntenie
PAG1452UP	YBR268w	MRPL37 Mito protein of the large ribosomal subunit	1	syntenie
	YJL062w	unknown function	1	end of syntenie. Two genes with UP-SRS
PAG1453RP	MITO-DNA		1	
PAG1453UP	MITO-DNA		1	
PAG1454RP	YBR228c	protein with sim to alpha 1,4 glucosidase.	1	syntenie
PAG1454UP	YBR225w	YBR225w-Ybr229c Syntenie. YBR225w, YBR226c both of unknown function. 227c: protein with sim to E.coli ATP-	1	syntenie. Two genes with

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PAG1458UP	YGR099w	protein with sim to mannosyltransferase, has strong sim to Pmt3p; has 6 predicted transmembrane domain unknown function	1	SYNTENIE YJR087w: len 116: unknown; YJR086W: len 107: STE18: Guanine nucleotide binding protein gamma subunit of the pheromone - pathway
PAG1459RP	YJR088c	unknown function	1	syntenie
PAG1459UP	YJR085c	unknown function	1	syntenie
PAG1460RP	YFL049W	sim to NPL6: Nuclear protein localization factor	1	syntenie; YFL048c: EMP47: Golgi membrane protein with C-terminal KXKXX ER-retrieval motif, len 445aa
PAG1460UP	YFL047w	unknown function	1	
PAG1461RP	YIL017c	with sim to adenylate cyclase	1	
PAG1461UP	YBR256c	Riboflavin Synthase, last step of riboflavin synthesis, converts 6,7-dimethyl-8-ribitylumazine to riboflavin	1	
PAG1462RP	MITO-DNA	align		
PAG1462UP	MITO-DNA	align		
PAG1463RP	YDR232w	5-Aminolevulinate synthase, first step in heme biosynthesis pathway (pyridoxal-5'-phosphate is essential cofactor)	1	

PAG1463UP	YBR057c	MUM2	1	protein with sim to ubiquitin C-terminal hydrolase	1	syntenie; YOL118c:unknown, len 102 YOL117w: unknown, len 645
PAG1464RP	YOL119c		1	with weak sim to mammalian monocarboxylate transporter proteins	1	
PAG1464UP	YOL116w	MSN1	2	transcriptional activator for genes regulated through SNF1p, multicopy	2	syntenie
PAG1465RP	YFL046W		1	suppressor of invertase defect in snf1 mutants	1	syntenie
	YFL045c	SEC53	1	unknown function	1	syntenie; end of syntenie
PAG1465UP	YLR078c	BOS1	1	Phosphomannomutase, involved in the synthesis of GDP-mannose and dolichol-phosphate-mannose	1	defined; two genes covered by RP-SRS
PAG1466RP			1	Vesicular transport protein Synaptobrevin (-SNARE) homolog	1	
PAG1466UP	YMR196w		4	involved in ER to Golgi transport	4	complete gene should be on this plasmid
PAG1467RP	YIL144w		1	unknown function	1	syntenie; YIL145c: len 345aa: with sim to E.coli pantoate beta-alanine ligase (pantothenate
			1	protein with sim to myosin heavy chain, possible coiled coil	1	

PAG1467UP	YIL146C	unknown function	1	synthetase)	1	syntenie
PAG1468RP	YER133W	protein SER/THR phosphatase PP1 required for glucose repression,	1			
PAG1468UP	YGL200c	probably functions antagonistically to SNF1p component of the COPII coat of certain ER derived vesicles	1			
PAG1469RP	YHR098c	protein with unknown function	1	Syntenie		
PAG1469UP	YHR097c	unknown function	1	syntenie		
PAG1470RP	YOR172W	protein with sim to transcription factors, has Zn(2)-Cys(6) fungal-type binuclear cluster domain in the N-terminal region	1	identical to 1155,1470,1527,1535,1546,1595		
PAG1470UP	YNR043W	Mevalonate kinase, generates mevalonate-5-phosphate from mevalonate, needed for ARS-CEN plasmid stability (regulation of autonomous replication)	1	identical to 1155,1470,1527,1535,1546,1595		
PAG1471RP	YHR096c	Highly similar to hexose transporters HXT2 and HXT4 (<i>S. cerevisiae</i>)	1	syntenie due to the transporter genes ; continued syntenie with plasmid PAG1469RP/UP		
PAG1471UP	YHR094C	HEX1:Hexokinase II, converts hexoses to	1	chosen due to syntenie, the		

		hexose phosphates in glycolysis and plays a regulatory role in glucose repression	other hits(YJL214W:HXT8;YDR3 45C; YLR081W) had no higher sim.
PAG1472RP	YDR016c	unknown function	1 weak case of syntenie
PAG1472UP	YDR014W	hypothetical protein	2 weak syntenie
PAG1473RP	YMR097c	has ATP/GTP-binding site motif	1 syntenie
PAG1473UP	YMR094W	kinetochore proteinCbf3, subunit c	1 syntenie; YMR096w: len 297aa, slm to YFL059p and YNL333p.YMR095c: len 224aa, slm to YML334p
PAG1474RP	YOR070c	unknown	1
PAG1474UP	YKR081c	unknown	1
PAG1475RP			4
PAG1475UP	YPR190c	RNA-POL III, third largest subunit	1
	YGR049W	Similar to Scm4p (SCM4_YEAST), possible Cdc4p-interacting protein.	1
PAG1476RP	YML091c	Ribonuclease P of MT, generates mature tRNA molecules by cleaving their 5' ends	
PAG1476UP	YML126c	3-hydroxy-3-methylglutaryl coenzyme A synthase, functions in mevalonate synthesis	1 located near TUB3/YML124c

PAG1477RP	YER093c	unknown function	1	syntenie	
	YNL116w	unknown	1		
PAG1477UP	YER091c	Homocysteine methyltransferase, methionine synthase; 5-methyltetrahydropteroyl triglutamate--homocysteinemethyltransferase-	1	syntenie.YER092w:len 125:unknown	
PAG1478RP	YER022w	component of RNA-POLII holoenzyme and Kornberg's mediator (SRB)			
PAG1478UP	YER021w	subcomplex, required for basal transcription	1	syntenie	
PAG1479RP		Component of 26S proteasome complex	1	syntenie	
PAG1479UP	YJR091c	protein that when overexpressed can suppress the hyperstable microtubule phenotype of tub2-150	4		
PAG1480RP	YMR167w	Mismatch repair protein and homolog of E.coli MutL involved in repair of small insertions	1	almost all of the ORF on this plasmid starting from codon 20	
	MLH1		1	syntenie; YMR168c:CBF3b, len 608aa YMR169c:ALD3, len 506aa	
PAG1480UP	YMR170c	Aldehyde dehydrogenase	1	syntenie	
PAG1482RP	YLR214w	Ferric (and cupric) reductase, acts on ferric iron chelates external to the cell	1	syntenie	
PAG1482UP	YLR215c	unknown function	1	syntenie	
PAG1483RP	YDL171c	Glutamate synthase, involved with glutamine synthase in glutamate biosynthesis	1		

PAG1483UP	YNR013c	protein with sim to Pho87p and YJL198p, member of the phosphate permease family, 12 TMD	1	
PAG1484RP	YNR006w	protein involved in vacuolar sorting	1	
PAG1484UP	YPL256c	G1/S-specific cyclin, interacts with CDC28p		
		protein kinase to control the events at START	1	
PAG1485RP		pre-tRNA-leu	1	redundant
PAG1485UP	YGL170c	with sim to phosphoribulokinase precursor (phosphopentokinase)	2	
PAG1486RP	YNL161w	SER/THR protein kinase of unknown function; related protein from N.crassa is required for hyphal elongation, has sim to DBF2, DBF20, YPK1, YPK2, and TPK2, strong sim to cAMP-dependent protein kinases like cot-1 and human myotonic dystrophy kinase MDK	1	
PAG1486UP	YHR142w	unknown function, has 7 potential TMD	1	
PAG1487RP	YOR036w	PEP12:Syntaxin(t-SNARE) involved in Golgi to vacuole transport, len 288aa	1	disturbed syntenie . Two genes covered with RP-SRS
	YDR267C	protein with sim to SEC13 and other proteins with WD-40 repeats; has sim to transcription factors	1	disturbed syntenie
PAG1487UP	YOR038c	HIR2:Histone transcription regulator, required	1	disturbed syntenie

PAG1488RP	YIR007W	YIB7	sim to endoglucanases	1	
PAG1488UP	YOL027C		unknown,sim to YPR125p	1	
PAG1489RP	YBR001c	NTH2	alpha, alpha-trehalase, converts alpha, alpha-trehalose to glucose, promoter contains the stress-regulated CCCCT-elements (STRE)	1	CEN-
			common to stress-induced genes, repressors:		PLASMID,HISTONES:SYN
			glucose		TENIE
PAG1489UP	YBL003c	HTA2	Histone H2a	1	syntenie
PAG1490RP	YMR167w	MLH1	mismatch repair protein and homolog of E.coli MUTL	1	syntenie:YMR170c:ALD5.Y MR169c:ALD3
					YMR168c:CBF3B
PAG1490UP	YMR170c	ALD5	Aldehyde dehydrogenase	1	syntenie
PAG1491RP				4	
PAG1491UP	YNL082w	PMS1	protein required for mismatch repair, homologous to MutL	2	
			unknown function		
PAG1492RP	YKR070w		unknown function	1	two genes covered by RP- SRS
	YOR052c		unknown function	1	two genes covered by RP- SRS
PAG1492UP	YLR292c	SEC72	SEC72:Component of ER protein-translocation complex that includes		

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Gene	Accession	Protein	Function	Count	Notes
PAG1497UP	YPL016w	ADR6	SWI1; Component of the SWI/SNF global transcription activator complex, acts to assist gene-specific activators	1	end of gene covered by RP-SRS
PAG1499RP	YOR021c		unknown function	1	
PAG1499UP	YPR133c		unknown function	1	
PAG1500RP	YOL094c	RFC4	replication factor c	1	
PAG1500UP				4	
PAG1501RP	MITO-DNA		align		
PAG1501UP	MITO-DNA		align		
PAG1502RP	YLR056w	ERG3	ERG3:C-5 sterol desaturase, an iron non-heme oxygen-required enzyme of the ergosterol biosynthesis pathway, ER retention signal	1	syntenic;
PAG1502UP	YPL055c	SPT8	member of the TBP class of SPT proteins that alter transcription start site selection, functionally related to SPT3p and TBP	1	syntenic
PAG1503RP	YNL297c		unknown	1	syntenic
PAG1503UP	YNL294c		unknown, has 6 potential TMD	1	YPL296w: q-ORF, len 104. YPL295w: len 524, unknown
PAG1504RP	MITO-DNA				
PAG1504UP	MITO-DNA				
PAG1505RP	YOR007c		sim to protein phosphatases	1	
PAG1505UP	YML002W		unknown function	1	syntenic. Two genes

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Accession	Gene Name	Protein Name	Function	Notes
PAG1514RP	YNL126w	sim to YJL207p	1	same as PAG1699
PAG1514UP	YHR121w	unknown function	1	same as PAG1699
PAG1515RP	YFR007w	unknown function	1	
PAG1515UP	YGR021w	unknown function	1	
PAG1516RP	YPL072w	LPF12	1	syntenic
PAG1516UP	YPL074w	YTA6	1	syntenic; there is no YPL073
		strong sim to YTA4p, member of the CDC48/PAS1/SEC18(AAA) family of ATPases and probable regulatory subunit of the 26S proteasome complex		
PAG1517RP	YPR190C	RPC82	1	syntenic
	YPR189W	SKI3	1	two genes covered by RP-SRS. Syntenic
		end of gene on this SRS Antiviral protein with tetratricopeptide (TPR) repeats, part of a system to protect cells from dsRNA viruses		
PAG1517UP	YPR189W	SKI3	1	syntenic
PAG1519RP	YBR112c	SSN6	1	
		sequence begins at codon 504		
		general repressor of trans-cription that is brought to target promoters by sequence specific DNA-binding proteins, has tetratricopeptide TPR repeats		
PAG1519UP	YPR070W	unknown function	1	
PAG1520RP	YDL100c	with sim to E.coli arsenical pump-driving ATPase, has amino- transferases class-V pyridoxalphosphate attachment site	1	
		unknown function		
PAG1520UP	YMR157c		1	
PAG1521RP	YDL145c	RET1	1	
		RPC128:RNA-POL III , second largest subunit		

PAG1521UP	YLR213c	unknown:has WAP-type 'four-disulfide core' domain signature	1	
PAG1522RP			4	
PAG1522UP	YPR015c	YPR013c:with sim to mouse REX1 encoded transcription factor, contains C2H2-type zinc finger domain; YPR015c :same type of zinc finger	1	
PAG1523RP	YML006C	unknown function, has prenyl group binding site (CAAX)-motif	1	
PAG1523UP	YDR421W	unknown function, has a (P-loop)	1	syntenie
PAG1524RP	YPR049C	unknown function, has a probable coiled coil	1	syntenie. Two genes covered by UP-SRS
PAG1524UP	YPR048W	protein with sim to NADPH-cytochrome P450 reductase, has a MT energy transfer proteins signature	1	syntenie overthree genes
	YPR047w	also YLR168c:protein possibly involved in intra-mitochondrial sorting	1	
PAG1525RP			4	
PAG1525UP	YOR362c	proteasome subunit Y13	1	two genes covered on UP-SRS
	YAL047c	unknown function	1	two genes covered by UP-SRS
PAG1526RP	YJL111w	component of chaperonin-containing T-complex	1	
PAG1526UP	YNL135c	(FKB1) FK506-binding protein, homolog of human FKBP12, human FKBP12 is functional	1	

PAG1527RP	YOR172w	ERG19	1	identical to 1155,1470,1527,1535,1546 ,1595	in yeast, has peptidyl-prolyl isomerase activity; produces lethal complex with rapamycin with sim to transcription factors
PAG1527UP	YNR043w	ERG19	1	identical to 1155,1470,1527,1535,1546 ,1595	Mevalonate diphosphate-decarboxylase, functions in the polyisoprene biosynthesis pathway
PAG1528RP	YLR430w	SEN1	1	one gene on plasmid; covering codons 1356 to1588	positive effector of tRNA-splicing endonuclease, required for intron cleavage for all ten precursor tRNA families
PAG1528UP	YLR430w	SEN1	1	one gene on plasmid covering codons 132 to 365	
PAG1529RP	YLR187w		1	syntenie	unknown functionhas strong sim to YNL278w
PAG1529UP	YLR188w	MDL1	1	syntenie	ATP-binding cassette (ABC)-transporter family member, equivalent to a "half-molecule" ABC protein plus an ATP-binding domain, has sim to mammalian multidrug resistance protein and peptide transporter TAP
PAG1530RP	YGR277c		1	syntenie, same as PAG1538	sim to CTR1 (cholin permease)=HNM1; has multiple membrane spanning domains
PAG1530UP	YGR279C		1	syntenie.YGR278w:unknow n, same as PAG1538	unknown function
PAG1531RP	YCL057w	PRD1	1		Proteinase yscD, saccharolysin, homologous to

PAG1531UP			4	rat metallo- endopeptidase, contains zinc metallopeptidase motif HEXXH	
PAG1532RP	YIL144w		1	protein with sim to myosin heavy chain, possibly coiled-coil	syntenic
PAG1532UP	YIL145c		1	sim to E.coli PANTOATE-BETA-ALANINE LIGASE	syntenic
PAG1533RP	YJR052w	RAD7	1	nucleotide excision repair protein involved in G2 repair of inactive genes	
PAG1533UP	YPR194c		2	unknown, has sim to S.pombe C-terminal region of ips4	
PAG1534RP	YOR165w		1	unknown function	syntenic
PAG1534UP	YOR163w		1	unknown function	syntenic.YOR164c:unknown n function
PAG1535RP	YOR172w		1	sim to ts factor	identical to 1155,1470,1527,1535,1546,1595
PAG1535UP	YNR043w	ERG19	1		identical to 1155,1470,1527,1535,1546,1595
PAG1536RP	YJR085c		1	unknown function	
PAG1536UP	YPR040w		1	unknown function, has sim to a C.elegans protein	
PAG1537RP	YER164w			with sim to mouse chromodomain-helicase-	

Accession	Gene Name	Protein Name	Function	Similarity	Notes
PAG1537UP	YGR277c	YGR277c	DNA-binding protein, contains putative Myb DNA-binding domain	1	
PAG1538RP	YGR277c	YGR277c	protein with sim to CTR1:copper transport protein, required for high-affinity uptake of copper (=HNM1)	4	YGR278w: unknown, len 577aa.syntenie same as PAG1530
PAG1538UP	YGR279c	YGR279c	unknown, but related to YMR305p	1	syntenie.same as PAG1530
PAG1540RP	YML061C	PIF1	single-stranded DNA-dependent ATPase and 5'-3' DNA helicase required for maintenance and repair of MT-DNA, also functions in nucleus to regulate telomere length	1	syntenie
PAG1540UP	YML060w	OGG1	DNA glycosylase, excises 7,8-dihydro-8-oxoguanine and Fapy residues from DNA	1	syntenie
PAG1541RP	YDR035w	ARO3	2-dehydro-3-deoxyphosphoepoxide aldolase, phenylalanine inhibited	1	
PAG1541UP	tRNA-Asp	tRNA-Asp	closest to YDR035w is a copy at YDR058	1	
PAG1542RP	YIR019c	STA1	Glucosyltransferase (alpha-1,4-glucan glucosidase), extracellular enzyme	2	weak similarity based on Ser/thr residues
PAG1542UP	YMR241W	YMR241W	protein with sim to MT-carrier family proteins, has prokaryotic	1	
PAG1544RP	YDR316w	YDR316w	membrane lipoprotein lipid attachment site unknown function; Weak similarity to E. coli hypothetical 28.1 kD protein in udp-fah region	1	

PAG1544UP PAG1545RP PAG1545UP PAG1546RP	YHR070W YLR043c YOR172w	TRX1	1 4 1 1	ot. accession number P27851) and Lactococcus lactis hypothe- tical protein 2 (pip 3'region) (PIRaccession number B48653) unknown function Thioredoxin 1:required for vacuolar inheritance protein with sim to transcription factors	1 1 1 1	identical to 1155,1470,1527,1535,1546 ,1595 identical to 1155,1470,1527,1535,1546 ,1595
PAG1546UP	YNR043w	ERG19	1	Mevalonate diphosphate decarboxylase, functions in polyisoprene biosynthesis	1	identical to 1155,1470,1527,1535,1546 ,1595
PAG1547RP	YDR371w			with sim to chitinases, has chitinases family 18 active site signature, has sim to Aphanocladium album chitinase	1	
PAG1547UP	YOR122c	PFY1	1	Profilin, can act to prevent actin polymerization and to complex with monomeric actin; C-terminus is implicated in actin binding	1	two genes covered by UP- SRS. Syntenie
PAG1548RP	YOR123c	LEO1	1	unknown function, extremely hydrophilic	1	syntenie
	YER056c	FCY2	1	Cytosine/purine permease	1	syntenie;between 56c and 62c are 56cA(L34, len 121), 57c(unknown len 129), 58w (PET11, len87aa), 59w (sim

Accession	Gene	Protein	Function	Notes	Redundant	Other
PAG1548UP	YER062c	HOR2	DL-glycerol phosphatase, strong sim to GPP1	to PHO80 and other cyclins, len420aa), 60w	1	
PAG1549RP	YNL162w	RPL41A		(FCYY, len 528aa), 60wA	1	
PAG1549UP	YNL163c	EF4	translation elongation factor EF4	(FCYX, len530aa),	1	
PAG1550RP	YLR440C		unknown function, has carbamoyl-phosphate synthase subdomain	61c(CEM1, len 442aa);	1	
PAG1550UP	YML060w	OGG1	signatures	syntenie	1	redundant clone?
PAG1551RP			DNA-glycosylase	syntenie	1	redundant?
PAG1551UP	YLR095c		unknown function		4	
PAG1552RP	YDL008w		unknown function		1	end of syntenie; two genes covered from RP-SRS
PAG1552UP	YBR011c	IPP1	Inorganic pyrophosphatase, cytoplasmic	syntenie	1	
	YBR009c	HHF1	Histone H4	syntenie; YBR010w=HHT1	1	which is Histone H3
PAG1554RP	YGR277c			redundant? Syntenie	1	
PAG1554UP	YGR279c			syntenie, redundant?	1	
PAG1555RP	YDL080w		unknown function	syntenie; redundant?	1	
PAG1555UP	YDL081c	RPS29B	YEAST 40S RIBOSOMAL PROTEIN YS29B.	syntenie; redundant?	1	
PAG1558RP	YPR070w		unknown	syntenie	1	

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	protein		1	Syntenie; YGL121c:unknown
PAG1563UP	Nuclear poly(A)-binding protein, required for proper polyadenylation of pre-mRNA and for mRNA export	NAB2	1	syntenie
PAG1565RP	YJR156c:protein with strong sim to THI5 and YNL332wYDL244w:has99,7% identity to THI5;YNL332w:THI5: YFL058w: biosynthetic enzyme involved in pyrimidine biosynthesis pathway above the hydroxymethyl-pyrimidine precursor leading to the thiamine moiety. S.pombe homolog nmt1	YJR156c	1	
PAG1565UP	protein with sim to acylglycerol lipase	YJR107w	1	
PAG1566RP	C-8 sterol isomerase, enzyme of the ergosterol biosynthesis pathway: null mutant is lethal in the absence of exogenous ergosterol	ERG2	1	syntenie
PAG1566UP	Phosphofructokinase beta subunit, converts fructose -6-phosphat into fructose -1-6-bisphosphat: key regulatory step in glycolysis	PFK2	1	syntenie; YMR203w: TOM40-MT integral membrane protein involved in protein import, forms the outer membrane import-channel.YMr204c: unknown, len 420
PAG1568RP	subunit of eIF3 initiation complex, required for	PRT1		

				initiation of protein synthesis, has an RNA recognition domain	1	syntenie
PAG1568up	YOR362c	PRE10		Proteasome subunit YC1	1	syntenie
PAG1569RP	YDR238c	SEC26		coatmer complex beta chain (beta-COP) of secretory pathway		
				vesicles,required for transport from ER to Golgi	1	syntenie
PAG1569UP	YDR236c			unknown	1	syntenie
PAG1570RP	YKL054c			unknown function, glutamic acid rich	1	
PAG1570UP	YOL048c			unknown function	1	
PAG1571RP	YLR077w			unknown, has regulator of chromosome condensation signature		
				(RCC1)	1	syntenie
PAG1571UP	YLR075w	GRC5		ribosomal protein of the 60S subunit (rat L10), len 221	1	syntenie;YLR076c:unknown .len 140 overlapping ORF's anyway
PAG1572RP	MITO-DNA					
PAG1572UP	MITO-DNA					
PAG1573RP	YJR066w	TOR1		Phosphatidylinositol kinase (PI kinase) homolog involved in cell growth and sensitivity to the Immunosuppressant rapamycin, kinase domain is essentila for G1 cell cycle functions; depletion causes starvation response but not through RAS/cAMP pathway	1	hit no 1 (YKL203c: TOR2) neglected due to syntenie
PAG1573UP	YJR065c	ACT4		actin related protein , essential, len 449	1	syntenie

PAG1574RP	YML070w	(=ACT3) unknown function, has sim to dihydroxyacetone kinase	1	syntenie
PAG1574UP	YML069w	YML069w:has sim to HMG1 proteins	1	syntenie
PAG1575RP	YOR009w	weak sim based on Ser-residues	2	
PAG1575UP	YNR044w	weak sim based on Ser-residues	2	
PAG1576RP	YML125c	protein with sim to NADH-cytochrome b5 reductase	1	syntenie, same as PAG1688
PAG1576UP	YML124c	TUB1:YML085c: tubulin alpha-1 chain, required for mitosis and karyogamyTUB3:YML124c: tubulin alpha-3 chain, non-essential, null mutant has poor spore viability; TUB1 and TUB3 each have an intron in CODON 9	1	syntenie.C-term of TUB3 on plasmid
PAG1577RP	YJR117w	protein with weak sim to tetracycline resistance proteins	1	relaxed syntenie
PAG1577UP	YJR106w	unknown function, with sim to a C.elegans protein	1	relaxed syntenie
PAG1578RP	YDL220c	protein proposed to regulate generation of single-stranded tails at telomeres; required for passage through G2/M; required in meiosis after DNA replication but before chromosome synapsis or recombination mutants are arrested At the RAD9 checkpoint;	1	
PAG1578UP	YNL192w	Chitin synthase I, has a repair function during	1	

PAG1579RP	YMR160W		cell separation; major form of chitin synthase	1	
PAG1579UP	YMR205c	PFK2	representing 90% of activity, null mutants	1	
PAG1580RP	YLR368W		resistant to calcofluor, and with lower mating	1	syntenie
PAG1580UP	YLR370c		and sporulation efficiency	1	syntenie, two genes with UP-SRS
	YLR369w		unknown function	1	syntenie
PAG1581RP	MITO-DNA		see 1566UP		
PAG1581UP	MITO-DNA		unknown function		
PAG1582RP	YLL023c		unknown function		
			protein with strong sim to HSP	1	
			unknown function	1	syntenie; two genes on RP-SRS
	YLL024c	SSA2	HSP70 family, cytoplasmic	1	syntenie
PAG1582UP	YLR314c	CDC3	Septin:Component of 10 nm filaments of mother-bud neck	1	N-Term up to codon 240 on the plasmid
PAG1583RP	YCL039w		unknown, probably a member of the beta-transducin (WD-40)		
			repeat family	1	syntenie
PAG1583UP	YCL040w	GLK1	Glucokinase, specific for aldohexoses, sim to YDR516p	1	syntenie
PAG1584RP	YKL062w	MSN4	Zinc-finger transcriptional activator for genes regulated through Snf1p		

				homologous to MSN2	1	
	PAG1584UP	YMR035w	IMP2	Inner membrane protease of MT, acts in complex with Imp1p but has a different substrate specificity for removal of signal peptidase	1	
	PAG1585RP	YGL162w	SUT1	protein involved in sterol uptake; expressed only in anaerobic conditions	1	syntenie
	PAG1585UP	YGL163c	RAD54	DNA-dependent ATPase of the Snf2p family, required for recombination and repair of X-ray damage; required for an early step of mating-type switching; mutant cells die if mating-type switching is attempted, mutants are unable to repair double-strand breaks	1	syntenie
	PAG1586RP	tRNA-Val			1	
	PAG1586UP	YDR420w	HKR1	Hansenula mrakii K9 killer toxin-resistance protein	2	
	PAG1587RP	YAL036c	FUN11	YAL036c:unknown, has GTP-binding motif	1	
	PAG1587UP	YOR346w	REV1	protein required for mutagenesis by physical and chemical agents, has some sim with E.coli mutagenic repair protein umuC	1	
	PAG1588RP				4	
	PAG1589UP				4	
	PAG1590RP		MITO-DNA			

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Accession	Gene	Protein	Function	Length
PAG1596RP	YNL294c	Syntenie	YNL294c: unknown, 6 potential TMD	1595
PAG1596UP	YNL297c	Syntenie	YNL297c: unknown, 6 potential TMD	104aa questionable ORF
PAG1597RP				YNL295w: unknown, len 524aa
PAG1597UP				
PAG1598RP	MITO-DNA			
PAG1598UP	MITO-DNA			
PAG1600RP	YEL023c		unknown function	
PAG1600UP	YJR035w	RAD26	putative helicase homologous to Cockayne syndrome B gene ERCC-6, involved in transcription-coupled repair, has putative NLS	
PAG1601RP	YBR041w		protein of unknown function, probable ATP-binding protein, with 4 potential TMD	
PAG1601UP	YBR043c		member of major facilitator superfamily (MFS), multidrug-resistance	
PAG1602RP	YPL059W		proteins family 1	
			protein with sim to Legionella pneumophila LPNTSAA_1	
			glutaredoxin-like protein	

PAG1602UP	YBR162c	protein with sim to AGA1	1	1	
PAG1603RP	YJL190c	ribosomal protein	1	1	syntenie. Same as PAG1670
PAG1603UP	YJL191w	ribosomal protein	1	1	same as PAG1670
PAG1604RP	YJL069c	unknown function	1	1	same as PAG1670
PAG1604UP	YGL123w	ribosomal protein, E.coli S5, rat S2	1	1	
	YDR172w	=SUP2; omnipotent suppressor with sim to EF1-alpha, protein responsible for the (psi+) phenotype probably through a prion mechanism, required for G1/S-transition; has EF-TU homology domain, C-terminal 2/3 homologous to EF-1alpha, N-terminal domain has tandem oligopeptide repeats and has structural sim to mammalian prion protein	1	1	
PAG1605RP	YDR170c	data on length vary, but it should be larger than 1800aa	1	1	this clone contains the N- terminus down to codon 432 syntenie with upstream genes
PAG1605UP	YDR172w	=SUP35;	1	1	syntenie YDR171w:HSP42
PAG1606RP			4	4	
PAG1606UP	YNL254c	unknown function	1	1	
PAG1607RP	YBR214w	protein with sim to moc1 protein of S.pombe	1	1	
PAG1607UP			4	4	
PAG1608RP	YNL287w	Coatomer complex gamma chain (gamma-			
	SEC21				

Gene	Accession	Protein Name	Function	Notes
PAG1608UP	YBR025c	unknown, probable purine nucleotide-binding protein	essential	1
PAG1609RP	YJL041w	TFS1:suppressor of CDC25: has affect on the phosphorylation state of two proteins whose phosphorylation varies with the cell cycle		1
PAG1609UP				4
PAG1610RP	YNL267w	PIK1:Phosphatidylinositol4-kinase, generates PtdIns4-P; overproduction causes increased sensitivity to growth arrest by alpha factor		1
PAG1610UP	YNL268w	Lysine specific permease		1
PAG1611RP	YMR061w	component of pre-mRNA 3'-end processing factor involved in poly(A)-site choice		1
PAG1611UP	YKL075c	protein with sim to HEX2, histidine-rich protein		1
PAG1612RP	YJL004c	protein of unknown function, probable membrane protein		1
PAG1613UP	YJR019c	unknown function		1

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PAG1618RP			4	
PAG1619RP	YOR085w	OST3	1	syntenie
				member of a complex of 6 ER proteins that transfer core oligosaccharide from dolichol carrier to Asn-X-Ser/Thr motif
PAG1619UP	YOR86c		1	syntenie
PAG1620RP	YKL217w	JEN1	1	CHIMERIC-PLASMID
				unknown function
				protein with sim to E.coli osmoregulatory proP
				proline/betaine transporter and KgtP alpha-ketoglutarate transporter, member of the major facilitator superfamily
PAG1620UP	MITO-DNA			CHIMERIC-PLASMID
PAG1622RP	MITO-DNA			
PAG1622UP	MITO-DNA			
PAG1623RP	YDR150w	NUM1	1	syntenie
PAG1623UP	YDR152w		1	syntenie,
				YDR151c:CTH1:1en 325: protein of the inducible
				CCCH zinc-finger family
PAG1624RP	YIL093c		1	
PAG1624UP	YNL023c			unknown function
				protein with sim to human DNA binding protein
				tenascin and
				Drosophila shuttle craft protein
PAG1625RP	YLR180w	SAM1	1	high degree of identity to
				S-adenosylmethionine synthetase 1;repressors:

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PAG1628RP	YKR092c	SRP40	suppressor of mutant AC40 subunit of RNA- POL I and III, overproduction is lethal	2	
PAG1629RP	YNL257c	SIP3	interacts with SNF1, contains PH-domain	1	
PAG1629UP	YGR255c		protein with sim to E.coli ubiH protein	1	
PAG1630RP	YLR424w		protein with sim to retrovirus-related proteases	2	
PAG1630UP				4	
PAG1631RP	MITO-DNA		align		
PAG1631UP	MITO-DNA		align		
PAG1632RP	YNL068c	FKH2	Homolog of Drosophila forkhead protein	1	
PAG1632UP				4	
PAG1633RP	MITO-DNA				
PAG1633UP	MITO-DNA				
PAG1634RP	YBL085w	BOI1	BEM1p-binding protein, has a SH3 domain and a PH domain; involved in bud formation redundant with BOI2p	1	
PAG1634UP				4	
PAG1635RP	YDL052c	SLC1	Fatty acyltransferase	1	two genes covered by RP- SRS,same as PAG1664
	YLR377c	FBP1	Fructose-1,6-bisphosphatase	1	two genes covered by RP- SRS,same as PAG1664
PAG1635UP	YDL054c		putative transmembrane protein	1	same as PAG1664
PAG1636RP	YLL055w		protein with sim to DAL5 and members of the allantoate permease		

PAG1636UP	YKL215c	1	family of the major facilitator superfamily (MFS)	1	
		1	protein with sim to Pseudomonas		
PAG1637RP	YER157w	2	hydantoinases hyuA-hyuB		syntenic, same as
			unknown function		PAG1060
PAG1637UP	YER155c	1	bud-emergence protein		codons 403 to 218
					including N-
					term+promoter(?)syntenic
					YER156c:unknown
					function, same as PAG1060
PAG1638RP	YCL037c	1	with sim to SLF1, has a motif in common with	1	syntenic.YCL038c:unknown
			conserved sequence in LHP1 but does not		function, len 528aa37c:is
			contain a RNA recognition motif		SRO9
PAG1638UP	YCL039w	1	probably a member of the WD-40 family	1	syntenic
PAG1639RP	YKL046c	1	unknown function, has 2 predicted TMDs		
PAG1639UP	YMR020w	1	sim to corticosteroid-binding protein	1	
		4			
PAG1640RP		1			
PAG1640UP	YLR196w	1	member of WD-40 repeat family		
PAG1642RP	YKR023w	1	unknown function	1	syntenic
PAG1642UP	YKR024c	1	unknown function, probable purine nucleotide-	1	syntenic
			binding protein		
			protein that amplifies the magnitude of		
			transcriptional regulation		
PAG1643RP	YMR179w	1	at various loci	1	syntenic; YMR180c:len

PAG1643UP	YMR181c	unknown function	1	syntenic	320, unknown
PAG1644RP			4		
PAG1645RP	YDR089w	unknown function ; with leucine zipper pattern	1	syntenic, two genes covered by RP-SRS ending syntenic	
	YER161c	HMG-like chromatin protein that interacts with SNF1p through a conserved domain	1	syntenic, two genes covered by RP-SRS ending syntenic	
PAG1645UP	SLU7	pre-mRNA splicing factor affecting 3' splice site choice, required only for the second catalytic step	1	syntenic	
PAG1646RP	NDI1	NADH-ubiquinone oxidoreductase	1		
PAG1646UP	ERG9	Squalene synthase (farnesyl-diphosphate farnesyltransferase), branch point for isoprenoid biosynthesis pathway	1		
PAG1647RP	GLO1	sim to glyoxalases	1		
PAG1647UP	PRP2	RNA-dependent ATPase of DEAD box family required for first catalytic event of pre-mRNA splicing	1		
			4		
PAG1648RP					
PAG1648UP	FAS3	first and rate limiting step in fatty acid biosynthesis pathway	1		

PAG1649RP	YHR206W	SKN7	1	Transcription factor with homology to response regulator proteins of bacterial two-component systems and DNA-binding region of Hsf1p, may be involved in the response to oxidative stress. May act in parallel to PKC1-MAP kinase pathway to regulate growth at the cell surface, but is not in the same pathway as PKC1, null mutant w/O phenotype, high level of overexpression is lethal: Has a potential coiled-coil domain	1	syntene; two genes covered by UP-SRS
PAG1649UP	YER183C		1	unknown function	1	syntene; two genes covered by UP-SRS
	YER182C		1	unknown, but essential	1	syntene; two genes covered by UP-SRS
PAG1650RP	YOR317W	FAA1	1	:long-chain fatty acid CoA ligase (fatty acid activator 1), can incorporate exogenous myristate into myristoyl-CoA and other fatty acids to the CoA derivatives	1	
PAG1650UP	YMR100W		1	unknown function	1	
PAG1651RP	YNL121C	TOM70		MT specialized import receptor of the outer membrane, has tetrapeptide repeats	1	syntene
PAG1651UP	YNL123W		1	unknown function	1	syntene; two genes covered by UP-SRS

	YNL122c	unknown function	1	syntenie; two genes covered by UP-SRS
PAG1652RP	YOL095c	sim to DNA helicase pcrA	1	syntenie
PAG1652UP	YOL094c	Replication Factor C , 37kD subunit	1	syntenie
PAG1653RP	YHR047c	see ATP8,ORC6;Highly similar to aminopeptidase yscII (<i>S. cerevisiae</i>), AMPE_MOUSE, and several other zinc metalloproteases	1	
PAG1653UP	YHR074w	Weak similarity to spore outgrowth factor B (sporulation protein OUTB, <i>B. subtilis</i>)	1	
PAG1654RP	YMR196w	unknown function	1	very end of the gene
PAG1654UP	YMR196w	unknown function	1	very start of gene, w/o promoter
PAG1655RP	YNL202w	sporulation specific protein, probably peroxisomal, ends in SKL*	1	syntenie
PAG1655UP	YNL200c	contains a possible signal-peptide, predicted to be extracellular	1	syntenie; two genes covered by UP-SRS
	YNL201c	protein involved in the regulation of carbon metabolism	1	syntenie; two genes covered by UP-SRS
PAG1656RP	YHR201c	degrades polyphosphate, converting ADP to ATP	1	
PAG1656UP	YJR141w	unknown protein	1	
PAG1657RP	YJL130c	multifunctional pyrimidine biosynthesis protein	1	from codon 1781 to the C-terminus
	URA2			

PAG1657UP	YKR051W	unknown protein	1	
PAG1659RP	YBR038W	Chitin Synthase II, responsible for primary septum disk; Mutants resistant to calcofluor white, 8 TMD, mutant is unable to grow on non-fermentable c-sources Membrane location is altered in an rho0 strain unknown function; has 12 TMD	1	syntenie
PAG1659UP	YBR037C	SCO1		
PAG1660RP	YBL004W		1	syntenie
PAG1660UP	YBL004W		1	codons 800-1033
PAG1664RP	YDL052C	SLC1	1	codons 2167-1951; C-terminus missing
PAG1664UP	YDL054C		1	syntenie, same as PAG1635
PAG1666RP	MITO-DNA		1	syntenie; same as PAG1635
PAG1666UP	MITO-DNA		1	
PAG1667RP	YMR061W	RNA14 component of pre-mRNA 3' end processing factor involved in poly(A) site choice, interacts with Rna15p, Fip1p, and Pap1p	1	same as PAG1611
PAG1667UP	YKL075C	unknown protein	1	same as PAG1611
PAG1669RP	YLR277C	BRR5 protein required for processing of mRNA 3' end	1	syntenie
PAG1669UP	YLR281C	unknown, however there are other overlapping ORF's	1	syntenie; YLR278c:protein with sim to transcription

							5 10 15 20 25 30 35 40 45 50 55	factors, has Zn(2)- Cys(6) fungal- type binuclear cluster domain in the N- terminal region, len 1341aa syntenie; two genes covered by RP-SRS, same as PAG1603 1 syntenie, same as PAG1603 1 same as PAG1603 2 codons 442 to 655 promoter and terminator missing; regulatable promoter? 4 splP24197YIGID_ECOLI HYPOTHETICAL 28.3 KD PROTEIN IN T...-3 73 1.2e-10 5 1 syntenie 1 syntenie; two genes
PAG1670RP	YJL191W	CRY2	ribosomal protein rp59 (E.coli S11, rat and human S14)	1				
	YJL190c	RPS24A	RPS24A:ribosomal protein RPS24 (E.coli S8, mammalian S24)	1				
PAG1670UP	YJL069c		unknown protein	1				
PAG1671RP	YBR112c	SSN6	has 10 TPR repeats (TPR-Tetratricopeptide)	2				
PAG1671UP	YML042w	CAT2	Carnitine-o-acetyltransferase, peroxisomal and mitochondrial, not required for growth on fatty acids, Catalytic activity: undetected in cells grown on glucose, increased on glycerol or acetate, very high on oleate	1				
PAG1672RP								
PAG1672UP	YDL203c		unknown, has weak sim to SKT5	1				
PAG1673RP	YDL104c	QRI7	sim to E.coli orfX gene; may be in a cold spot for recombination	1				
	YDL105w	QRI2	unknown	1				

PAG1673UP	YMR166c	sim to members of the MCF MT carrier protein family	1	covered by RP-SRS not in syntenie to RP-SRS
PAG1674RP	YPL072w	unknown function	1	syntenie
PAG1674UP	YPL075w	required for expression of glycolytic genes. binds to DNA with high affinity but low specificity , motif CTTCC, contains a leucine zipper that is necessary and sufficient for homodimerization	1	syntenie; YPL074w:YTA6:CDC48-ATPase- family
PAG1675RP	YMR259C	unknown, has sim to YGR273p	1	
PAG1675UP	YML100w	alternate third subunit of the trehalose-6-phosphate synthase complex, probably regulatory	1	
PAG1676RP	YLR429W	unknown, with WD-40 repeats	1	syntenie
PAG1676UP	YLR426w	rotein with sim to FOX2p, E.coli 3-oxoacyl-reductase and insect-type alcohol dehydrogenase/ribitol dehydrogenase family	1	syntenie, YLR427w:len 670aa,unknown function
PAG1677RP	YNL116w	unknown function	1	
PAG1677UP	YNR044w	sim relies on Ser-residues	2	
PAG1678RP	YLR347c	karyopherin-beta, acts to target proteins with nuclear localization signals (NLS) to the nuclear pore complex	1	syntenie; YLR345w : len 509: sim to rat fructose-2,6-bisphosphatase;YLR346c :len 101: unknown

PAG1678UP	YLR344w	RPL33A	1	syntenie
PAG1680RP	YLR107w	Similar to <i>S. pombe</i> hypothetical protein C22G7.04p	1	syntenie; YLR108c: unknown, len485aa; YLR109w: sim to <i>C. boldinii</i> peroxisomal membrane proteins A and B complete gene
PAG1680UP	YLR110c	cell wall protein, probably highly O-glycosylated, null mutant fails to flocculate; repeat domains account for 70% of the protein FLO1 homolog	1	
PAG1681RP	YER172C	BRR2	1	syntenie
PAG1681UP	YER171w	RAD3	1	syntenie
PAG1682RP	YKL214C	transcription initiation factor TFIIB(factor b) and the nucleotide excision repairosome	1	syntenie; two genes covered byRP-SRS
PAG1682UP	YKL212w	SAC1	1	syntenie
PAG1683RP	YDL077c	unknown protein	1	start of gene to codon 164,

PAG1683UP	YDL077c	1	same as PAG1133 very end of gene; maybe including terminator, same as PAG1133
PAG1684RP	YLR425W	1	syntenie
PAG1684UP	YLR424w	1	syntenie; somehow disturbed by overlapping hitno 1
PAG1685RP	YNL330c	1	Transcription modifier required for full repression or full activation of many genes including PHO5, STE6, SPO13, HO, TRK2, and TY2
PAG1686RP	YLR129w	1	DOM34p interacting protein, with WD-40 repeats.
PAG1687RP		4	
PAG1687UP	YOR240w	1	unknown function
PAG1688RP	YML125c	1	sim to NADH-cytochrome b5 reductase
PAG1688UP	YML124c	1	TUB3 rather than TUB1 due to syntenie
PAG1689RP	YKR059w	1	Translation initiation factor 4a eIF4A of the DEAD-box family
PAG1689UP	YJL140w	1	RNA-POLII, fourth largest subunit
	YJL139c	1	Mannosyltransferase of KRE2/KTR1/YUR1

Accession	Gene Name	Protein Name	Family	Overlap	Notes
PAG1690RP	YDL033c	sim to H. influenza protein HI0174	family	1	overlapping genes
PAG1690UP	YDL035c	unknown function; putative transmembrane protein		1	syntenie
				1	syntenie; YDL034w: unknown, len 114;
				1	overlapping with YDL035c
PAG1691RP	YHR023w	Myosin heavy chain (myosin II), involved in septation and cell wall organization; null mutant has abnormal nuclear migration and cytokinesis, has delocalized chitin deposition, are defective in cell division, are osmosensitive,, and have an altered budding pattern, mutants show wild-type movement of actin cortical patches. Molecule is a dimer with two heads and a long coiled coil tail	MYO1	1	N-Term down to codon 198
PAG1691UP				4	
PAG1692RP	MITO-DNA			1	syntenie
PAG1692UP	MITO-DNA			1	syntenie
PAG1694RP	YBR280c	sim to SRM1/PRP20		1	
PAG1694UP	YBR281c	unknown, with WD40 repeats		1	
PAG1695RP	YPR194C	unknown function		1	
PAG1695UP	YFL010c	unknown function		1	
PAG1696RP	YCL036w	unknown function		1	syntenie. Hit no1: YDR514C:unknown has sim to YCL036w

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Table 2:

Ashbya gossypii sequences with (>100 codons) ORF's that show no homology to *S. cerevisiae*

5	PAG1002RP	open frame > 450 nt in -2
	PAG1005RP	open frame > 350 nt in -1
	PAG1005UP	open frame 300 nt in -3
	PAG1006RP	open frame > 450 nt in -3
	PAG1006UP	open frame > 350 nt in -1
10	PAG1010I1	open frame 350 nt in +3 and -2
	PAG1010I2	open frames whole length in +3 and -3
	PAG1018UP	open frames whole length in +1 and -3
	PAG1019UP	open frame whole length in +1
15	PAG1022RP	open frame whole length in -1
	PAG1022UP	open frame > 350 in +1
	PAG1024UP	open frames whole length in +3 and -2
	PAG1033UP	open frame s whole length in -2
	PAG1035I1	open frame 300 nt in -3
20	PAG1035I2	open frame > 350 nt in -1
	PAG1035RP	open frames > 350 nt in -1
	PAG1036RP	open frames 350 nt in -3, 300 nt in +2
	PAG1038RP	open frame whole length in -3
25	PAG1042RP	open frame > 300 nt in -2
	PAG1042UP	open frame 300 nt in +1
	PAG1046UP	open frame 350 nt in +1
	PAG1053RP	open frame whole length in -1
	PAG1054RP	open frame whole lenght in -2, 350 nt in +1
30	PAG1054UP	open frames 350 nt in +3, +2, and -2
	PAG1055UP	open frames 350nt in +3 and -2
	PAG1057UP	open frame 400 nt in +3
	PAG1062UP	open frame 300 nt in -1, many stops in other frames
35	PAG1071CRP	open frames> 350 nt in +2 and -3, possible chimeric plasmid, hybridizes to A.g. chr. II and III
	PAG1071CUP	open frame whole length in -3, possible chimeric plasmid, hybridizes to A.g. chr. II and III
	PAG1081RP	open frame whole length in +3
	PAG1083RP	open frame whole lenght in -2, many stops in other frames
	PAG1214RP	open frame whole length in -2
40	PAG1216RP	open frame >300 nt in +2
	PAG1220RP	open frame 350 nt in +2 (S-rich)
	PAG1223UP	open frame whole length in -2, open frames > 350 nt in +2 and -3
	PAG1224UP	open frame > 300 nt in -1
45	PAG1225UP	open frames > 500 nt in +2 (S-rich) and >450 nt in -1
	PAG1226RP	open frame whole length in +2
	PAG1231RP	open frame > 350 nt in -1
	PAG1231UP	open frames > 400 nt in +1
	PAG1233RP	open frames whole length in +2 and nearly whole length in -3
50	PAG1245UP	open frames > 400 nt in -2 and > 300 nt in +1
	PAG1247RP	open frames whole length in -3,open frames > 400 in +3 and +2
	PAG1251RP	open frames > 450 nt in +1 and > 400 nt in -3
	PAG1253RP	open frame > 500 nt in +2
55	PAG1263UP	open frame > 400 nt in -1
	PAG1265RP	open frame 450 nt in -1
	PAG1266UP	open frame > 400 nt in
	PAG1267UP	open frame nearly whole length in +1

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Table 2: (continued)

Ashbya gossypii sequences with (>100 codons) ORF's that show no homology to <i>S. cerevisiae</i>	
5	PAG1272UP open frame whole length in +3
	PAG1275RP open frame whole length in -3
	PAG1277UP open frame > 500 nt in -1
	PAG1280RP open frame whole length in -2, two separated short blocks with high homology -> funct. domain?
	PAG1286RP open frame > 400 nt in -3,
10	PAG1286UP open frames > 500 nt in +1 and -3
	PAG1293UP open frames 300 nt in +2 and > 400 nt in +1
	PAG1294RP open frame > 300 nt in +3
	PAG1299RP open frame > 350 nt in -1
	PAG1300RP open frames > 350 nt in +1 and -2
15	PAG1303RP open frame > 350 nt in +2 or ending frame > 250 nt in -1
	PAG1303UP open frame whole length in -2
	PAG1305RP open frame whole length in -2
	PAG1306UP open frame whole length in +2
	PAG1311UP open frame 500 nt in -2
20	PAG1312UP open frame whole length in +1
	PAG1314RP open frame > 350 nt in -3
	PAG1318RP open frames > 300 nt in -2
	PAG1318UP open frames > 450 nt in -3 and > 600 nt in +2
25	PAG1331UP open frames > 400 nt in +2> 350 nt in +3 and > 350 nt in +3
	PAG1332RP open frame nearly whole length in +1
	PAG1334RP open frame whole length in -2 and +2
	PAG1335RP open frames whole length in -2 and 300 nt in +3
	PAG1356RP open frame whole length in -3
30	PAG1357RP open frame whole length in -2
	PAG1362UP open frames > 350 nt in +3 and > 300 nt in -3
	PAG1363UP open frame whole length in +2
	PAG1365RP open frame whole length in +3
35	PAG1366RP open frame whole length in +2
	PAG1387UP open frames > 450 nt int -3, >350 nt in +1 and +2

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1001RP

	GTGATTTCGTC	CGAGATTGAA	AAGTCCCTAA	CAATCAAAAA	CAACGGGAAG	GCGTACGAGG	60
	AATGGCTGGA	CCTGGGTAAT	GGGTGCCTAT	GTTGCAGTCT	GAAGGACGTA	GGGGTGAAGG	120
5	CCATCGAGGC	GATGGTTTCG	CGGTCCGCCAG	GTAAAATCGA	CTACATCATA	CTTGAGACAA	180
	GCGGGATAGC	GGACCCAGTG	CCGATCGTGA	AGATGTTCTG	GCAGGATGAG	GGTCTCAATA	240
	GCTGCATCTA	CATTGATGGG	ATTGTGACGG	TGCTGGACGC	AGAGCATGTG	ATGACATTGC	300
	TCGACGAGGT	GGCCCTCCCG	CGCCAATTGC	GCGGCGACCA	GGTGCTGATG	GAAAACCAGA	360
	TGACCCNNGG	GNATCTTCAG	GTTGCCATGG	GGGNGCGGGG	GNGTTGATTA	AATCNACCCC	420
	TGNAGGCTGN	NTAAAAATCT	TGGNNGGGAA	AANGGTGANT	ATAAGCGGCC	TTTTTCGGCN	480
10	AATNCGGGAN	TTTNGNTANN	AAAGNTNT				

1001UP

	TGATCCGACC	AAGAGCAGGG	CTTTGGTGCG	GTGAATCTCG	AACTCCTGCC	CCTGTGTCAG	60
15	CTCACCCCGG	CCGAAGTCCT	TCCAAAGAAG	AGCTTGTAAG	AAGTGTTCCT	CGAACCCTC	120
	GAGCTCAGCC	TTGTCCGCGA	GCGGCCGGCA	GGTCAAGGTG	ACCGTGGACA	GCCGCGGATC	180
	ATGGTAAGCC	ACGTGGGCAT	CGGGAATGTC	AGAGGCACCA	AAAGCATGGA	GATTCAAGTA	240
	CCTTGTTTAT	CTCCAGATCG	CCGAACCTGG	TCCCGATAGA	TGGGCGCGAC	TGCATTAAATG	300
	CTACGCACTT	TTTCTCCAA	CCACAGCGAT	TCGTCAATCA	NGCCTCCCAG	CCNGTCGGAT	360
20	TTATCAAAAC	AACCNNGTCC	GCCATGGCNA	GTTGNAGATG	GCANGGCACT	TTNTTCCAC	420
	AGACTGGNGG	CCGGCAATGG	GGGGGGCACC	CGCGACATTA	NAATTNTGTC	AGACCNAAAC	480
	CNCAATTGNN						

1002I2

	GATCTTCGAG	TGGGCGAGGG	ATAGTAGCGA	CCGTGGCAGA	CATTCACTCT	GATCAATTGA	60
	AGCGCCTGCT	CCATGTCCCT	GATGAACCTG	GGAAATAAAT	GCCTATAGAG	TTGGTGTAAC	120
	AGGGTAACGA	CTTCTCTCGA	TTGCCTATCA	AAAGACTGAA	AAGGTACGTT	CGGCAGCACA	180
	CAAAACAGCG	AGTTCGGCTG	GTGGACTGTT	CGCGTGTAAT	ACGCAGTACA	CATATACCTA	240
	AGATAAAGAG	GTTTCATGAAT	AAGTGGTTAG	CCACTATATT	CAATTCATTT	GGAGGAAATA	300
30	ATACTACTAG	ACGTGGATTG	TTGGTGCCAC	TGGGTTCCAA	TCGATAGCTA	CTTCAAATTT	360
	CCCGGCTACA	CTAAAAACGG	GCGCTCTTGT	CCTTCAAGGA	TAGAACGCTT	CCGGAGTACC	420
	TCCCTGTTTC	ATGCACAAAA	GCGAACTACT	CTTGGCACCA	CCGCCGGAGG	AGACAAACTT	480
	TGGGGCAATC	CTTTGAGATT	TCGACACCAN	TGNAAAAGNT	N		

1002I1

	GATCTCCGCA	AATTCTCCCA	AAATGGTAAG	TCGTTATCCA	CCTTAAATGC	TTGCTCGGGT	60
	AGCTTGTTCC	CCAATAAATA	ACGTGACCCA	TCATTGAGAT	CCAATACCTG	GGGGAGCAGT	120
	TCGCTCCAAT	CGCGTACTTT	CTTTAAAAAC	GGAAATAGTT	CATGATGGAG	AGAGTACAAG	180
40	TTTATGTCCT	CACCAAAAAC	CTCACGAAGA	CCTATATCTC	CTTGCAATGAA	ACAAGTGTCTG	240
	AACACTCGTA	GTCGTTCCAG	CATGGCAGCT	GTCACCGAGG	CATCCTTCAT	GCGACCACGC	300
	GACCTTTCGA	TAATTTTCGTT	CAGCCATTGT	TGTCTCTTTT	TCCTTCGCAA	AGTACCACTG	360
	GCATTCTTTT	CCAGGGGGCA	TCTCCCGAAC	TGGGTTGGTC	AACAGAAATGT	ACTGTNTGGG	420
	GNGGGGTTTG	GTGTTGGACG	ACNTTTNGTG	AAGATGGGGC	ACAGTTNTGC	CGTTTTTGAG	480
	GNCAGGCAGA	TNTGAAACAA	ATTNNCGNNA	ANTTCGNTTT	CCCNACGCAC	GGGGCCCGAN	540
45	TTCAGGCAAC	CTNGACATTN	TCGAAGTACC	N			

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1002RP

	GATCTACTAA	GGAATTATGG	GAATCGTGTC	TTTTCTTCTT	AGAAATGAAT	TTGTTTGCAG	60
	TCGAAGACGA	GGTGGAAAGAC	GAGCGCGACT	GTTTACTCTT	GGGGAAGTTA	GTCAAACAAT	120
5	CGCTAGATTG	TATCCGCATG	GTATCACCTG	AGTTTCTATC	TATAGGAATG	CTACTATYAC	180
	GGAAGTTGCG	ATGCTGATGG	GCATGGTTGT	CATGAAAAAT	AGGATGTTGG	CTCCGGTTAG	240
	ATGACTGMCC	GAATACCTCT	TCTATGATTA	ATTCCTWCAA	GCGGGTATTG	ATTAATGTCT	300
	ATCCTGTGGC	GTATGATGAA	ATGACTGCCG	CGTCATTGCC	GGTACGCCCT	TGGAGTGTTC	360
	GGANTTGACA	AGAANNCGCT	CTTAGGTGCC	NGGATTCCCN	GGGTGGGAAA	GATGATNGCG	420
	AATNCCAATT	TNGGTCCAAT	AGGGAATCTG	GNATTATTTG	TTATTGCAAT	NAGGATNCCC	480
10	GGGAGGGGGT	TNCNCTACGA	AGAAGGATTA	GGTTTNNC			

1002UP

	GATCCACGKG	AGTCGCAGCG	CCAAAGGCCG	CTGGGCGTCA	CGATGCAGGT	TATGCTGTCT	60
15	CGTCGACAGA	GTGCGCCCCG	CTGGATGAAG	CCCATAAGAC	TATTGAGCCA	CTATATAATA	120
	CCAGCTGGTT	ACMTGATACT	ATATGGTCAT	AGCATCAATT	GTAGTAGCCA	GGGCAGTGAG	180
	GCTATAGCAG	CTGGAAAGGC	GACTCTGAAA	AGGGATTAT	GCCAAGAGCT	TCAGAAGTGG	240
	ACTCAGGCCA	CGCATCCAAC	GGATTCTTCC	TCAATTCTCT	TATATTGAGC	CAGAGCTCCA	300
	TCTTGACCGA	GGTCCCTCAT	TCATATTTCAT	ACGAGTTACT	TGAACATCCA	ACAGGTGCCA	360
	TATTTAGKTT	GGGGGGGTAA	GTACAATANC	GNTGNNGGCC	GTGGAACCCC	GGTCCGTTCC	420
20	CNNGGTTTTG	GAATTTTNG	G				

1003RP

	GATCGCTCAT	GACCAAAACA	ACGAAATCCA	CTACATTTCT	CTTGCCACTG	CTCACCAGC	60
25	GAAGTTTGCG	GACGCTGTGA	ACGAAGCTCT	CTCCTCTTAC	GATGACTACA	ACTTCGATGA	120
	CGTTCTTCCA	GACCGTCTAA	GACGTCTAGG	TGACCTTGAG	AAGAGAATTA	AGTACGTGGA	180
	CAACACCCGAC	GTTGATGTTA	TCAAATCTAT	CATTGAGGAG	GAAGTATTA	ACATGGGCAT	240
	TTACAATCCA	TAGATGATCT	GAAGTCTAGA	TGATTTATAG	ACTATCTAGT	TAGCCTTCTA	300
	GTCCTATATA	CCTAATTCCA	ATAGGCAGGG	GGGCCTATGT	CAAGTTTAAA	TCCATTTTGC	360
	CTTCTACTGC	CGCAACGTGG	TTTTTTTGCAA	AGCCAATTTT	GCCGTCGGGG	CCAACCTCAC	420
30	CTCANTACCC	AGNTCTGNGA	GTCATCANCA	TTCCCCGCTN	TAGGCCCCAG	TGANTAGAAG	480
	TGGTCTAGGT	CGTTTCAAGA	GGAACATNAA	TNT			

1003UP

	GATCTTTAGA	CAATTATGAC	ATCCAAGTTT	GGTCCGTTCA	GACTGGTCAG	TTGCTTGACA	60
	CACTCTCTGG	TCACGAAGGC	CCAGTCTCTT	GCTTGTCTTT	CAGCCGGGAA	AATAGCATAC	120
	TAGCCTCTGC	CTCTTGAGAC	AAAACATATA	GAGTGTGGCC	GATATTTGGG	CGGCCCCAGC	180
	AAGTCGAGCC	TATAGAAGCA	TACTCTGATG	TGCTGGATAT	TTCCATGAGA	CCTGATGGTA	240
40	AGCAGGTCTG	TGTCTCCACG	CTGAATGGTC	AGCTGTCAAT	CTTCGACGTT	TGAAACCTCA	300
	CGGCAGGTTG	GCAACAATTG	CTTGCAAGAG	GGACATCATA	TCAGGACGCC	ATTTAGAGGA	360
	CCGGTTTACT	CAAAGAACTT	CGGCAACGGC	CCAAATATTC	ACAACAATCC	ACTACAGTTC	420
	GGCGGCTTTC	AATGNTGGAG	NTGGGANAAA	ATCTNNTGGT	NTAGAATCCN	ATAAGGGTAT	480
	AANCGTCATG	TTCCANAAAT	NATC				

1004RP

	GATCTTAAAG	AGGCTCAGTA	TGCAGAGGCA	GTTTCCAGAA	GAAGACAGGC	TGGGCTTCGA	60
	AATCCCTCAG	CTCCCGCCGT	GGAAGAGTCC	GCAGATGAAG	CAACACACAC	AACAGGGCCA	120
5	GCAAACGCCG	CTGCGGCGGC	CGCGCTGCAT	CCTCGGTGCC	CCTTATGAAC	CGAGCAGGGC	180
	GTCGTCCACT	GGTGCAGGCC	AAAAGCGCGA	CTACGACTAC	TCCGTGTTCA	ATGAGAGCAG	240
	GCTCCTCACT	GAGAGCAAGA	TAGACCAGTA	CTTGAAGAGC	GAGGCCGCAA	CGCACAAACG	300
	CGTATTCCAC	CCGCGACCGC	CCCCACGACG	ACAGCTACCC	GCCCCGACTT	TGCAGCCCGC	360
	TCTGCTTGCG	ACAAGCTTCG	GACGANGAGG	GAGAGCCCN	CCCCCTCNC	AGAGNGCGCN	420
	TTNGNGACCC	CCCNNTGGNTG	TTCATCATCC	CCCCANTCCT	CCAGGAGAGT	TTTNGAAAGG	480
10	GCGCCCCNA	NACNCCNTAG	GATTCGTGGA	GGATGGAGTN	GGGCCCTTTT		

1004UP

	GATCACCAG	CCTAATGAGT	GGTGCTAGGG	TAGCGGTTAT	TACCGGTACT	AATAGGTATG	60
15	TTAATATGCC	ATCAGTGTCT	GAGCTCACGA	CTGACATATA	TTAGCAATCT	TGGCCTGAAT	120
	ATCGCATACA	GGTTGATTGA	GCAGTTTACT	GATGACAGCA	AGTTGGTTAT	CGTGGTAACA	180
	TCGCGTACGC	TGCCAAGAGT	AAGGGAGGTG	GTAGACCTAA	TCAAAACATA	CGCCGAGAAA	240
	TGTGGYAAGT	CTGGAGCAGT	AGATTTTCGAC	TACCTGCTGG	TGGATTTTAC	CGACATGGTT	300
	AGTGTGCTGG	GCGCGGCATA	CGAATTAGAA	AAACGATATG	ACGCTATACA	TTACTTCTAC	360
	GCTAACGCTG	GCAGGCTGTG	TATTTCCCGA	ATTGATTGGT	TGGGTGCACC	NGGTGTTTAC	420
20	GGGATCCNCG	GGTGTGTGAT	ATCCNCGTTA	GNCNGGGTGG	ANNAATCAGG	ATGGTNGGTT	480
	AGTTTCAAGC	ANTC					

1005RP

25	GATCTCCCC	AGGAACCGCG	ACGGGTACGC	AGTCGTCGTT	CTTCCCAGCG	TGGTCGTCAC	60
	GAATTCCATC	AGCATGTGGA	ACTTCAGCGC	GAACATCTCC	TCACGCAGGA	TCCGCGTCTT	120
	CCTCCTCCTC	TGCGGCCACC	GAGAGCTCCG	CCAGCTGCTG	GCACCCGGTC	AGGAAGCACT	180
	CCCGCGCGTT	CCCCTCgCGC	cccacCTCCC	TGAAGCAGCC	CACCAGGAGC	CGCCACACCA	240
	TATCATCCCC	GAGCCCTTCG	TTGAGGTTGA	AGTTGTCTGC	CCTAATGCAC	CGCACAAGCA	300
30	CCTTCGGGAT	ATCCCaACCC	AAATCTCCCA	CGAGTGCagG	GTGCTCCCGG	AGCTGCTCCC	360
	AcAGCGCCTC	CAGGAAGCTC	GCCAgCCGCC	CCGCGTTACC	GcTCGCAAGC	GCCTGCTcCG	420
	CGCACAACTC	GATCCCCGCT	GCGAgCGAgA	TcTCGTcCCC	GCCTGcTCCG	CGAATAGCaC	480
	GCCCAGACTC	TCaCCTTCCG	TATTGCGTGG	cGTTTCATAg	AATcAcTCT		

1005UP

	GATCTTGAG	TTAACGGTTC	TTCCATCAAG	GGACAAATGG	GCGTACCGAA	GCTCTTAGCC	60
	CAGCCAAGTA	TCCCACAGCT	GCACAATGCT	AAGGGTGAGG	TAATTGATGT	TCAGTCCCAG	120
	CCCCCGCGG	GCTGGCGGCA	GGTGCTACTA	NAGCATGGCC	CAGAAGTATT	TGCGAAGAAG	180
40	GTGCGTgAAT	TCGATGGAAC	ATTGCTTACA	GACACTACAT	GGAGAGATGC	CCATCAATCA	240
	TTGTTGGCAA	CTAGGGTGCG	TACTTATGAC	CTAGCTGCTA	TTGCACCTAC	CACTGCACAT	300
	GCaTTAGCAG	GAgCCTTTGC	aTTAGAgTGT	TGGGGTGGCG	CTACGTTTGA	CGTTGCCATG	360
	CGGTTTTTGC	ACgAAGACcC	aTGGGAgCGC	TTGAgGACAC	TGCGGAAATT	GGTGCCAAAC	420
	ATCCCATTC	AGATGTTGCT	TCgTGGTGCC	aACgGTGTTG	CTTACTCCTC	TCTGCCTGAT	480
	AATGCGAATG	ACATTcGTCa	AACAAGCAAA	GGAgAATGGT	GTC		

1006RP

	NNNNNGNNNN	NNNNTGTGGG	GCGTGGTAGA	NTAGTGGGTC	TCGTAGACAA	TGGATGCCTG	60
	TAAGCATgTG	TAACGGGTAT	CGTGGAGGGG	TCCCTTCCCG	CCTCCGAAGC	CTTCTTCGGT	120
5	TTCTCAATTT	CCCATAGcAA	TGGCGACTCG	CACCAGTAAA	TCCTCCTCTG	GGTAGGCTCC	180
	GCTCATTAGT	CGAACGGTTC	TCCGTAGCCC	ATCCTCGTCC	AGTTGCGGCG	CCGCGAAAAC	240
	AAACAAACAC	TGGCCGCCCC	GATAACGTCA	GTAGcTATGT	TTCAGcAGAT	TCCGCGGAAA	300
	CCGTCCAACA	GATCGTCTGT	AACCGGTGcA	GATACGTCTG	GGcAGcGGGT	TTTAACTGCA	360
	GCCAGTGcAG	ATTTAACGTG	CGATGGAAGC	CTGCGCGCGG	TTCTGGcTGC	CCGCCGGTGG	420
	CTCCAGCGGA	GCGAGCGCGC	GCGTCGCGAT	GCGCGGcGTa	AGTCTGTgAT	CGcCGGGAGC	480
10	TGAgTAGcGC	TAGCGAAGGT	CACACGGACG	CCGGATAGTA	GaTGGAGcAA	GGGGCCTCTT	540
	TGGACGGTTT	GGTTACGAAA	TNCCGGG				

1006UP

15	GATCTCTGTT	CTTTTTTTTAC	CTCTGAAGGT	GCCGAATGTG	TGCGCGTGAA	ACCACTCTTT	60
	CGCGATGGGA	TGTTTCCTGA	TCTCCCTCGC	GAGCTGTTTC	ATGTATTACT	TCCTTGTAAG	120
	GCAATCGCCA	CGCAGGACAG	ACCGAGCTGG	TGCCAACGGT	TTCTCCGGCG	TGCCPTTGCT	180
	GAGATGCGTT	CGCATGTTTT	GACCCAGCT	CTGGAATATG	CGCGCGGTGC	GATGCTGCGT	240
	GTGGTACGAT	GCAACGTCAG	CGATCCCGCA	GGGCGGgGGT	GCAGgGGTGT	ACTTCGATCG	300
20	TAGGCCGCTG	TAAATGCTCC	TCTGGGACGC	CGCTCCCGCC	GATCTTACTG	TCCGCCATGA	360
	ACGATGGGAC	AgAgTAGcCG	GGATGGTTCC	CTTTGcAGAT	AGGAAATCTG	GAAGAATTG	420
	GTCCCgctCC	gcCTGATTG	TtTATACAAA	AAATTGGCCA	TACATTCCCTT	G	

1007RP

25	GATCTTCTCG	CCGAAGTACT	GCACCATGTC	ATTTCTCTCC	GGTTCACCAT	GAACAAGGAC	60
	ATCTAGGCCG	ACCTCCTCCT	GGAAAGCGAT	GACTTCCTCA	ATCTGAGAAT	TGATGAAGTT	120
	GGTGTACTCC	TCCGTGGAAA	TCGCCCCCTT	TGCATGCTTG	TTTCTGTTGA	TCCGAATGTC	180
	CTTAGTCTGT	GGGAAGGAAC	CGATGGTGGT	GGTTGGGAAT	AGCGGGAGCT	TGAAAATTGG	240
30	CTGCTGCTCC	TTGAGACGCT	CCCCGAATGG	TGCGGCTCTC	GTGGATAGCT	TCTCGTTCAA	300
	ACCAGCAACA	CGTTCTTGGA	CAGAAGGATC	GTTGGGTGAT	CGCAGAGGCG	GGACGCGCAG	360
	CAATCGAGTC	TGCATTTGGC	TCCAATCTCAG	AGGAAAAGTC	TTCGCCAGAG	CGTCCTTAGC	420
	GAGGAAACAA	ACTCATGCAG	TTCTTGGMTG	AAAAGAGAAC	CAGCCTGGCT	TNTTGTCCAA	480
	GGAGATCGTT	TCCAAGTAAC	TGGNNTTGAA	NAAGGAGC			

1007UP

35	GATCTTGTCG	AGCTCGCCAT	GACAGATGAG	AATCCGACAG	CACGTTTCAC	GGCATTTTAT	60
	GCGCTGGGGC	TAATTAGTAA	AACGGAGGAA	GGCTGTGAAC	TATTGGACGA	GTTGGGCTGG	120
	GACTGTTGCA	TCGATGTTCTG	TCGCCAGCCA	GTTGGTATTT	GGGTACCAA	TAACATCACC	180
40	ACCTTTCTCA	GTTATCCTCA	AGAGAGCGTC	GAGAAAACAA	CCGTTTCGGA	AGGTATCGAC	240
	CAATTTGGAC	CACGGAATTT	CGGGAGGAGG	GACTTCCCCC	CACTGGAGGG	TATCACAAAT	300
	ACAAGTTGAT	ACAATACTCT	GAAAAGGTAG	GAAAGGGATG	TCCTGACAGA	CAACCAAGAG	360
	CTTAAATCCA	TCCTCGCACA	CAGGGGTAGA	CAAGTGANTG	NAAGCGGNGA	TTGATCTTCC	420
	CATGGAGNTC	CAGGATGACC	AGCTCCCCAA	GATTTCCGTT	CGTGGGAANC	GGAATCATTT	480
45	NTACACAGNG	GA					

1008I2

	TCGAGACCGC	ATCAAATATC	TGTCATTATG	TAAATGTGCA	TATTATAGAC	TTCTATTTC	60
	AGTACCAGGC	AATTGTGTCC	GATAAATGAG	GTGCAATGAG	CACCCGTCAT	CACCGGACGC	120
5	GATAAATTTT	TTTTTGGGGG	TCAACCATTA	AATCTACGTG	CATCTAACGC	AAGGAGCAAT	180
	TTAGCTAACA	ACTCTTCTTA	TCTTAAGAAT	CGGGTATACC	TCCTCTTCGC	ACATCTTCGC	240
	CTTCTTTAGT	CTCGAGTCTT	AACTACGTTT	AACAATGTCA	GCCTCCGATA	AGATGTACAT	300
	GTGCTATAAC	AACATACACA	AACTGTGTCA	GCAGGTAGCT	GGCCAAATTA	TGGAGCGTGG	360
	TGACAGACCG	GACGTGATTA	TCGCCATTAC	CGGCGGCGGC	ATGATTCTCTG	CAAGAATCAT	420
	CCGGTTCGTT	CTCAAGGTCA	AGGGCCAGAA	AAACATCCCC	ATCCAGGCGA	TTGGGTCTTT	480
10	CTTTGGTACG	AGGACTTGGG	TTTGGGAAGAC	GGGACGGAAA	GCATCGGCAA	GGAAGTTATC	540
	CGGATCAAGT	GGCTAGACTT	TGGGGGCCTT	GGGCAAACAC	TTTGGACTCA	ACTGATTGGA	600
	AGAAGGTGTT	GGATTGGCGC	CGAGTTGGNC	GANACCCNGA	CACGTCCCTA	CGGTTGTNAC	660
	CGANTTGGGG	AGGGGGNCAN					

1008I1

	TCGAGTCATT	TCTTGTAAGT	CAGTGCATCG	ACAAAGTCGT	CTGCTTCGCC	GTTGGCATA	60
	GTTATTTTCG	TTCCATACTC	GGCATCATCA	GCGTCCTCAA	GCGCGACCTG	AGACAACTCC	120
	TGGCGCAACT	TTGTCTGGGC	GCGAAGCATC	TCCAGGGGAC	CCCTGCATTG	ATAACAGGAT	180
20	CGGGAGCGAG	TCGGAACCTG	CCTTGAGGTT	CGCGCGAAGA	GCCTTGATTT	CCTTGTTACC	240
	CCGCGGCTGC	AAGGAATCTA	GGTGAGGAGC	ACGCAGTCGA	AGCAACCACT	TAAACCACCA	300
	ACGGATCGCT	GAGCTTTCTG	TCCAAACGTC	AGAGGCCACC	CGCTGGCTCA	CGATGACAAA	360
	ACAGTTCATT	GNANCGCNAT	GGAAGGNGAT	NCATGTCCGN	NANATCTTTT	NNTTCTTTCC	420
	TCGGACCANG	NGTNANAAC	NACAGTCCCT	GACGANTTCC	TCACCTANGT	CNCCGCAGGG	480
	GATNNTTTCA	ACGCCGCNCC	GTCTNNCCCC	CTCNCNCTCG	NNNACCTTCT	TTGTTNNNGG	540
25	TTTTCTTTTN	CCNNCNCNCC	TNNTNCCNAC	TTNGGTTTTT	NNACNCCNTC	NNNAC	

1008RP

	GATCTGTCTT	GGACGATATC	AACGTCTATG	CCATCTTCCA	AACCGTCTTT	TCCACATTGC	60
30	AACAAAATGA	CTCTACAAAA	TACCAGTTAG	TCCTAGAAAA	TATGTCACAG	GACGAACAGA	120
	TGCACCTAGC	ACATATTACA	TCGTTATGAG	CACCATAAAT	CTCATAGTCT	TCCTACTTTA	180
	TCTTTAATAT	TAATAGTATG	TGTATGCCAA	TCGGCGCGTT	ATGCCCGGGT	AACAGTAGTT	240
	TCTTTTCTTN	GAACATCTGA	AAAATTTTCA	CCGATGAGCT	CTCTTGTTGC	AATGGCGCAT	300
	CGAGCTACAA	GTGCAGGTGT	ACCATTCACA	TCCCTATCGG	NATTCGGCTG	TTGNTAGAGC	360
	TGTTAAAATG	ATTGCTTCAG	AAGATACGAG	GTCCCTGGGA	GTTTTTCGGC	CGATGAACGN	420
35	GGTCGCATTG	CAAGCCAATG	CGTGGAAGG	ACTCATTGAA	TTTTCANNGA	CCNGNAGAAT	480
	TAANGGNAAA	GTCANCNGTA	ACCNATTGT				

1008UP

	GATCAAGCGG	GAATTTTCGG	GCAAAATGCAC	GTTAATGCTC	ATATTGTTAA	CAAGCTCGGG	60
	GCAGAAGTCC	GCCGTTTGGA	GCTAGAAATT	TCCACATTGA	AAGCGTTCAA	TAACACATTA	120
	GAGGAAGAGA	AAGCTCGTGC	AGAAGATGAT	ATTTTGAAGC	TGCTAGAGGA	AAATCACACT	180
	GTGCATCATT	TGAAGACTAC	CAACGAAGCG	TTGACTACCA	AGGTAGCCGA	CTATAGCAAT	240
	AGACAAGATA	CGATTCTCCA	GCTGTTGGGC	GAAAAGACGG	AACGTGTAGA	GGAACCTGGA	300
45	AAATGACGTC	GAGGACCTCA	AGCAGATGCT	GCGGATGCAA	GCACAGCAAC	TTGGCCGACA	360
	TGCAAGAGAG	GTTAAGAATT	TAGATTCCCA	TATCTTATTA	ACATTATTNA	TNCAANCGGC	420
	TTGGGTTNGT	TAATCAACTT	CNCCAGATGC	NTAGATTG	GTAGTTAGNC	ANTTTTTTCGA	480
	NGTGGNTCAA	ATGGNGGCC					

1009RP

	GATCTTTCGCT	TGGGGCCGTG	CGTTCACGGT	CTTAGAAAGC	AAGCGTGCAA	GCGATGTCTT	60
	GCCTACCCCT	GGGGGGGCCC	ATAGTATCAT	CGAAGGTATT	GTTCCCTGGC	TCACATATTT	120
5	GTATAGTGCC	CCGCTTTCCCT	GGGAGAGAAT	ATGCTGTTGC	CCCACGTACT	CCCGCAGCTC	180
	GCGGGGACGA	AGTTTCTCAC	TTAAGGGCAA	ATGTGCCATT	TTCTGCAGCT	CACGCTGATC	240
	TGAGTTCACC	GCCCCGTGTG	GACGTGCCCC	CTTCCGTTGG	GGAGAGTCGT	CCATCTCTAT	300
	CACCTCACTA	TCCTCCATAT	TAACGTCCGA	GATCACAGAC	ACGCTATCCT	CATCCTCCAG	360
	CTTATGCTTG	CGCCCCAGCA	TCTCAGATAC	GGACGTGGTC	CTCGCTCCTT	TCGGCTCCTC	420
	CTGCAGGGAT	GCACTCTAGAT	GGTATGGATG	TGATGAATGG	AAAGCCTGCA	ATCTGGNAAT	480
10	GGTAAGTCTC	CCCCCCGTAT	CATTTN				

1009UP

	GATCATGCTA	GTTCTGCAGC	TGAGTTTTTA	AAAACGCAGT	ACTGGAGATG	TTTCGCTTTA	60
15	TGGTATCGCT	CCACTAGCGC	ACGGACTGAC	TTTGGTAAAC	GGCTTAGCAC	TGATGCCGGT	120
	ATTTGGAACG	CCCGTCCCTAA	GAAGCTTGAG	TTCCGACCAT	CAATGAAGGG	AGCGCAAGTC	180
	GAAATTTCCC	AGCCTAGAGG	CATGTCACTA	GGGTCAAATA	CGTCTTGTTT	TGGATCGCTC	240
	TGCATCATGA	TATCGACATA	GTAGTCGCAC	ATATCGATGG	AGACGACCTT	GCCGGGGTCA	300
	AATTTGTTAA	ATTGGTTCAA	TCCCTCAGGC	ACTTGGGTGA	TAACCTCAAG	TAGCGGCATT	360
	TCTTCAGGGA	AATCGCCCCG	TAGGAGGGCA	TCGAAGNCAG	AGTTNGACGA	ACCNCAGGCG	420
20	GGGGGANTCT	TTGAAGGGAG	AAAGAGGCCG	GGAANTGGTA	CCACTCCGCT	CCCNCTCANA	480
	AGTTGGCCCC	AGCCTCAATN					

1010I2

25	TCGAGGTGGC	GGGCGGGAAA	CCCCTGCGCA	ATCCTGGCCT	CCAGCGCCCG	GCTGACTGCG	60
	GGTACCGTCA	AGCACTTGAA	GTGGCTCCGC	TCAAGATAAT	CCACCGCCTC	GTTCGCCCCG	120
	AGCCCGCGAC	TCCCGTGCAC	ATCCCGCGGG	ATCAGCTTGA	ACTCCCCCGC	GCTCAGCCAG	180
	AGTCGGTTGT	TGCCCACCGG	GTAGTCGTAC	TCCTCTGGCA	GCGCCTCGCT	GCTCATCATC	240
	AGCAGAAAGT	CGCCCTCTGT	GTCGCACATC	TTGATGAAAA	CCTCCGCGCC	CTGAGCCCCG	300
30	GAGAATCGCT	GCAGCACCCC	TGCCACCAGC	GCCTCCTCCT	CCTCGGGTTG	TCCGCGACTT	360
	CCACTCCGCC	AAGCACCATC	GCCTGCCCTC	CCGCGCCCCG	CACCGCCCCG	AGGTGCACCC	420
	GCTGTACCCC	TGNCACGGGT	AGTGGTCAAT	CCACGGCCGG	AACACTCCTC	AAGCTGAGCA	480
	TGTTCTTGGG	ATCTTTGTCT	GGACGTCATC	AAAATTGTCT	ATTTGAAAAA	CGATACAATA	540
	NAGNGGCTCN	GGGGTNGAAA	GTCACACCNA	TCACTCTGGT	TCAAAGCATG	TCTCAATNTG	600
35	CGGGGCATAA	CCAATTCNCN	GGTANGCA				

1010I1

	TCGAGGCGCT	TACGTGGGTC	CACCTGAAGA	TGCGGCAGAC	GGCGCACGCG	GAGCTGGTGC	60
40	GGGCGAACCC	CACCGTGTTC	CCCCTGCTGC	TGGCGAACTT	TCTCAGAAAC	GATCTGTGCG	120
	TGACCGGGGC	TGCGATGGAG	GGCCAGGAAG	CGAAGTGCAG	CGACGTGCAC	GTGCTAGTAC	180
	CGAAAACACA	CGCCGCGCTG	GCGTCTCTCC	TGCTTGACAC	TAGTCCCGTG	GCGCGGGGTG	240
	GCGATCTTGG	CATCACCTTT	GGCGACATTT	TATCGTTGTC	CCTGCAGGAT	GCACTAGACG	300
	CGGGCCAGTT	AACGACAGCT	GAACCCAAAAG	GAAAGTTAGA	GGGTGACCTA	GTAAGCGCTC	360
	TGGTACATAC	AAAACAGCTA	GAGCGCCCCG	TGGAGTTCTC	TACGACTGAA	TTAATACGGA	420
45	GGTACCGACT	TGCGGACAAA	GAGGCGTCTA	TGGATGCCTT	GGCCTGTGCG	TGGAGATTTT	480
	CTGACAGATT	TAAAGATGAC	GATGAGGTAG	AATGACATTT	CTTGTCAAGG	TCTCAAGTGG	540
	GATGAGAGGT	CGGCATTTTC	GAAGGAGNNT	GGTTTATNAN	NANATCTTGG	ATTTTCTGAG	600
	GGGGCTNAGN	TNCAAGAAAG	TCANATN				

1010RP

	GATCCGGCTC	GCAAAGGAGA	AGATAGAAGA	GCAGAAAGAA	TACCCGGTGC	AGGAGTTTGA	60
	CAAAAAGCTG	TATCATAGCA	ACCCCGCAAG	GTA CTGGGAT	ATATTCTATA	AAAATAACAA	120
5	AGAAAAC TTC	TTCAAAGACA	GGAAGTGGTT	GCAGATTGAG	TTTCCCTCTC	TATACGAAGC	180
	TACCAAGAAA	GATGCTGGTT	CAGTGACTAT	CTTCGAGATT	GGGTGTGGTG	CGGGCAATAC	240
	CATGTTCCCG	ATCTTATCTG	CAAACGAAAA	CGAACACTTA	CGCGTTGTGG	GTGCGGACTT	300
	CTCCCCGAAG	GCCGTGGGAA	TTGGTAAAGA	CGTCGCAAAA	CTTTAACCCC	TCGAATGCCC	360
	ACGCGACGGT	ATGGGACTTT	AGCCAACCCT	GATGGTCTTT	TGGCCGATGG	TGTCGAGCCG	420
	CATTCCGGTCG	ANATCGNAGN	AATGATTTTTN	GTTTTAGTGC	CTNGGNGCCC	ACAGGGGGCC	480
10	AGGNTNTTGGT	TATTGGANAA	AGTCTTNANC	AGNGGGT			

1010UP

	GATCAGGACA	G TAGCAGCTT	GA CTGAGTAT	CAGCAGGAAA	AGCCTAGCTA	ATTGGCGCGA	60
15	GTACAATTAC	AAGTACCTGT	CTGACTACTT	CTTTGGGTGG	GATGCCATAT	TTTTTAGGAT	120
	GGCCTGCAAC	GGGCCGGTGG	GGGCGCCATC	CAAATTTATG	GAGTTGAAGA	GCTGTTCAAT	180
	GCCCTTTTATC	CCATCTGCAC	CGTCTTTTATC	GCCGAACATG	GCATGCAACT	CTTCAAGCAT	240
	GATATCTTCT	TCCTCGTGCT	CTGATCCGGC	GTTGGTCGTC	GTTTGGGCAG	TC TCGTAGG	300
	CGCCATTTCT	GTAATGTTGA	AGCTGGTCTT	TGGTCATCTT	CAGACCTTCC	CGTCAGGAAA	360
20	TATCAAAGAA	ATCGGCTTCA	CTAATATCTA	CGCCTCACTC	TCGAAAAATG	TCCGAGGCTC	420
	TTCATCCCCA	GCTGAAGGAC	CCTGACCAGA	AAAATGTCAA	TGGTACTCAA	CGCAACTTTA	480
	ATNTTNCAAG	AN					

1011I2

	GATCTCTTGC	ACCAGTCCAA	ATCAGCGGGG	TCGTCCACCT	TTCTCTCCATA	TATGATTTTTG	60
	CCGATGGTGT	CGCTGACAAG	CTTCCAGGGC	ACCAAATCGG	GGTCGACATG	CTCCTTGCCG	120
	TTACTGCTCT	GTTCAAATAT	GTGGTCCAAA	AACTTGCTAC	CTGCGTGGA	GTCACCATCG	180
	TGGAAGTCGT	ACTTCTTGGT	GAATCCAATA	GGCGCGAGAC	GGCACCTGGC	CATGATAATA	240
30	GAGTGGAACC	ACACGAGGAT	GAAC TTGCTA	TGAAGTTTTT	CTACTGGTTT	GACATTCTTC	300
	AGTTCTCTG	ACTGAGTCCG	CCACAGCTCG	CAGACTGTGT	TTAGAACGCC	GGGCTCACCC	360
	TCGTACGCTA	TCTTATAGTT	CTGCTGAGCA	AAGGAACCAC	TAGAGGCTTG	CTTTGGGATC	420

1011I1

	GATCTGCGCG	GCGGATGTTT	AGCAGCGACG	CGTATCTAAA	CAATTTGCAA	GTTGTCCAAG	60
	GCCTGACCGT	TCCAATAGAC	CGCTCTAGCT	ATTCCCACTA	TGACAAATGG	TTTAAATCGC	120
	TAGATGCAGC	TGCAGAACGT	ACAAC TGCT	GGTTAGAGCT	GTCGGATGCT	TCGGCCCTGC	180
40	AAAAC TTCTA	CGCTCACGAG	GCCAGGATGA	TCTGCAAAAA	AATCATCCAG	ACCAATGGCC	240
	CCACATCTTT	AATTCACTGA	GTGTAATGTC	CATACCTCCA	GTA CTACCA	GTCTTTTGGT	300
	TTTCTGGATG	TCAGATACCA	GACTATGTAC	TGAATAGCGA	CAACATTAGA	TATCTAAAAA	360
	GTCTGTGCGT	TTACAATCTT	AAGGTGCGCT	GAAAGAAGAG	AAACAATCTT	CGAAAACAAT	420
	ACTAAGGCGA	ATATATCAAC	GTAATATGAC	CGCTCAGGCT	TCGGATAACA	TTCCGATATC	480
	AGAGGGAGAA	GACTCCGCNG	GNGTCTTGNC	NNTCNGGCGN	AAATTGCNCA	GTNTTNATCC	540
45	CGGNAGCCNC	CCACNGGTTT	TCANACCCCT	TTTTNGNGT	TCNCGNCAAT	NAAGGGNGNC	600
	CTCCTGCANT	TACCCTANNA					

Pag1011rp

5 1 GATCCAAAGC AAGCCTCTAG TGGTTCCTTT GCTCAGCAGA AGCTATAAGA
51 TAGCGTACGA GGGTGAGCCC GGC GTTCTAA ACACAGTCTG CGAGCTGTGG
10 101 CGGACTCAGT CAGAGGAACT GAAGAATGTC AAACCAGTAG AAAA ACTTCA
151 TAGCAAGTTC ATCCTCGTGT GGTTCCTC TATTATCATG GCCAGGTGCC
201 GTCTCGCGCC TATTGGATTG ACCAAGAAGT ACGACTTCCA CGATGGTGAC
15 251 TTCCACGCAG GTAGCAAGTT TTTGGACCAC ATATTTGAAC AGAGCAGTAA
301 CGGCAAGGAG CATGTCGACC CCGATTTGGT GCCCTGGAAA GCTTGTCAGC
20 351 GACACCATCG GCAAATCAT ATATGGGAGG AAAGGTGGAC GACCCCGCTG
401 ATTTGGACTG GTGCAAGANA TCTGCGCGGC GGATGTTT CAG CAGCGACGCG
25 451 TATCTAAACA ATTCGAAGTT GTCCAAGGGC TGACCGTTCC ATAAACCGCT
501 CTANCTATTC CCAGTATGAC AAATGGGTTA AATCNCTAAA NGCANCTGCA
30 551 GAACGTACAA CTGCCCTGNT TANANCTGTC GGATGCTCGG CCTGCAA ACT
601 TCTACNNCNC GAGGCCAGNA NGATNGGCAA AAAAATCTNC AGANCNANGG
35 651 CCCCTCCTT TAATCCCTNG ANTNTNATNT CCAACCNCCN TTNCCCCATC
701 TTTTGNNTTT TGTTNTTAAA AACCAAATTN TC

40

45

50

55

1012/RP

1 GATCCTAACC CAACTGCACA AAATTGTCAG TCATATGTTG GGAGGCAGTT
5 51 TACCCTTCCG CCGCAAATA CATACTTCTC CTTAGGAAAC GTCCTCGCT
101 CAGGACTGCA ACTGCATTGA CGAGCAGCAG AATAACGTAG AATAGCTTTC
151 CCAGGCCAAA TATCATCCCT CCACGTACAG TCTATCAGCA GTGTACTGCG
201 CTGTGCGAGA AGTGGCATTG ACAAGATAAG CAGAAGTAGT TCTAAAAATC
251 AGTGGTCACC AACGCGAGGC TGCAAATCG TGTTGTTTAT TCCCATCTCA
10 301 AAGCATCGCC TGAAAACAAA GGCTCACAGT TGCAGGTGCC CCCGCGTGAT
351 AACAGATGAT AATTTATATT TTAAGTTATA TTAACACACA TATACAAAAA
401 GATTTGGTAG TGGATTAATG ATGATTTGCT TAATCAGCGT TACGTCTTGC
451 GGCCTTCTTA GCCAATCTCT TACCGGTACC AAAGACCTTC TTACCTCTGT
15 501 TCTTTCTTTG CTTTCTCTGT TGTCTGGAAG CCTTCTCAGC CTTCTCAGCC
551 ATGCCGTATC TGACCAATCT GTANGTTGGC TCGAACTTCT TGGCGTCNGC
601 AACAGAGTTG TAGATCAAAC CGAAACCGGT GGAATTGCCA CCACCAAAC
20 651 GGG

1011UP

	GATCTTCACA	CGCACTATTT	GTCCAAGGGG	CTTCAATCGT	CATTGCATTA	CACGAAGAAA	60
	CAATACTTAC	ATGAGAATGG	AACAATAATA	AAC TAAGCGT	ATGGTGCC TA	ATGATTGTCC	120
5	AGATGGGCGT	TGCTGTTTCG	GAACAGTAAA	TGCTTGGCAA	ACTCATAAGA	TGTCCACGAT	180
	ATAGCAGTTG	CAGGCATGTT	GCTGATAATT	CTGGGTTTTA	GGCCCCGAAA	GAAACCGGAC	240
	CAACCATATG	TTTTGTGGAT	TGCAGATGCA	GCCTTGCGGA	ATGTGTCAGC	CTCCTTGAAC	300
	AGCTGACTTT	GAACAGAATC	TGCACCGCGA	ATCTGCAATA	CTGTCTTCAC	GCAGTCTAGC	360
	GGTGTGGGTT	ATGGCGGCAC	ATGTTGGCGC	CCGGATATCC	CACCGCACAG	ACAATGTATC	420
	CAGGGGTTTG	TAGCTGGTTA	CTCGGATTGA	TTATTTTGGT	GGATGATTCA	ATAAATTACA	480
10	AAAATTCAAC	GCTGCGACGG	ATTGTTTATA	GCAATAGTTG	TCCGGTTATG	ATTAGAAAAA	540
	CGCTTGAAAT	GCCCCCTCGT	GGTCAATCCG	CACGGGGCAT	CCC GCAATGG	ANCANTGGGG	600
	TGAANTGAAC	TCTTTGGTGG	GNGNNANCGG	TCCNNAGGGA	C		

1012UP

	GATCTTCCTC	GAGCGCACCA	CGCCGCCCCA	CACAGACTCC	GAGAACCTGC	TCTTCCTGGA	60
	GGGCACCAAA	ACATGCTTCC	AGATGTTTAC	GCAGCAGGTG	GAGGTGCGCG	CAGGCTCGGG	120
	CCAGGCGAAG	ATCCTGGTCG	GCGTCGTCTG	GCGCTTCTGC	AAGCTCCTGT	TCGAGCGCCA	180
	AAGCCACTGG	ATGCAGGCCA	TTTCGTCCGA	GGTCAAGAAG	TGCCTCCAGT	ACAACCACAA	240
20	GTATGAGAAA	GACCCCGACA	ACATCGCGCA	GGAGGAGGAG	TGCGCCGGCG	GCCTCGTCTG	300
	GTACCTCGTC	GCGGTCGCCA	ACGACCAGAT	GAAGGCCGCA	GACTACGCCG	TCGCCATCTC	360
	GCAGAAGTAC	GGCTCCATGG	TCTCCAAGGT	GCACGAGCGC	ACCATCACGA	ACCGCATCGA	420
	GGAAGACCCT	CGACGGCTTC	GCAGAGGTCG	CCAAGTGCAG	CAACAGCGGC	CTCGTCGCCC	480
	TGATCTTCGA	CGACCTGCGC	CGCCCCTACG	CCGAGATCTT	CAGCAAGGCC	TGGTACTCCG	540
	GCAACCAGGC	GCAGCAGATC	GCAGACACCC	TCTACGAGTA	CCTCGCCGAC	ATCCGCAGCC	600
25	AGATGAACCC	TTCTGCTACT	CCACCCTCGT	CGAGTCCGTC	ATCGAAGAGA		

1013I2

	TCGACAAGGT	GACCAAGGAG	AAGTCCAACG	GTGCCCTCCGT	GCCATTGGAC	GTCCACCCAT	60
30	CCAAGGTTGT	CATCACCAAG	TTGCACTTGG	ACAAGGACAG	AAAGGCCTTG	ATCGAGAGAA	120
	AGGGTGGCAA	GTTGGAGTAA	ATGCATTCCA	CAGGTCAGCC	AGCATATTAT	AAGTAATTAT	180
	GTTCTACCAA	CTCTCCTCGA	TATATAGTAA	GTTCAGAAAG	TCGTGTTTCA	CTAGTGTTTA	240
	TCAGTGGGGA	TAATGACTGC	TCTGGTGCTC	CGCTCGTGCG	CAGCCATTCT	TGGCGGACAG	300
	CCATGACTCC	CGCGGACCCG	TGAACAGGCG	CGAAATTCCG	TTCTCCGGGC	CGACCACCNT	360
	TGGACTCTTA	TTGATTTCTT	TCCGCCCTAA	GAAAGTAGAC	AGCGCCTACA	TATATGACAC	420
35	ATCCCTGTCT	GGGTGTTTAA	GGAGCACC GC	TCTGAAGAGC	AGGGAAAACA	CGGAGTCACT	480
	AGGCTCTGCT	ACGGCTCGAG	GTTTTTGAAG	TGAGTTTGNA	ATTATTTCGT	CNNTGAGAA	540
	TGANAGGGGT	GGAGGCCGTC	ACCCGATCAA	CAGACNANCA	GGCAATGGTN	TGAGTNGNAA	600
	CACAGCNCGG	CGAGAACGTG	GCAANCNTCN	ANGNA			

1013I1

	TCGACGCGGA	CAGCGTACTT	CAATCTGTAG	ACAGAAGAAA	CCTTGCCCTC	TTGGCCCTTC	60
	TTGGAGCCAC	GCACAACCAT	AATCTCGTCG	TCCTTTCTGA	TTGGTAGAGA	CTTGATGTTG	120
	TACTGCTCTC	TCAACTCCTT	GGATAGAGGA	GCAGACATGA	TCACGCGGCG	CTCGGAAGAT	180
45	GGCGCGTTGA	AGTACGCCTT	TCTGGCCTTT	CTTCTGTGCG	AGGAAACGTC	TGCAGACATG	240
	TTAGTACTGT	GCCGGGCCAC	CAACTTGTTT	CACGCACTGG	ATTATGCTAG	GTCCGCCTGC	300
	GCGCTGGGCC	GTATGCCCCAG	GTTACCACGG	ATCGCAGCGC	CAGAGACGCT	CATTCCCAAT	360
	GTTTCGGGAG	CCACCATCGT	TCTGTACAT	ACCTAGAGAT	TGCTTAGCCA	TTGCTGATTC	420
	GCCTGGTGCT	GTGTAAGAAC	CTCTGTTTCA	NNATGTGNAN	AATCTCAATN	GTGNAACCT	480
	TTTCANNTTG	TCCCGNCTAC	GCTGNACCCN	CTNNCNNTCG	TNAANCNNCN	NNNNNNNNCN	540
50	CAANCGTTTC	GCTANNNTNN	TCCTANANAC	NNANANNNNNT	CNNCNNNNA	NCCCNNNNN	600
	CACNNNTTTC	NACCNCCNNN	CAANNNNNNN	NNCNNNNNNN	NANCCCNNNN	NATNCNTCAT	660
	NCCCCCTTNC	NNNACTNNNN	ANCCNNNNNC	TNNNNNNNAN	NTNNNNNNNC	ATNNNAACNA	720
	NAACNCC						

1013RP

	ANAATGGCTG	GTAGTTATTG	TTAACCACTA	GTTTCTCCCC	GAAGTTGAAG	TACTTCACAT	60
	AACTCAGCCC	CTCCGAGGGA	CTCATCTCCT	CGTACAGAGG	CCTATTCAAC	TCAATGCGCT	120
5	GCTTGTAGTC	CTCCAATGCA	TCCTGCCTAT	TCCAACCCCT	GTNGTCTGCA	GAGGCTGCTG	180
	CCATCTCCAC	TGTGCGCGCC	CTCAGAATTG	ACTCGCTCAC	GACAGACTCA	ACGAAGAATA	240
	CTTTTACATT	AAGAGCAGCA	AACTCCTCGG	CGAGCATTCT	GCGCTCCTCG	CGCATGATGT	300
	TCATCCCATC	ATAGACAGNA	AGCTGTCCCT	GCTCGAAGAA	CTTCTTCATG	TCCGCTTGA	360
	TCTCGGCTAT	CAGCGTGCGC	CGCAGTCTGA	TCCCTTCCGG	CGTAACTGGT	CTGGTAGAGA	420
10	AGTAGTCCAG	CGGTAGNTTC	ACCATCCCCCT	GCGGGACCCG	NGNCCNNCGA	TACTCGGACA	480
	CANTGAAGGA	TTGTGTGNGC	ACCCCNAGCC	ACCCCCGTAT	TGCGTGTATT	GNCACCGNAA	540
	CAANNNTTTT	GGGTGNTCGT	TGNAGGCCAC	CCAGGACGNA	CCAAAATTTT	TCCCCGNTTG	600
	GAAANCCCCC	CAGNTCCCAN	NNNGNAAATT	GGNCCCCGGG	AATTTTPTNG	CCCTNGGCNC	660
	CNCCGNCNG						

1013UP

	GATCGCTTAC	CAGCCCAGTA	GTGCGCCACA	GGAACTTGAG	GTGGCTATC	CGGCTGACAC	60
	GAAGTATATC	GACCCTTTGG	CAGAAAGTTGA	CATATGTAAA	CGGGATTTCG	CGCATTTGAA	120
	AAAGCTCGGA	GTCAATACCA	TTGCTGTTTA	CTCCATTGAT	CCAACCAAGC	CACATGACGT	180
20	TTGCATGGAG	GAGTTGAGCA	AGCTGGGAAT	CTACGTTCTC	ATCGATTATAT	CAGAACCAGA	240
	CACCTCTATA	ATTAGGGAAA	CACCAACATG	GGATGTAAAA	GTATTCCAGC	GGTACAAAGA	300
	CGTAGTAGAC	TCCATGCAGA	AATACAATAA	TGTTCTGGGC	TTTTCTGCTG	GTAACGAGGT	360
	CACTAATGAC	CGCACGAACA	CAGACGCATC	GTCTTTTGTG	ACGGCGGCTA	TCAGAGATGT	420
	CAAAAACTAC	ATCAAGCAAA	TGGGATACAG	AACTCTTCCG	GTTGGTTACT	CACCATCGAT	480
	GACCAGGAGA	CGAGGGATCA	CTGGCCTGAT	ACTCCCTTC	GGTNGCGTAT	CTNCAGANNC	540
25	TTTTGGCATA	ANTTTGTCCG	ATTGGGCCGG	CATCCACCTN	CNGACGANCG	TTCAAGAGAG	600
	NGGCTTNCNA	TTCNNGAACT	CCCCTTGCCG	CC			

1014RP

	GATCAAACTG	CCGTCTTGGC	GCAGCACGCG	GCCgcgCGAG	TTGGATACGC	GGTCCGCGTC	60
	AAAGGCCACG	CCgAGCGCGC	CAAACCTCCG	GAGGGGCTGG	CCGCGGTAGC	CCAGTGACGT	120
	GATAAGCACG	TCCAATTCTG	AATCCAATTG	CTCGTCCAGG	TGACGTACAA	CCTTGTTTTC	180
	AGGGGTCAGG	GAGTTTTTGC	AGACGGTCAG	CGCAGATATC	GCGCCGGCGC	CGTCCCTGCG	240
	GATGTAGAGC	GGCGTCTTGA	GATAGTCGGA	CACCCAGGCC	TTGGAGTAGC	CTTCCGCCGG	300
35	AGGAGGGTAT	TTACTCGCGG	ACTTGCTGCC	GCGGGCGGCG	TACGGCAGCA	GGTACTGCTG	360
	GCACATGTCA	ATGCGGCGTT	TCGTGCGCGG	GTCgAgCGGC	AGCgCCGcCC	ACGCCTcGGG	420
	CGTGAAGTGC	TCGGGCGCGA	TGTGGCCGCG	CACGCCGCAG	CGCTCGAGCT	CCCACATCTC	480
	GCGCAACTcC	TTGNTCGTGA	ACTTGCTGcC	GAGGAAGTCC	CGGCGCCCGA	TGAGACGCAC	540
	CTCCTCGAGC	GGCgCGCGCC	GcAaCGCCTG	CAGCGCGTgC	gGGTTTGATG	TCGGtCTGGC	600
	CC						

1014UP

	GATCAGTGTT	CGGGGCGAGC	CGGAGAGcAt	ACTGCTGTCA	TGTCATATACC	AGGAGCTGCT	60
	CTCGCGGGTC	ATTGAGGAGT	CCAAGCGTTT	TGCAGACAGG	GACAGCACCA	AGCACATCAC	120
45	AGCCGAGCAC	CTAGATGAGG	CGGTGGAGGC	GTTGCTGGGA	GATGTAGACC	GAGGCGCGGA	180
	CGGGGCATGG	CCTTGATGTA	AGTCTATGTA	CAGGATATTA	GCTTTCAAAA	TGCATGGTTG	240
	GGGTACTTCA	GCGTTTCCAC	CATGGAAAGG	GCGCTGGCGG	CGTCGTTTTT	GTTGAGCACG	300
	AAGAGGCCCT	GGAGCTGCGC	GGtCGACACT	GGGACGCCTA	GCGCGACGGC	CTTGGCGACA	360
	AACTcCGGgC	AGAGCGCCgA	GTCGTCCGGG	TAGAAGCGCA	gGAACATCTG	CTCGATCTGG	420
	TGCGGCGgTTG	CGTTCCCCAC	AAGGACCTTG	TAGTCGATgC	GGCCCGgGCG	CaGCACGGCG	480
50	GGGTGAGGGA	CCTCGGGATG	GTTGGTGGTC	ATAAAGGTGA	TCATCTTCTC	ACTGGAGGCG	540
	ACgCCGTcCA	GGGCGTTGAg	CAGCCCCGCTG	AaCGTGACGC	CGTTGGTGTG	ACCCTCGTCG	600
	TTCTTCTTgC	GCTTgACAAA	GGCGCGT				

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1016RP

	GATGTGAaTC	GATGTGTGGA	GACGAGTGTA	ACTAGACACA	AGCTGGCGAT	GCAGCGAGAT	60
	CTAACAGGAA	AGGTGCTGGt	TGGGGAGAAA	AGGTACTACG	AAGAGGTAGT	CACTAGTGTC	120
5	ACCTACAAGC	CTACACACCA	CCAACTGCGT	TACGAAAATC	TAAATACGTA	CCTCTATCCT	180
	ACAAACTACG	AGGTGcGCGA	ATtCCAATTC	AATtTTGTCC	ATCGtGCGTT	ATTCGAAAAT	240
	GTGCTCTGTG	CGATTCCCAC	AGGTaTtGGT	AAGACCTTCA	TTGCCAGTAC	GGGGATGCTC	300
	AATTACTATT	GGTGGACAGG	GGGCACAAA	ATTATTTTTA	CTGGTCCCAC	ACGACCACTT	360
	GTTGGGCAGG	AAATTAAAGC	ATTCCtGGGG	aTTACTGGTt	TTCCCCNTTA	TGATACGGGA	420
	ATNCTTCTTT	GACAAGAGCC	NNNNGCACAG	GGNACAGATT	TGGGNCAAAA	GAAAACGTTT	480
10	TTTTTTTCGN	NAACGCCCCC	CANTGGGGGG	GNAANTTTCC	CCNNCGAGAG	GGGGGACTTN	540
	NNTCCCCNNA	GANNNTNGGN	TTTTCTNGGG	NNTNNGNNGA	NGGNTCCACC	CCNGNCNNGG	600
	GGGGCCACN	NCCCCCNCNN	NNGGNNTTTT	NNGNNTTTN	TTTTNACAAA	ANTTNC	

15 1016UP

	GATCCATCGA	ACGTCCATTT	TATACGACGA	CATTTTTTATA	CAATTTTTTAT	TTAATAATGA	60
	GGATTTGGCA	TTCCCTCAAA	CTCGCTGACT	AGAAGTTAGC	TGGTGCTAGT	AGTGTAGCTG	120
	GGCTAATGTC	GACTGAATTG	CCGTTGCCGG	TGCTGGAGGA	TTATTTTGTG	TCCGCAGCTA	180
	ATGCCTTCCT	GCCAGATGAA	TTCCCAGTGA	AAGAATTGCA	AGATGAATAC	TATCGACCTT	240
20	GGGAAACGAT	TGTGAGTAAT	CTACCCGCGC	TATTGTTGGC	GCGACAGCTG	CGGGATGTGG	300
	TGGACCACT	GAAGGTGCTG	GAGGTGAAGA	AGGAGCTGTT	CGACGATATT	TCGGCAGGTT	360
	CGGCGCGCAT	ATTCCGGCGTT	GGGCTTCAAC	GTCAATGCGT	ATGTGTCGAG	CTACGACGAC	420
	CGGTTGACA	CGATT					

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1017I2

	GATCTTCTTG	GCGTCGGGCA	TCAGACAGGC	GTAACATAATT	TGATCATTTCC	TGGTGCGGGT	60
	GAGGCTAACT	ATGATGCATT	GGAAGTTAAT	CCTTACGAGA	CGACGAAGCA	AAGGAAAGAG	120
5	CAGGAGGTTA	GATCGCTACT	GAACAAATTA	CCTGCTGATT	CTATTGCATT	AGATCCAAAT	180
	GTGATTGGTA	CGGTCGACAA	GCGTTCTGCG	CAGATTAGAT	TGACCGCCAA	AGACCTGACC	240
	CAAATCGCAA	CTGATGAAGA	CATGAAATCT	AAGGAGAATA	GAGACATTCC	AAAAGCAAAC	300
	CCTGCTGTGA	AGAGTAAGAA	ATTCAGGTCT	GCGTACATT	CTCCGTAAGA	AGACGCAGAA	360
	TGTTGTAGAT	GAGAGGAAGT	TGAGAGTACA	GAAGCAGTTA	GAAAACGAAA	AGGNNGCCCN	420
	CTTGCGGAAG	CANCAAGCTG	CTGAGGNGAG	CTANCAGNAG	ATNCGANCTN	CCCTGNCCGAN	480
10	GCGTCAGCNA	GTCCACTCGC	NNTNNNCTCA	CCCNNTTTC	TTCTGTTNNCN	GAMTTTACNC	540
	CANNNCNCCT	CCCCNNCTNN	NNCTTNCNN	NCCTTNCNN	ACCNCNNCNC	TCCCNNTTCC	600
	NANCCACNC	CCCCNCCNC	NNCCCCNNCN	CCNNNNNNAN	NCNNNNCCCC	CTCTNCCCCN	660
	NCCCCCCNT	NCC					

1017I1

	GATCTTCAAA	TGGGACAAAT	GCAAGGCTAT	TGATCTTATT	CCCAGCAAAC	AAGTGCGACA	60
	TGTATGGTGT	ATTTTTGTG	GGCAACCGAC	TGCTGGTGAA	AACGGGCTTA	AAATCTGAGC	120
	TAGTTTTAAA	GGCATCCTTC	CAAAGTGTC	CATGTGGTCC	TCTCGACACT	GCAAGCAAGC	180
20	CCATGTCAGA	GATTTTCACA	TTGCTTGCTG	GTATAGGCAG	GTTTTCAACG	GAATGTAAGT	240
	CCTTGAAGTT	CCTGATATCC	CACAGTCTCA	TGGACTTATC	TGCTCCGGTN	TGTAGCCATA	300
	TAGTAACCTT	GCCTATCTAC	CGCGACACCA	GTGACGGGCC	CGGTACC		

1017RP

	GATCAAGGTT	GAAAACGAGC	AGCGTGATAA	AAAAGAGCAT	GACGCCGATG	TCCCTGAAGA	60
	GGAATTTAAG	ATTAAATATA	CCTCGACCTA	CTATAAGGTT	GAGAATATGA	CGCGTGATGT	120
	ACCACAGCAA	TTAAATATA	TTGCATTTCC	AAAGGATGAG	AGATTTACTC	CCGCTCGCAA	180
	GTTTAAGGGT	AGCAATGGCG	TTATAGTGCT	ATCGGACAAA	ACTCCTGACG	AGCCGGTCTGA	240
	AGTAATCAAA	ACCGCTAGAC	AGGAAAAAGA	GACGGATGCT	CCTCTGCCTG	CTCCCTTCAA	300
30	GGTTCAGGAT	GACTTAGAAT	TCTGAAGTGA	TAATTAGGAA	GCGTCGATTA	TGTTTATTAG	360
	GAAAAAGGGT	ATTTTTTCTA	GAAACGAAAG	AACTTACTGA	TGCGAGCTCT	CTCTAAACAA	420
	GTATATTATG	AGGTGATTTA	TTTCAACTGA	ATCTGGCTAA	CGCCCGGCAA	CTAGGTCTTA	480
	TCTTCTTGTA	GTCACCCTAG	AGGTGGTGGT	CCCCAANCGG	CNC		

1017UP

	GATCTCCATC	CACGTTTTTG	CCTCGTTTCT	GAGCTCCTCT	GTGACTTTCAT	CCTTGATACG	60
	CGCAATTAAG	CCAGGGCCTC	TGTATGCGTA	CGCAGTGTAG	AGTTGCACAA	AGTGCGCCCC	120
	CGCTTTGGCA	AACTCGATGG	CATCCTGGCC	ACTACTGATA	CCACCACATC	CAACCAAAAC	180
	CAGGTTCTGT	TCCTTTGTGT	ATTGGTGTAT	CGTGCGCAAA	GCTTTTAGCG	CAAATGGTTT	240
40	CACGGGCTTG	GCGGACAAGC	CGCTGCCTG	GTTTTTCAGC	TCCTCATCGA	CAGTGACAG	300
	CGAGTCTGGC	CTTTGGATAG	TAGTGTGTTG	AAACGATGAT	ACCCCAATA	CTCGATTTTC	360
	TTGGGCCGCC	TCTGCGATCG	ATTGGAATCC	TGGCTCGGTC	AAATCCGGTG	CGATTTTAAC	420
	AGGAAAGTTG	GTTATGGTTA	CTGGACCAAG	AAAAATGCCNC	CGTGGNCAAA	GATTGGGTTA	480
	GCANAACAAG	NTN					

1018RP

	GATCATCGTC	GAGGAGTACA	CGCACTCGCT	CTgcgCGTGC	GTGAACTTCG	CCGCGTGACA	60
	CCCGtaCTTC	TTCGACGCCA	CCGTGTTTCA	GAACCGGCAC	CCGGCCGCGT	CGTACAGGTG	120
5	CATGTTGTTC	CACGCCGTTG	CGCTCAGAAG	GTACTGTCCA	TGGTCGTCTGA	ACGACAGCGA	180
	CGTGATCGGG	CCCTGTTCCT	TCTGCGCCAC	CTTGAAAGAC	TTGACCGCCC	GGAACCCCGC	240
	CAATGTGTCT	TTGTTGATCC	CGATACTCAT	CCCGCTCGTC	TTGCAGCTTC	CGGTCCTTGG	300
	CCCTCTCGCC	GCTGCTCTGC	ACTGCTGGCT	AGCAGAGCTC	ACCAAAATTT	TTATAGCCAT	360
	GGCCAGGCCA	AACTTcaCTA	ACTGGGGAAC	CACACGACCA	CAGCAAGCAA	TGCCCTCAGT	420
	ATGTcgGtCG	GtCGCACCGT	CCTGGGATCG	CTACTAACCC	GCACAGCTCA	AGCAGATGGT	480
10	GCACTTCAGC	GCCgACCTCG	CGCTGGtGGC	GATGGtGCTG	GCC		

1018UP

	GATCGCGTGT	ACGACTTCAT	GCGGATGCac	tACGTTATCA	CCCAGATGGT	GGTGCGGCGC	60
15	GACTTTCCGT	TCATGCGCGA	CTACCTGGAG	GTCTTGCGCG	GCCGGCTCGA	GCAACACGAG	120
	TTGTGCGATG	CCCCCATGTC	TGCCGCTGTG	CAACGGGACC	ACATTGCCCG	ATACACCGAG	180
	CTGCTGATGC	TGTATGCGCG	GAAGTCTGGG	GATGAGAAAA	TGCTGGCGGA	GCTCTTTGCC	240
	TCCTTGGTCG	ATAGTCTGCC	TCGCGGGATG	GGCGGAGCCA	CTCTTCGTCA	GCCATTGCAT	300
	GAAGTCATGA	CGTACCTGAT	CAGCGAAAAC	CAGCCGCAAC	AGGTGCTGAA	ACTGGTGGCG	360
	GGCATGCGCA	AGGCGGAGCC	CAATCGGCGG	CCGGGCAAAAT	CCTCCGTTCC	AGGCACCTTG	420
20	GCGCTGGTTG	TTTCCGCGTT	GCGACAGTTC	AACAATCCTA	ATCTCGTCGT	GAGCTTTATT	480
	GTGCAGGCAT	ACAGAAAGAC	GCAAACGAGA	GTGCTGCTGG	GACAACTCgG	GCTATGGTCT	540
	CTGGCATTTC	ATGGCCGCGC	TGTTGCGCTC	TCTcCCGagG	CGGCGAAgTC	GCCGCAgGag	600
	CTGGCGCagA	TATCGcCTGT	GGACCTGCCG	AAGGAGCTAA	TACTGAAGTC	CGtACCTgac	660
	AGCTGATAAT	GTGCgAGCTC	TATCAGCGAA	TCTATcCgAG	AAgCgATCGc	AGGTGCCCGc	720
25	GGAgGagTAC	CgCGAGATTT	AATCCAgCTa	TTTGCgCTTT	AcCAGGACTT		

1019RP

	GATCCATGAC	CCATGCTAGG	TGGAAGGAGC	CCTTACCCGC	TAACTCGGAC	TCCCTCTTCA	60
30	ATTGCCTTAT	CAGTTTGTA	TCCACAGCAC	CCACGTCGTA	CAACAACCGC	CCCATCAGCG	120
	TAGACTTGCC	CGCATCCACA	TGGCCTAGAA	CAACAAACGA	CATATGGGGC	TTCTTCTCAC	180
	GTACATATCG	AAGGATGTCG	AATGGGTTCC	GCGGGTTAGT	GGGCTGCACA	ACCTTCTTGG	240
	CCGACGGCTG	TTCGCCCTCC	TTCCGCCGCG	AATCCTCCTC	CTCGTCCTCG	TAGTTCTTCG	300
	GGGCCGCGCT	CTTGTTGTTG	AATTTTCAGAT	CGGCCACCTT	CTCGGCCACC	TGCTTAATCT	360
	CAAAGGCTCG	CTTCTGGGAT	TCCAACACCA	CGTCATCCGG	CGAGGGCTTC	ATGAAATTGG	420
35	CACTGGCCTG	CTTCTTAGCT	GCTTTATAGT	TGTTAGGATA	AAAACTGAG	AACACCTCCT	480
	CCACTCGCCT	CTTGAGCTGG	GTTTTGCGTG	GTTCGCGCA	TCCTGTCTGT	CTCGAGAGGA	540
	GCACGCTCGA	CAGCTGCAGT	GCAgGGCGCG	CTGCagGCTT	GAAGGACGGc	TGACGCTGCA	600
	GAAGAgCCCC	CagGGcCATc	CACTGGTCTT	GcCgtgCCTc	CGTCTTTGCG	GGGCGCGCTG	660
	cAACAgGCTT	TGcCTcAGCG	TCGcCGCGCG	ACTGcTTCGC	AgAGACgACA	GCGTcTGCAT	720
40	cAgCgACgCG	CCCCG					

1019UP

	GATCGCAGAT	TCATCATCGC	TGTTATACca	gGCTCTATCT	TCCTCGAGGT	CCTCGGGACC	60
45	AAACCGGGCG	CTCTCTTGTTG	TGCCAAGAGG	TGCAGGACCC	TCGGCGCGAT	CCTCGGCCAG	120
	CAGAGTGGCA	ATCTGGTCTT	CATCCGCTAT	CGCTGTCAGC	TTAGGCACAA	AAGCCAGTTT	180
	TTCCGTTTTC	TCGCCGTGAT	CATCCTGCTC	GAGCGTGCTC	TTCTGATCTC	TGCGACCCCTC	240
	TGCAAACTCT	TTGAGCTGCC	TTGCTGCTGC	CTTGTCAGT	CGCTTAAATC	TCAGCGGTTT	300
	CTGTTCTCTG	CCACCGCTCC	CCAAGCTCTG	GTCCGGCTCC	AGTGCTGTTT	CCAGTTCGTC	360
	GTCCGAATCT	TCGAAGCTCA	gCGCGACCAA	GTTTCTGGAT	GTGTTTCCCT	TCACGCGCTC	420
50	CCCGTCAAGG	ACAGCCTTCA	CCGTGGTGT	TGTGCGCTCC	TCCTGCGTAC	TcCGCAGGGA	480
	TACTAGCAGC	TcATGCAGGA	ACTTCTCtC	CCCTTAAACT	TGCCAAGCGC	CATGCagCTC	540
	TTAgTGAAct	TCACTGGATC	GTATGCATGC	ACGCGCGCTA	TATTGCATAT	CGGCTGcACA	600
	AACTTTCTGT	GACATTGGAT	gCGGATGTTG	GTGGATCACT	CCTTcAGCCG	GGGtCATCGT	660
	CTTAGCTCCT	ACCGTACTTG	cTcTCTcAgA	TgCatGATGt	GTaCCATcGc	ATcTTcAGcT	720
55	tGaCAGACTT	CCATATACGt					

1020RP

	GATCGTTCCT	GTTCCTGCGG	GCAAAGTTCA	GAATTGACCT	AGTGCCAGAC	ATGACAGTAT	60
	CGTTCAAAC	CCTCGGAGAG	TTAGCCTTGG	ATATCCACCA	TGAAGACAAA	AACCAGAGAC	120
5	CAACaGCGGA	TCCTACCAAA	ATGGcCAGAA	TACCGAAAAA	CCAGTGCAAT	TCTCCGGTTG	180
	CTTCACCTGG	GACAGTGACG	TTCATCCCAA	ATAGACCCGT	AACAAGATTC	AAAGGAACTA	240
	ACATTGTTCC	AATCATAGTG	ACCTTTCCCA	ACaTTTCaGT	AACaCGATTG	TTACACCGGA	300
	AGGACTCAAC	TTGCAATTGT	GCCAAGTAGT	TACCAtGTGA	ACGGGAGAAA	ATCTTCTCAT	360
	agGACAgTAA	aTTTTGAAAC	aTCGGGAGGA	CaTGGTCCCTG	AAATATCTCCC	AAATAGAGCG	420
	CtATATCagC	TCTTGGTTgA	gTGCGCTGGA	CaTGATGAtG	TTGTATGTTT	GAGCCTAgCC	480
10	TGGCagAcAg	AgGGTcgTgT	cCGCTAgCCT	GCAAgTTCgC	aaTGTTTTaTC	tCGAGGT	

1020UP

	GATCAGCACC	GTGCCCTTCG	TGTACGCCCTG	CTTGGACATG	GTGTGCGACG	ACCGTGTGTCT	60
15	GCATTTCTTA	CACGTGAAAG	CAATCATCAT	CATCGGCTTG	TCCACCTTTTA	TAGACCCGAT	120
	ATGCCGAAAC	TCATCTGCAA	TAgGCGGTTT	CTGGCTGTTT	TGCAGCTGCG	GCGAACCGCT	180
	GTGGAACCGA	TGAgCTACCA	AATGCCCCCC	AAACACCGGA	CCCAGCACGT	ACTGCATGCA	240
	GTTACGGCTT	GGGCGGAGTA	AACCAGCAAT	CCTGAGAgGC	CCCATCGAAC	GTCTAAGCAT	300
	TTTAAACAGT	TATACGTaGT	CAGCGGTTTT	CCTAAAACAG	GACATGAgAg	TGCGTCGAAA	360
20	GAAgGcGTCA	TCTCAAATTT	TTCAACTTTA	GAAGCGCTGC	CCGAAAAAgC	ACCGTCaCCA	420
	TTTATCTATT	ACAAGATGAA	CAgTTAGTGG	TGCCGGCaAT	TGTGTcAGAt	ATATgTcTCT	480
	GGACATGGAT	ACAAGACACT	CTCgCCaCaG	AAgGAGCAGG	AgATAgCaTC	gAAAATCTTG	540
	CagAAGGCTG	AgCTGGcTCA	gAT				

1021I2

	GATCTGCGCC	GGATGGCTGC	GAGTTGAGCG	CGGCGAAGAT	GTGTGACTCC	TGCAGAAAAAC	60
	GCTGGAGCTC	GATGTCCTGT	TCCAGCAGCT	GCTTCTCGTC	GCGGTGCGCC	GCGGCAGATT	120
	TCGGCGCGGG	CTCGGTCTCT	AGGCCCGGCG	CCTTGCCGCT	GCGGATGCGG	CGCAGTTCTC	180
30	GTGGAGAAGG	CCCGCTGTAG	GCATCTGACG	GCGCGCGGAA	CGAGATCACG	CGCGGCGTAT	240
	GGGCGGCCTC	GTGCTCGGAG	CTGGCTGAGG	CGCCGTCCAT	TTCCGACTGC	TCGTCTGGATT	300
	CAGACTGTCC	GGAGCGCGCG	TCGCCCTCGC	TCTCCGGGTC	ACTGTGCTC	TCGGAGGCGC	360
	TGGTGCTTGT	GTGCTGCTT	TGTGCAGCAC	GGGTCTTGTC	TACATATCCC	ATATCCTCTA	420
	GGGAGCCAAA	CTGGGCCTCG	AAGGCCCTCC	CCTGGGNCCC	GACNTGCTTG	NATTTATCTT	480
	CAATTGTTCG	TCATCCNNGG	GGGTTCCTTG	GCCCCANGAA	GTNTNTNANC	AGGAANCCCT	540
35	AGNANNANGG	TTTTCAAATT	CC				

1021I1

	GATCTCACCC	TGCGCACCAT	CGACAACCCT	GCATACGCCG	GCGGTGAGGT	CATCGGCAAG	60
40	GCCCGTGCCC	GCACACTCGA	GATGCGCCTC	AATGCCCTGT	CCGCTACCAA	TGGCGCGGCA	120
	CGAACCCCTCG	AAACCGTGCC	TATGAACATA	CGCAAAGGCA	TGGTTTCCAA	GCACCGCAGT	180
	CGCATCCGGG	AGCACGAGCA	GCTGGCCCCG	GACTCCGGCA	CCGTCTTCGC	CAAGGTCCGT	240
	CGCGGAGAGT	TCCGGAAGAT	AGACGCAACC	TACAAAAAAG	ACATCGAGCG	TCGCATTGGC	300
	ACGACCATCA	AGGCTGCAGA	CCGTGCCCGC	AAGAAACACC	GCGATC		

1021RP

	GATCCTCGAG	TTTGTGCGCG	GCGGGTCCCG	CTCATTTACC	TAATCCTGTC	TATAGTAAAC	60
	ACGTTGTTGT	ATCTACATAG	CGCACCTGTT	GTAACTTACG	CTGCACGCAT	GCGCGGGCGC	120
5	ACGTCCCCCA	CCAGCGCCCG	GTAGAACGCC	TGGCCCCGCG	GCCGCCCGCC	CAGCATGCAC	180
	AGGCGCAGCC	ACGGTTTCAT	CGTGATCAGC	AGGCCAGTCC	ACAGCGGGCC	CTGCACCAGC	240
	GGGATCAGCA	GGACGTCCCG	CACCACCACC	TTGGCGACGA	CCAGTGCCTG	GATCCCCGTC	300
	TCGCCGTCCG	CCGTCCGCTC	GCCCTCCTTC	TGTGCCCGCA	GGTGTCTGCT	GCGCGCGCTT	360
	TCCTTCGCCA	GCGTTCGCGC	GAACGTCTTT	TTCGAACCTG	ACGTCCGGTA	TCGTTATTGC	420
	TTGGGGTCCA	TTGGAACGGC	TGTTCCGGGT	CAGAGGGAGG	ATTCTTCGCG	TGGTTTGGTT	480
10	TTTACGAAGA	CGACCCTCGG	TGAGAATGTC	AGTTTGGCCA	CTNGGCAGCC	CCAGGAAGGA	540
	CCGNGAATTC	AAACCACCTG	AGTNGGGCGN	CGNGTAAAA	ACGCTAAGTT	AGTGCNNTGC	600
	ANACCCNCCT	C					

1021UP

	GATCGCGGTG	TTTCTTGCGG	GCACGGTCTG	CAGCCTTGAT	GGTCGTGCCA	ATGCGACGCT	60
	CGATGTCTTT	TTTGTAGGTT	GCGTCTATCT	TCCGGAACCT	TCCGCGACGG	ACCTTGCGCA	120
	GGACGGTGCC	GGAGTCCCGG	GCCAGCTGCT	CGTGCTCCCG	GATGCGACTG	CGGTGCTTGG	180
	AAACCATGCC	TTTGCGTATG	TTCATAGGCA	CGGTTTCGAG	GGTTCGTGCC	GCGCCATTGG	240
20	TAGCGGACAG	GGCATTGAGG	CGCATCTCGA	GTGTGCGGGC	ACGGGCCCTG	CCGATGACCT	300
	CACCGCCGGC	GTATGCAGGG	TTGTCTGATG	TGCGCAGGGT	GAGATC		

1022RP

25	ANNNNNNGNN	NNNANGGTGG	GGCGTGTTNG	AaTAGTGGGT	CTtTCTGcCG	GGGTCTGTGC	60
	AGAAAACGAG	ATTCTGGGGA	GTATCTGAAA	TECTTTGTTG	CGCCGAGCCG	tCTGGGTCTG	120
	CGTCAAGCGA	CAGCGAGTTt	GCGACAGGAA	CTGAAGCTAA	TTTCGTGTGCT	GGAGGTGTTT	180
	TGGGGCTTCG	CGTTTTcCAGC	CTTTCAGGAA	ATCTAGAGGG	GCTGTGTGCT	TTGAGGCTGA	240
	AATCAGGGGA	ATAGCCTGAA	TTTGCGAGCG	TGAATTGAGC	GGTTATATGG	AACTGTGGTA	300
	CATCGNCACA	CTGTaCCACG	AGGACAGCGA	ATATCTGACA	GTAGGGcGTC	CTtCGtAAGA	360
30	ACACAGtGTA	TCGCGTgAGA	TAGGTGTtGA	TTGAGTCTAG	CGTgCTAGGT	ACTCTTtAAC	420
	TTtCAGtCGG	tGTttttt					

1022UP

35	GATCCAGCAG	ACGTTTTAAT	CACCGATTTT	TTCGGTAACA	TTCAAAATAT	AATTCTCGAT	60
	GACAGTGAGA	TAGATGGTGA	AACTCCAGCT	GGACTTACGG	AATCTGGCCG	GACTCGCAAT	120
	CTGCTAGAAT	TCGCAAAAGC	GAAATTTTTT	GGCANTGTAG	ACGCAGAGAC	TAATGGCACG	180
	CATAAAAACG	TGATTCCAAG	CTATCCAGTG	GTAAATGAGG	ATTTACTAAG	TGGGGNANCA	240
	AATGCATCCA	CAAACAAAAT	GATAAAATTG	TGGGGGATTA	TCATCTTCCt	GGcACTAACG	300
40	TCATTAATGA	TGAAGTACGC	CAACACTGAA	AACATATCGG	GTAGTCGAGc	ACTATTATgT	360
	TTCTCTTAGA	AAAATGCTTC	AtGCTTCATG	GAATTAAGGc	GGcaACAAGT	GCAAGGTTAa	420
	GAACGGaaTT	TTaCTATaG	CGCGAAATTT	GtaTaTaTTa	T		

1023I2

	GTCGAGGGAA	GTAACCAATA	TATTACAGAG	GGCTACCTAT	GGCATCAATG	AGACGTTCCG	60
	AACCAAAGAT	CGTCGGGTCC	TGGGTGATAG	CGCTTCTGTG	TGGGGTCTTG	TGTGCAAGCG	120
5	ACAACCTTCA	TACACGCGAT	ACTTCCTGGT	TAGTGTTAAT	CTCAACAGCG	GTGAAGTTAT	180
	CTTCGATGAC	TTCAAAGAGG	AGCGTTTTCT	GACGGAGGCT	TTGGAGACGC	GAATAAAATA	240
	CACAAACCCG	AGTGAAGTTG	TGGTCGGAGA	TGGCCTTGGC	TCAGAAATCG	AAAAGGTGTT	300
	TCATACTTCA	GATTCCGATA	TCACTCTAAA	TAGGATCGAG	CTCGTCGGGT	TGTATGAAGA	360
	AATCTTTCAGT	GAGCCGCACC	CAGCCTTTAG	GGGCAACGTT	CCTCTGCAAA	CAGCGCTCAT	420
	GCTGGTGCAT	GGCTACCTAA	CAAACTTCAA	AAATGAGAGT	TTACTCTTCT	TCAAGGAAAA	480
10	CTTTAAACCA	TTCTGCTCGA	AGACGCACAT	GATTCTTCCC	TTCTAGCGCT	ATTGGAAGCT	540
	TAGATATTTT	GGGGACAGTA	CAGATAGGAG	CAGTAAAGGT	CCCCTGTTAT	GGGTNTTAGG	600
	TCAANCTAGA	ANAAC TAGGG	TTAAGGACTT	GGAGGACTGG	NTTGAAAGGC	CTTNTAATTT	660
	GGTCAAGTCA	ANAGAGTTGN	GGNNGCCAAN	GATTACACNAG	GNGGGNATTN	TCATGGCTCG	720
	GAATT						

1023I1

	GTCGAGAAAA	CAGAGCTTGA	GGTCCCACTG	TTCTTTTTCA	CTGCGGATGT	CTCTGTCTGC	60
	TCCACGACCC	CCACTTTTCA	ATTGTGGTGC	ATCAAGCGCT	GCAAGTGGAC	TTCGAGACGG	120
20	GTGTCTGGGA	TGGTGCAGTA	CGCAAACCTC	TTGTGCTTGT	GATCAGCGGG	GTCGTCTCTG	180
	TGTACCGTAA	GCTTGCCGGG	CACCAGCTTG	ATC			

1023RP

	TGCCCCGGCAA	GCTTACGGTA	CACGAGACAG	ACCCCGCTGA	TCACAAGCAC	AAGAAGTTTG	60
	NGTACTGCAC	CATCCCAGAC	ACCCGTCTCG	AAGTCCACTT	GCAGCGCTTG	ATGCACCACA	120
	ATCTGAAAGT	GGGGGTCTGT	GAGCAGACAG	AGACATCCGC	AGTGAAAAAG	AACAGTGGGA	180
	CCTCAAGCTC	TGTTTTCTCG	ACGCTAGGGA	TAACAGGGTA	ATACAGATAT	CAGATCTAAG	240
	CTTGCCCTCGT	CCCCGCCGGG	TCACCCGGCC	AGCGACATGG	AGGCCAGAA	TACCTCCTT	300
	GACAGTCTTG	ACGTGCGCAG	CTCAGGGGCA	TGATGTGACT	GTCGCCCCGT	ACATTTAGCC	360
30	CATACATCCC	CATGTATAAT	CATTTCATC	CATACATTTT	GGATGGNCGC	ACGGCGCGAA	420
	GCAAAAAATTA	CGGGTCCCTG	CTGNAGACCT	GCGAGCAGGG	AAACGCTCCC	CTCACAGACG	480
	CGTTNGATTC	TTCCCCACGG	CGNGCCCN TG	TNGAGAAATN	AAAGGTTAGG	ATTNGCAATG	540
	AGGTNCTCCT	TTCANNTNCT	CCCTTTTNAA	ATCNNTGTNG	GTCAAGTCNT	CANATCAAAT	600
	TCCCAACATT	AACACCN TGG	TTAGGGGAAGT	TCANNTTTCN	GGGGCCNNGA	TTANTTCN	

1023UP

	GATCTCAAAC	CTGAGAATAT	TCTACTTCAT	CAATCTGGTC	ACGTTATGCT	TTCTGATTTT	60
	GACCTGTCAG	TACAGGCAAA	AGGAACCAGA	AATCCTCAGG	TTAAGGGAAA	TGCCCCAGTCT	120
40	TCGCTTGTCG	ACACAAAAGT	TTGTTC TGAT	GGCTTCAGGA	CTAATTC TTT	TGTTGGAACG	180
	GAAGAGTACA	TTGCACCTGA	GGTCATCAGG	GGAAATGGCC	ATACAGCATC	CGTGGATTGG	240
	TGGACATTGG	GTATACTTAC	TTACGAAATG	CTCTTTGGGT	TCACTCCTTT	CAAGGGCGAC	300
	AACACAAATC	AAACGTTCTC	CAATATTTTG	GAAGAA TGAC	GTTTATTTCC	CAAACAATAA	360
	CGATATATCT	CGCACTTGCA	AGGACTTGGA	TTAAAAAGTT	ATTGGGTCAA	GAAAGAGAGT	420
	AAGCGACTTG	GTCAAAGTTT	GGCGCCAAGT	GAGATTAAAA	AAGCATCCCT	TTCTTTTAAAG	480
	ACCCGTCCAG	TGGGCGGTTA	TTGGAGGGAA	CCAGGAACCT	CCCTTTTATC	CCCGTATTGA	540
45	CGGGAGATGG	GTACGACTTT	GGAAAGNTAT	CACATTAAAG	GATGTTAAAA	AGGCCGGGAA	600
	TCCGGCCAC	CCGGGTTAGT	CTCATATTCA	AAGGCGNGGT	TCNNCN		

1024RP

	ATNNNNNGNN	CANNNGTGGG	GCGGAGCGAN	TAGTGGGTCA	GCANGGTGCG	CTCGGTGTgT	60
	GCGCAGCCGT	TGGcATGCTC	GCGGATCCTC	GCGTCCAATA	TACCAGAATG	CATCATGCTT	120
5	CGCTGGCTCT	ATATTGACCT	GGTGGCCATA	TATGAAAAGG	CGGTCCTTGA	AGTTTtGTAG	180
	AAACTCGTCT	GCCTGAGATG	GCGTAGCGAA	CCCAAGGAAG	CATTTATTGC	GGCATTTACG	240
	AGGCCTGGAA	ACACTAACTA	CCCCGTACTT	CTCATCTAGC	AGTGAAGGG	GCACGTCTGC	300
	GGAAGGAAGC	GGCTCTGGCA	ACGTTTTCTC	CgCCGATAGA	GCATATGGGT	TATCCTtGTT	360
	GATGGACTTC	AACAGTTGTC	GAGCATATT	TATCCTGGAG	GCATTTGACG	CTGGCAAATT	420
	TGACAGGTAG	ACACTGgATG	GCGGcGTTAG	tATCGAATCG	ACAGcAGtAT	AGtGACCAGc	480
10	ATTCACATAC	GACCGGAGCG	ATgATaTTAC	TtCCTTGNGN	ACTTAANTTN	CCCAATCTTN	540
	NGCCAGATTN	ATTTTCG					

1024UP

15	GATCTAAATT	CCCACGCCGC	TGCGGCGGTT	TCTCTGCGAG	TCTTTGcCGT	GAAGCACGAC	60
	ATAATCGAGC	CCAAACACAG	CAAGATCGCA	GAGAATCAAG	CTTATGTAAG	TCTCACGTGA	120
	CTCGANGCGT	GCAGAACGGT	ACGGGTGTGC	ACTGCAGGTG	CCACGCCATG	TCTCACATGG	180
	TTGTaACACG	GcGCGACCGC	GGTTCGGAAT	ATCAAACAAA	CATATgTTTG	CCGCAAAAGG	240
	GACTGGTTCC	CGCAGCTGcC	ACCCgCAGGG	GCACAgcGCG	GcAATGCAGA	GTCGCGTTAG	300
20	GGtGCCgTCG	CcCCGATGGG	GCAGtGTCGC	CGCC			

1025RP

25	GATCAGCCCCG	TTGCCGCCGC	CGCCGTTGTA	CTTCTGGTTC	TGGATGGACC	CCGGCGTGAT	60
	GGCGCTCTCG	TTGCCGTACT	CGTCGCTGCT	GCGCAAGTCG	CAC TTCAGCG	CCACTAGCAC	120
	CAGCTTCACG	CCCTCGCAGT	GGTCCGCAAT	TTCGCTCACC	CAC TTGTCT	TGACGTTCTC	180
	CAGCGAGTCC	CGCGAGTCCA	CCGAGAAACA	CAGCATAATC	GTGTGTGTGT	CCGAGTACGA	240
	CAGCGATCGC	AACCGGTCAA	ACTCCTCCTG	CCCAGCAGTG	TCCCACAGGC	TCAGCGTGAT	300
	TGTCTGGTTG	TCCACGAAGA	TGTCATGGAT	G TAGTTTTCG	AATACCGTGG	GCTCGTACAC	360
	CTTCGGAAAG	TACCTCGCGT	GAACACGTT	AACAGCGACg	TCTTCCCGCA	AGCACCCTCT	420
30	CCGAgGATGA	CGATCTTGCG	CTCGATAgGA	TGCTTCGACG	AcGAgCTCGA	CCACACAGAg	480
	GCATCTTG TG	TTTGTAgAgC	TGGTGGTGGG	AGCTcCtCTG	ATGCCAGTCC	ACGCTACaAA	540
	TACAGCGTTT	GAgAcgAAAT	AcTAgCTGCT	ACTGTCCTtT	CTCTCTGACG	AgGTGCACGG	600
	cGCATCCCCG	TTATAACTGT	C				

1025UP

35	GATCCCCATG	AGAATGAGCG	CATCTTGGAT	ATGGCGGCGG	CACCCGGTGG	TAAAACCACC	60
	TATATATCTG	CCATGATGAA	GAACACTGGT	TGTGTCTTTG	CAAATGACGC	CAACAAGGCA	120
	AGAACGAAGT	CCTTGATTGC	GAATATTAC	CGTCTCGGCT	GCACGAATAC	AATTGTCTGC	180
40	AACTACGACG	CCCGCGAATT	CCCTAAGGTT	ATCGGTGGAT	TTGACAGAAAT	TCTACTTGAT	240
	GCCCCTTGCT	CAGGTACAGG	TGTTATCGGC	AAAGATCAAT	CTGTGAAAGT	AAATCGTACT	300
	GAGAAGGACT	TTATGCAAAAT	TCCACACCTG	CAAAAGCAAC	TGATATTATC	TGCAATTGAC	360
	TCTGTTGACA	GCAACTCCaA	GCACGGcG GT	GTCATTGTCT	ACTCTACTTG	TTCCGTTGCG	420
	GTTGAAGAAA	ACgAgGCCGT	GGTCGAATAC	gCCTACGGAA	gAgACCTaAT	GTCAGCTGTT	480
45	GAAACCGGCT	gGcTATTGGT	AAGGAAGGCT	CaCTAgCTaC	GA		

50

55

1026RP

	GATCCAATTG	CTGGTCATAC	AtaCGCATTA	ACAGATTTTA	TTACTATGTA	TCCAACGTGA	60
	ATTGCTaTAT	GTACCTTATT	ATCGGTTTCA	TAAAgATGCT	TTAATTTCTT	ATTCTGAATC	120
5	GGAGTCgTtT	GACCGGCGCT	TAgaCTGGTT	ATGCCTCtTG	CCATCGTTTT	TCTCGAAAAT	180
	GAAAAATCTA	GCTTCACGCT	CgGCTGCAGG	CTTAgtTCGTa	TCTTGCTCAT	TGTTAGTTCT	240
	CCTAtGACgG	TATCctGGGA	AgGTATCCCA	cTGGAAtTTg	TgCgACCTCT	CAAGCTTtaA	300
	aCCATgCTCC	TTGGCaaAGTA	cCTtAgGCTG	CCaAGAATCg	TaTgGATCAC	CGGCAAAATag	360
	GGACAAAATG	ATCctCCCCA	TATCATCAGA	TGATtGttCT	TtttCCTACT	tCatATCCGG	420
10	AAAGATGGGC	AACAACtACC	ttCTTATTTCG	cCAGcTTGAT	AGttGtttAC	AGcTATCAAA	480
	AATATCCCga	TaGAGcTCTG	aGcTCTCT				

1026UP

15	GATCTAGCAG	ACTAGACTCT	CTATCGCATC	AAGTTTCTGT	TTTCAAGTCT	GGGTTTCTTG	60
	AGCAACCTGG	TGCCCCtATA	CCTGTGTcAG	ACGCACAGCG	AAGCAGACGT	CTATCGACGA	120
	TGTCGAACtT	ACAGACGAAA	AAACAGCGCC	CGCCAGCTAT	TCCAGAGGCA	GACGTATCAC	180
	TCCAGGCTAT	CAAGAAGCGG	CGCATGTCCG	CCAGGTCTTC	TACCTCCCGT	AAGTCGGGTT	240
	CTGCCcAGCG	TATTAGTgTT	GTGCCACGGG	CCGCAGCTTC	AGAGTCATAT	GTGGTTCCAC	300
	TTGCTGGTGC	TCCTCTGAAG	AAAGAGTCTG	CGGATGACTT	ATTTCAAACG	ACTGCTTCCT	360
20	TTTATGAACG	TTACACTATT	TCCACACTGA	AAGAAATACC	GAAAAACATT	GCAGATGAGG	420
	ActCTGCcCG	ATATACCGTt	aACGAgGATA	GCaTCaCTAT	GGCTGAcTTT	TGCaaACCTC	480
	TATtCcCGAT	AGGTGAAGTa	tCTGATAATT	TCACCGGGCG	AAAGAAGcTG	CAAAAGCCAA	540
	GATGGAAGCT	CGGAAGAAGC	GCCGcGAACt	CCGACAGATg	GcTaAgCGTc	AATC	

1027RP

25	CATATCGACG	TACTCTGGCG	TTTGTTCCTC	TTCGTCAGCA	GGAACGCCGT	CCGGCATAGG	60
	CTTACTGACT	TtCACAGACA	TGATTCTTTt	GCTGCAAGTA	AAGTATATTA	ATGGCGCTGT	120
	CAAAAATGGT	AATAGTACGG	AAAGAGCAAC	CTGAGAAGCG	TCCAGGGCCT	GCGATAAGCC	180
30	GTTTTTACCT	AGAGCAGTGG	ATACAGCTAA	TGTtGGAATC	AATGCAATGG	CTCGTGTcAG	240
	AATTCTCCGT	TTCCATGGGG	TTATAGTCCA	GCGTaTaTGG	CCTCCGCATA	CTATTTGTCC	300
	AGCTATGGTA	CAGACAATNC	CTGCCGATTG	GCCCGAGATT	AAGAGTGCGA	GCATGAATAT	360
	GGTACCTGCC	GCTGGTGCCA	AAGTGTtGGA	TAATAGGTGG	tGTATCGtGT	ATAGATCCgC	420
	ATCGATGGcT	TCCGGGGTAT	CATACAGtGc	GcTA			

1027UP

35	GATCAACGAG	TAAAAATGCC	AGGTGTTTTCC	GTTAGGTACG	TGTCATGAGT	GCTAGTTTAT	60
	GGTTTGGTAC	GGCTGCTGGG	GGGCGCTTTC	TGGGAGGTTT	CAGCGCTCAT	ACGTTATGTG	120
	AAGATGCTTC	GATCGNGAGG	GTTGCGAGAA	GGAATGGGAA	TGTGCCAAGC	AGGACTTGGT	180
40	GATTGGTTC	AGAACGTCCG	TGACTGTGTC	AAATATGAAA	TCATTGGGCG	AAACTTAGCT	240
	TGCTACGGAG	TCCAGCATGC	AGAACGTGCG	GCCGAAGCTA	GCTGAGGCTC	GATGAGACGG	300
	TGGCGGAAAT	CCTTCGATCC	CAGGCCAAAG	CAGACGTACC	TACCAGCTTT	TAATGTGCCC	360
	GCCTACTAAC	ATGATATACA	GAGACGTTCC	AGCTCAAGAG	TTCATCAACG	CTTACGCTTC	420
	TTTTCTTGCA	AAGACAAGGT	AAGTTG				

1028RP

	GATCATGCAA	ACGGAGAGAA	GGAGAAGAAG	TCTAAGAAAG	AGGGCACTAA	AGAGAAGAAA	60
	GCCaAAAAGC	AGGAGAAAAA	GGAACTGAGA	AACATCATTTG	AGGAGTCCGT	TGAGCAAAAT	120
5	AAGCTAGCAC	TGATAGAAAA	GGTGGAGGAA	GAAAGAGGCC	GCACGAAGGA	GAAAGACCTT	180
	GACATCaAGT	TCAGGTaTCG	GGAAGTTTCG	CCaGAAAGTT	TTGGCTTGAC	CACCCGTGAG	240
	ATATTTTATGG	CTGACGACGC	TGCCTTGAAT	GAGTaTATTG	GCCTCAAGAA	ATTTGCACCA	300
	TATAGAGCAA	AGGAGTTGCG	CaACAAAGAT	AAAAGGAAGG	TCaTGAaGC	TAAGCGTCTA	360
	AAAGAATGGA	gGAAAAAgGT	GTTCaATAAC	GAAAAATGGGT	TGGCCGATGA	gGATgAgGcC	420
	CTTGATACCC	AgGCgGCTCC	TAAAAAGGAg	AAAAGCcgtTT	CTAAGCaCAA	GACAAGTAAG	480
10	TAATATTACC	GTCTTTTATGT	aCgTTCTcGCC	gTAATTATAT	TTTGCTATaC	aTaTaTATTA	540
	ATTTAAACTT	T					

1028UP

15	GATCCGCGCC	CGGCACAGGC	CTGGCAGCAC	CCATCGCCGC	ATGCTGTGCC	TAAGATGTCT	60
	CAGAATTACG	CGGCCGCTCA	GGCGGGCGCC	AGCCCCTCCA	TGCTTTTGGG	CCAGGAAGCC	120
	TTCCACGAGC	TGGGCGACTC	GCCTGGCATG	TCAATGTACA	TGTCGCCCCA	GACCCATAGG	180
	CTCAAGGGCA	ATGGCGGGTA	CCTGTTGCCG	ACCGCTTCTA	TCTCCGACCC	TTCCGTGCTC	240
	GGTGACACCG	GCCGCCCTCC	GTCTTCTCAG	TCATTGACAT	CGCACCTTCT	GCGTACCCCCG	300
	AACTTTAACA	TGAATGACTA	TGTGCATAAC	CTTTTCAGCC	CCTCACCAAG	AATAGaCCCG	360
20	CCAGGTaGCT	CTGGGAATAT	ATaGGGcCTC	GCACACATTT	AGCGCACAGT	ATACTAgCTA	420
	ATCCTACATT	CTCTGTCATA	gTAATGCCTA	TGTCAGCACA	CCTGCCGTAT	AATTTcATTA	480
	TTTCTGTMTT	CATAAATGCT	GaCATATGTc	ACGTGGCTGG	ATCaGCaCgT	gATGGCAAAA	540
	TTCTTATGAA	TGAaCCTGTT	CATCTCGTCA	gACAATACAT	TATACACgCa	TCCaTCTCTC	600
	GGTATGAaAC	GGACTCTCTC	ACaCTGGA				

1029RP

	GATCGTAACA	CTCTGGAGAA	GTGGAAAGAG	CTAGTCCCTC	CGAGCTGTAA	ACGATGCATG	60
	GATGCGCTTC	ATCACAACCG	GTACGACACC	GCCGAGTTTC	CGGAGCACAC	GCTCGAGGAT	120
30	GTGGGAAAAG	GGGTTCGCGC	CGATGCAGTG	GTATACCATA	TTGCGCCACT	GTGGCAATTT	180
	CCGATGGGAC	TGGATCGGGC	CGTGCTGCAG	AGCTCAAAGA	AGGTTTGTGT	GCTATTCTCG	240
	AAGATCGATA	TGGTGGTGCA	GAGACCGTCG	CACATGCCGC	AGGACGTAGG	TGCATTTTCT	300
	CAGAGCTTGC	TTTATCATGA	CCTGCATGTC	AAGATCACGA	ACTTCCGCTT	CTTTTCTGCG	360
	CTGAAGCAAT	GGAACATCCA	GACGGTGCGG	AACGCTCTGA	GTAAAGAAAG	TTACTTACTT	420
	GGCGGGCCAA	ACGCGGGCAA	GTCTGTCATTG	ATCAATGCCC	TGATGAAGAC	TGTTGTTTAC	480
35	GAAAGTCGGC	GTCTCGTATC	CTCAAAGCAG	TCCTCTGCCA	CCCCTGCCGA	CCTGCCTCCA	540
	AAAGCGCATT	TGGACATCCA	TTCTGCGGGT	GTGAGCACA	TACCGAACTT	CACTCGCCAA	600
	CCCAGCAATA	CGATATAAAG	GGCAAGATCT	CCACGATTTT	CAGGCTACCG	CACAT	

1029UP

40	GATCTCGTGG	TGTTTTGCAA	CTTGGTGCGT	GACGCGATAT	CTCAGGCTTT	GCGTGCTGAG	60
	CATGATTATG	AGGTGAACAA	GATGCGCCGC	GCGCTCTCCT	TACTCCAAAA	GCTGTATATT	120
	AGGGATAGAA	GGACCAATTT	CCTCTCCGCG	GCCAAGGGGG	ACGACTTCTG	GGTCATTGCG	180
	GATACCACGG	TGAAAAACTG	CGACATTACA	TCTCTCCTTC	TTTACTTTGA	TGAGTTCTAC	240
	AGAGAACAGT	TGGATTTGTT	CCTGGCGCAG	GGCCGTGCTC	GGCACGAGGT	CCCCAGCGGC	300
45	GATCTCGTAG	CGTGGGAAAA	CGATATAAAA	GTAAAGTTCT	TTAGCGAGAA	GTCATCGAAG	360
	CACGCTTTCG	GGGGTTCCCT	TGCCCTGCGG	AAATTCGAAC	TCGTACTGCG	CGCTCCGTTT	420
	CTGTGCCCC	TTTCGCGAGCG	GGTCGCCTAC	TTTGAAACGC	TGATACACCA	CGACCGACGG	480
	CGGTTGCAAG	GACGCCACAC	AGGACCAGCC	TTGCGCCTGC	CCGACCTGTA	CTTCCCCGTCG	540
	TCGCGGCGGC	AGCGTGCGAT	TATCTCCAGG	AACAACATCC	TGGAAGATGC	ATACSAGGCG	600
50	TATTATCCGC	TGGGCGAAGA	CTTTAAGGAC	CAGCTGGC			

1030RP

	GATCTGCTTG	TTGCGCAACG	CTTCCCAATC	GATgTCGCTG	AGAAAGGGGT	GGGCGCGGAC	60
	CTCTGCGCCG	TCGTTGACCG	CACCGAGGCG	GTGCTTGGGA	TTGCGGTTCA	AAAGGCCCTT	120
5	GACAAAGGAG	CGACCTTCCG	GCGATAGCAC	GTCCCTGGGG	AATTTGACCT	TGCCAAACGC	180
	AATCTTCTGG	TACATCTTCT	GGTTGTCCCT	TGCAAAAAAA	GGCGACCAGC	CACAGCACAT	240
	CTCGAATATC	AAGACGCCCA	GCGACCAGAA	GTCAACCAAT	TTCGTGTAGC	CGGTCTCATC	300
	GAGCAGCAGC	TCGGGCGCTA	GATACTCGGT	GGTACCAGCAG	AACGTATTGG	TGCGATCCTT	360
	TAGGTCCGCT	TTTGAGAGGC	CGAAGTCACA	TAGTGCAGTA	TTGCCGtTGG	CGTCTAAAG	420
	GATGTTTTCT	GGCTTGAGGT	CGCGGTACAC	GATATCATT	TCGtGAAGGT	ATTCCAACGC	480
10	AAGCACCAAC	TCGGCAATGT	AGAACTTTGC	CCGCTcCTcC	GCGAACCAGC	CTTCTTTCTG	540
	AAGGTGCCAG	AAAAGCTcAC	CAcCGNTCAG	GAAGTcAGTC	ACCAAGTATA	AGTCtGtGGG	600
	CGTTTgAAAA	GAAAATTTCA	ACCAaCAATG	AAGGGACaCg	ACTTTgAgCA	gTaCgAACgA	660
	GATGTTgcGC	TCACCAATAg	TATGtGCA				

1030UP

	GATCGATTCC	CTGAGCATGT	TTTTCCCTAT	GCTGCAGGTT	TTACATGGTG	ACATTGCGGA	60
	TGCCGAACCTA	AAGAACCCTTA	TGTCTTTGAA	ACTCTGGAAC	ACTTACGGCG	GAATTCCTGA	120
	ACGCTGGCTA	TTCACTACTC	TCTACAAGAA	ACAGCAAGTT	ACCGTAAATG	ATACCGTGCA	180
20	GCTCGAGTGG	TATCCTTTAC	GGCCAGAGTT	TGTAGAATCA	ACCTATTCCC	TTTACAGGGC	240
	CACTAAAGAC	GCATTTTATC	TGAATATCGG	ACGAAGCATC	CTCCAGGCTC	TATCAACGCG	300
	CTTTAAACG	AAATGTGGGT	TTGCGGGCAT	ACAAAACGTC	ATAACGGGAG	AGCCACATGA	360
	TAGGATGGAA	TCGTTCGTTT	TGGGCGAGAC	CTTAAATAT	CTCTATCTCC	TCTTTGACGT	420
	ATCCAATGAA	TTGCATACAC	AAAAACGCAC	TAACCAAATA	TTTAGCACTG	AGGCGCATcC	480
	ACTGTGGtTG	ACTGCCTCGA	TGAAGgCTCG	CTACGAAAAG	AACAAGTaCT	GTGAAAACGA	540
	CgTGTATATA	CAGAACTTGC	GTcGcCTACA	gGAGCTTgac	CAGCTGAAAA	GcCgtGCCAA	600
25	TTCATTCACT	GcAGAGGaAG	cCATGATaCC	AGCTTCAGAt	TTCAAAACAG	AAGACTcCgA	660
	GGAGtCTTTG	AAGGACCGCG	TTGcAgcGCC	AtaCTaGAGG	CCTACACGTa	GAtaCgACaC	720
	gTTCGTGGaA	cATGCAGACC	TTTCGCGACA	A			

1031RP

	GATCTTAGTA	ATGATCACGT	GATTGGATTA	CCGCTTGTGC	GTTTTGCTCT	CCGCAAAGCG	60
	ACATTTACAC	GGGAAAAGCG	GTGAACTCCC	GCCGAAACCC	AAATACTCGT	ACACTATGAC	120
	TATAGACGAC	AATGTCGATG	ACGTGAGCAC	AGTTTAACTC	TAGTGTAACA	TCACGTGCAC	180
	ATACCTTCTC	TGCCACCCAC	ACATTAACCA	TTTATTTGTG	GTCACGTGAA	ATGAATCGAT	240
35	GCATTTTATA	ACTGCAGGTT	AGTTGAGCCA	TCTCGCCAAC	GATGTCCTGC	GACAGCATTC	300
	GGGGCACGGC	GCGTCATGAG	TGATTGGAAG	GAGGCACAGG	ACTCCACGGG	GCGTGTTTAC	360
	TACTATAATT	CGAAGGGGGA	AACGTCATGG	AATAAGCCCA	ACGACACGCC	AGTTGAGCTG	420
	GAACCGCGAC	TCGAAGAATG	TGGCTGGAAA	GTGGCAACGA	CGGAGGACGG	TAACGTGTAC	480
	TATTACAACA	GGGAAACTGG	CGAAAGCAGG	TGGGAGAAGC	CGGAGTTGGA	GCCAGCCGAG	540
	GAAGTGCCCC	GGGAAGARGA	CGAACGCGCG	CCGGAGGARG	AGAAGAACGA	GCCGTCCGCT	600
40	GCTGARGAGC	CCGGGGTCCG	GATCGAACTG	CTGCTCAACT	CAAAAC		

1031UP

	GATCANCGAN	CAGCACGGAC	AAATATAACA	GCAGCACGGG	CATTTGTCTA	GTCGGCTGGT	60
45	GYYYTGtGTC	CACCGTGACG	CTGGCGCTGG	GCTGGAGTGC	AAAAACCGGA	GCCACAAGCG	120
	TGCGCGTCCG	ACGGGGAAAG	CTGCGATCGT	GGCAGCAGCA	GAGAATGGGT	GCGGGAGTGC	180
	YAGAGCGGTG	CTGGGAGCGC	GCGGACGCGC	GCACGCTGCG	CGCGGCCGCG	CTGATGCTGG	240
	GCGCGGCATA	CCGAATCAAG	AAGGCACACG	CGCGGGCGCA	GCTGGCGATG	CAGGTGGCGC	300
	GGCTGCSCCG	CCTGCGTGAC	GTGCGGCTGC	GCCGCGGGCG	CGTCCCCTG	CTGGCKGTAC	360
50	ACCCCGGTCT	GGTGAAC TTC	GCGTAC				

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1032RP

	GATCTTTAAC	CTCTGGACTT	CAATCTTCTG	GGTaaaAGCA	CAAGTTTAGA	GATGTATGAT	60
	CCAAGCACCA	AACTACAGTC	TCGAGACAGC	AAAATAATCC	TACTTATATA	AACTGAACGT	120
5	TGCAATTCTT	TAAAAAATTT	ACTAACTTCG	ATTAATGCGG	CGCCGGTGAG	CGCCTCTGTT	180
	ATTAGCTGAG	TCATGCTGAG	GGTTTGGCTA	GGAAGCATCC	GCTCTTACTA	CGTATTTACC	240
	AAGGCACAGG	AAAATGTGGT	GGTATTCTTG	ATTTTCGGCGG	CGTTTTGTAC	ATTACTCCAT	300
	AGCTCATGGT	CAGCAATCCC	GTTCAATGGA	CATTTGCTCA	ATCGTGAGTC	TTCCACTGGA	360
	CTTGAAATCC	CGCAGGGATT	TTCCGGCTCCT	GGCTCAACCA	GGTCGCCCGG	ACACCTACAG	420
	CCGAAAAAAT	TGCTGCTTGG	ACTAGGTCCG	CTGACGTGGA	CATGCGAGAT	GACTTTAAAG	480
10	TGATACATTA	AAACCAGGGC	TGTATGAACT	CAGCAAAGGT	CTCTTTTATA	CAGTGTGCAT	540
	ATAATATTTC	GGGCGCTTGC	AATTACCTCA	TGCCAGGTac	TCGTAAGATT	CGCCGTCCGC	600
	GAGCGCTGTA	gGtATTCCCTT	GCTAATTAAAG	tTGTCgAtgG	CCTTCTTGAT	AGAGAtaCCt	660
	TTGCATTTGA	CCGTtGTgAG	AtTCgGCTAT	GCATTCGTCA	CCAAAGTgGC	ATGAGAgAcG	720
	ACCCGTTTGC	TTTCATAATT	CTGaCgATaC	AAGCTTCAGA	ACaATTGCTT	TCTTG	

1032UP

	GATCCCGAAA	ATAGACTACA	TCTGCCgcaa	gCAGCGCGCC	CTATCTGCAT	TTCTCTTCTt	60
	GGTGGTTGTC	ATGTGGGTCA	TCACGTTTAC	CAITAGCATT	CTAAGGGTAG	TGGAACGGGT	120
	GAGTTCACCT	TCACCCAGAT	AAAAGTTAAC	AGGACAAGTG	AAAAAAAACG	GGGATAAAGG	180
20	CATCAGTTAT	GTAATAAAGA	GCTATACGGC	AATAAACATT	TAAGTAACTA	CCATGGTATC	240
	TCCAGGGTAT	TACTAGGTTT	CCCTGAAGTT	TCCAATGTGC	CTTCGTTACC	CGGTGTTTAT	300
	GCAGGCTAGC	GCGACAAGAA	AAATGCGGTC	CCACCCATT	CACGATTAGC	GGTGGCAAAA	360
	GTCCATAAAG	TTAGGCAAAAT	AAACACATAA	CCATCCCTCA	AAAAGCGCTT	GAGCAAGGCT	420
	ATCGGGGGTC	AGAGCAGGTG	TAATATACAT	TAGAAGTGAG	CGATGAACGA	TAAATTGCCG	480
	AGAGCAGATG	ACTTGGAAAGC	CACTTGGAAAC	TTTGTGGAGC	CCGGtATCGG	GCAGATCCtG	540
25	GGCCGGGATG	GGTCGCCCCA	TGCAGGGCGA	GTGCAGAAAC	TGCTGtCAGC	TGCgATGTaC	600
	ATGGATGTCT	ACACGGcTAT	CTaCAACTAC	TGCGTCAACA	AGTCGCGGtC	CACCGGGCAT	660
	TTTCAGtCgG	ACTCGGCGCA	ACGGCAGTCG	AACCAGtCAT	CGAtCCTGSt	CGGAGGGAGA	720

1033RP

	GATCTTGTGCG	AACAGGTCGC	CCCCGTCCGC	CAGcTcCATC	GCGATCCATA	GGTACTCAGC	60
	TGACACATTG	CAGTCCAGCA	CCCTCACCAC	ATGTCGGTGC	CCCGCGCACC	GCGTCTGCAG	120
	CACCACCTCG	CGCGTCAGAT	CCTCGTCCGT	CATCCCTCGC	GCTTTGCAGC	GCTCGACGTG	180
	CACGAACCTT	ACAGCCACTA	TCGTCTGCGG	GTCTGCGCGC	AGCGAGGCGG	TTTGTACGAA	240
35	CGCGAACGTG	CCCTGCCCAA	TCGTCTCCCC	GAGCTCTAGT	TCCTTAATCT	CCGGCAGGCA	300
	TTCAGCTTGC	GACGACTCCA	TAGTAGCCCA	AAGTCGTGG	ACGGCCTTCC	AGGTGGCCCTC	360
	TAAGTGCTGG	TGATGGTTGG	TTGAAAAGTG	ATGCCCCAAAC	AATAGTGTGA	AAAACGGCAA	420
	AGTGGGCCCTT	ACGGGGGGAA	CAAAACAAGT	GCTAACTACA	CGGAAGCAGG	AATTAATTTG	480
	GGAAGTGGGC	TTGGAGCACG	GTATAGGAGT	ACCGGAGGTG	GATATGAgTG	TCgAACAGGT	540
40	GTCTGGTGCG	CACGCGTgCg	AAGAACAgtG	GGCACgGTTT	GAACGCAATG	TGGAgGCGCG	600
	GA						

1033UP

	GATCCGCGTC	GTCGAAAACA	GGTCCTTGgg	gTGCGATACC	GCCAGCACCT	TGCACGACGT	60
45	CCGCACCAGC	TGGTCGTGCG	TCTCCAGCGC	CGTGATGATG	TCCTCCACCG	AAAACACCTC	120
	CAGCACCGTC	TCAAACGGCG	CAAGCTTCAC	CACTGTGTCC	AGCAGCGACA	GAAGCCCGCT	180
	ATAGTCCAGC	CCACTCATCT	CCCCTGCCGT	GAGCACCTTT	TTCATCGCCG	AGAGTAGTGG	240
	CCGTGCGTCT	GCGTCGAGAC	GCACCATCAC	CCCCAGGTGC	AGCTGCAGCA	TGTCCACCAG	300
	CCCGTTTACC	GACCCACGCG	CGTGCTCCTC	GGGCGCCTCC	AGCACATCCG	CCAGCTGGCT	360
	CATTCCGTCC	TGGATCCTCC	ATTCTTCCAT	CGCGATATCG	ACTCTTCCGA	AGTAGCGTTT	420
50	TGGGGTTTGT	AAAAGTAAAG	GGCACTTTTC	CAGCACTTcG	CCACTTAATG	TCGTGAGGCA	480
	CAGAACCAGG	GCCCTATGTT	GCCGAGTCA	AGGCTTGCTT	CGCTATATTC	CGACTTCAGg	540
	AAGCTGCAAG	AGCTCAATcC	AGATGGGTTT	CAGGCTAACG	tTCTAACATG	GaAAGACCAC	600
	CTGATGAACA	CAGTGTGGCG	GGACgAGCTT	CTGATAGAAg	GGGGCGACAA	GCTGCTGGAg	660
	CGATTGAgCA	CCAAGGAGAC	GGG				

1034RP

	GATCATATTG	GTCTTGGCGC	CAGCATCGCC	TCTTCTGGTT	CTGAGCCAGT	AGTATGATAG	60
	CATGCCGCCG	ATGAACCTGG	CAATGGAGAA	ACTAGGTGAG	TTGTACATCC	CGACGCCAAG	120
5	GGCAACGCCCT	GAGGGTAACC	ACTGCGCCA	TCTGTACTTG	TCCTTATCAA	TACAAATCTT	180
	TACGAGGGAT	ATGACTGCAA	AGATGCTTCC	TAGGATGATC	GAACATTCCA	GTGCGTATGG	240
	TGGGAGTGCC	ATACCCATGA	CCAGACGTGC	GCAGTCTATC	CATACGAACG	CAGTTGGGAT	300
	CCGGAATTGC	TGGCTGGGGA	TTTCGTAGAC	CTTGTTGTAA	AAAATGTACA	TTACGCTAGA	360
	CAACACGATC	GACCAGCTGG	CGCCGATAAT	CTGCGCGGTA	AACTGAGCCC	TAGGAGAAGC	420
	ACCGATTAAA	TGCCCTGTCT	TAAGATCTTG	CATTAAATCG	CCCGCTTGCT	GAGCGCCCGC	480
10	CTCAGCTATA	CTTCCGGCAA	CCAAATTTAT	TAATACAGCG	GCCTTGTGAT	CCCTGGGTAC	540
	ACAAGAGCGA	AAATGATTTG	AGCCAGCTTT	CCGATGCCGC	TGAACGGGTT	GAGATCGGTT	600
	TCCCCAAGAC	CCGGACGCCC	AAAATCGATA	GAAAGATGCT	ATAAGGAGAG	CCA	

1034UP

	GATCACGCAC	AGCGGACACC	ACCAAAGCAG	AACCACGGTA	CCATATCTCT	CACACACGGC	60
	TCCCACTAGC	ACAGCGCCTC	CACCTGGCCG	CCCTGGGCTC	GGCCCCCGT	CGGCATAAGC	120
	ACGTCGGGGG	ACCTATTTAG	TTCCAAAAAT	ATTGTTGTAA	CAGTAATAAT	ATCCTCATTG	180
	AGGACATTTT	AGTTGTTACA	CTGAAAAGAA	CAGATACTAC	ACTTGATCTA	AGCCAAAAGG	240
	CAAAGAGATT	TGGTTTCTAA	AAGAAAAGAA	AACATGCCTG	TAAGAGGGAG	GGCCATCGCA	300
20	CATTTTTTCT	CTCCTTATAT	ACCAAGTAAA	ATTTAGAAAA	AGAAACGACG	CGGCTGCTTG	360
	GTCGGCGCCG	TCTGCCTGGG	ACTCCAGAGG	GGCTCACGCA	GGAATCCTGC	ATCCAGGGCG	420
	ATGCGATCAA	GCTCTGAACG	CCCATAGCTG	CCGCCATACA	CGCCGCCATT	CGCGAGCTTT	480
	CGTTGAGTTC	GTAAGCCATG	AAATCACAGT	ATACGATTCT	CGAGCGCAAG	TTAAAGAGAG	540
	CCCACTGGGC	ATACTGCTAG	GGCTACAAC	GCGCACCAGC	TGCGAAAGCG	GAACCTCAAT	600
	AGTTAAGGGC	GGGTGGCAAT	AGTATCTGCT	GCAAGCAGCT	TCTAGAATTT	GGTAGATGAG	660
25	TGCGTTCATG						

1035I2

	GATCCTTAAA	AGCTGGCCTC	CGCAGATAGA	CCTTCTGCGC	AGAGGCTGGA	AACCTCAACT	60
30	AGCAAGTCGC	CACCCGAATC	AGATAAGCAC	TAGAGTCGTT	CCAGTAACAG	AGGAAGCGAT	120
	CAAGGAAGAT	AGTAGAAGAG	GACACTGCTG	CCAGGCTTGA	TCGGACAGAG	GGTTTAGCTT	180
	TCTGTGTGAAT	TTTCAGAGTTT	CGGCGCTTTG	TTTACTTCGC	TTTCATTCTT	CGTGTAAGA	240
	AGCTGTTTTG	AGGATGTCTAT	CATTTGCCAG	TCGCCAGGTA	GGGTATTGCA	GGGCCGACGG	300
	AGTCGGTGAA	ACAGAGTCAG	GACCCGAGAAC	GCCGATAGAC	AGGCGTTTGG	TTTGTAAGCG	360
	GTGAGAGCTG	AAGCAGCTCA	AGAGGCCCGC	CTTGGTCAGG	TTGTGCGGTG	GCGGTAGAGC	420
35	ACAGCAGGGC	ATCCCTCGTC	GGTGGAGCGT	NCGGNCAGNA	GCCCAGGCGC	NTCGAACAGG	480
	GGGTGTTTAT	NANGANCNAC	CGACCACAAA	CACGCTNTNA	TTTCGNACCGG	CGGCCAGTTN	540
	CCTCANCNTG	GTTCCCGNGA	CTTGTTTTNN	GAGCCNATCC	TTGGCNCTCC	GCCNNAGNAA	600
	AAAA						

1035I1

	GATCTTTTGT	GGAACCAAGA	TCACCACACA	CGAATATGCG	ACGCCAAGCG	CCGGAACGAG	60
	CCACACATGG	GCCGCGGCGG	TAGCGGTGGG	CCCAAGCAAG	CGTATTTTGA	GGACCTGACG	120
	TGCTGTGGGT	GAGCAATCCA	GGGCATACTA	GGCCCAGGTT	GTCAGCTGAA	AGTGTGTTAC	180
45	CCGGTATCGG	TATTACCCGG	CTCGTATAAA	TGTTACCCGG	ATATGGTGAA	GCCAAAATTT	240
	TCCACGGCGT	AAACAACAGG	AGAGTGATCG	TGCATATGGC	GGCAGCAGCT	AGTGTAGCCT	300
	AGTGAGAAGA	AGGNCGTGTA	GCTAAGACTA	GCGAGGAGAC	GAGGATTGGG	CACTGATTGC	360
	GCGATGTCGA	TATTCTCTAC	GCCGCTGAAG	AGCAATGTNG	NATATNNGGN	CGCGCTNGTN	420
	GGCAACCNNG	GGNCCNNGG	AGAGNACCGA	GNTTGNNTNA	NGGNGNGGCG	CNCANAACCA	480
	ANNNNTNCCN	CAATCNCTTA	CNATCAANNC	CAANTTNCCN	CNNNCANCCC	CNNNGNNNAT	540
50	NNNNATTCCN	NCNNCNCN					

1035RP

	GATCTTAAAT	TGTTGCATTG	TGACCTGAAA	GTTGCCCCGT	AGACGCTGCA	TATTCAAGGT	60
	TPCCATPTCC	ACGGGACGTA	ACCTAATCCG	CTGCACTTTC	GACAAACGAC	TAATGTATCT	120
5	GTTCTCGGAC	TCTGGGTCAT	TCGCATCCCC	ACTCCACTGT	ACTTGTCCTG	ACTGTAGTTG	180
	TTGAAGCFTG	AGGTTATCTG	CCTCGAATGA	CTGCAGTAGT	AGTGATTTTC	GTCTCCCAAT	240
	CGTTTCTATG	GACCGCCTGA	ACACCGAACG	TGCCTCCGCC	TGGAAGGACT	CGAAAAGCCG	300
	CCGCTCCTCT	GCAGAAGGCG	GGAAATAAGA	CATAACTTGC	TCATCGCGTA	GGTAAATCTA	360
	CGTCATTATC	CGCGTCCACC	ATGTTCCGGCT	GGGATAAAAT	GGTGTTCCT	CCAGGGGGCG	420
	GGGAATACCA	CCCACCTCTC	AATCCTGCCC	CCGTTANTGA	ATNGNTTNT	TNATGGGGNN	480

1035UP

	GATCTGGCGT	ACGGTACCGA	TATATTTCAA	CTGAGGTATT	CGTTAGAACA	GCTACCTTCA	60
15	GTGGTTCCAC	GCTATATTGC	GTTGCAAATA	TGTTTGCGTA	CCCTTCTGGC	TTATCAGTGG	120
	CATTAAAGAG	CGCGCTAATG	GGGACTATCT	CTTTTACTGG	GCCAGTGGTC	TCCAAGAAGG	180
	AAGCATTTCT	AATATATTTT	CCGTGGTTTT	TCAGGATGCC	ATAATCTGGT	ACACTCACAA	240
	ACAATTTATG	TTGCACTGGG	TGAGATGCAG	GGGTATTAGT	ATTTGGAATC	ATGTGGGTGA	300
	TTGTCCCGGA	TGGGGTGCGC	TTCAACAACG	CAGAGGAAAA	AATATCCCCA	GGGGGATATT	360
	ATTNGTCGAA	GCAAGAATCG	CTTCGAGTAG	GGATTGAAGA	TTTCTTCTTG	ATACTTAAAG	420
20	CTGAATTGGT	TCANATGGGG	TCCAACGAAN	GANTAGGNTG	GATGGNCCCT	TNGGGGGGGG	480
	CC						

1036RP

	GATCATATTT	CAATGCAAGA	GCTCCATTAA	TAGGTATTGT	CTTGAGACAT	GCGCTCAAGT	60
25	CATTAATGTC	ATGGGAAAAA	TGCACCGTTC	CACCTCCTAT	CTCCAATGTA	TATTTTAGCA	120
	TTTCAAAATC	ATGTTTCTG	TTTACTATAA	AGTGCAACCC	ATTGAGGTCT	GCGGCTTCT	180
	TAGTAAAGCC	TCTAAAGGCG	TAATGCTGCT	CTTGTATACT	GCGTAGCTGT	GGGTCAAAAT	240
	CGGTAACAGG	CTGTGGAAGA	AGAGCGGTAA	ATTGTTTCAG	AAATTCGAGA	TGCAATATTG	300
30	GTATGCCTTT	AACAAGTGCA	AAACAAATAC	TTTTTCGGAA	TCTTGGTCAT	CTTCATGGGG	360
	TCTTAATAAT	ATGATGTGTA	GTGGGCCCTCC	GAAAAAGAGG	TCACCACTCG	TATTCCTAAC	420
	CCTTAATTAC	CTCAAGCAAA	GCAGGGCTTC	TTGTAACAAA	GTTTCGGGAC	CTGGACTCCC	480
	CATGGGCCCC	TCCAATNTGA	TTGGNCGGAT	NTGNCCCCCT	TCCNGATANA	GGNCTGGATG	540
	GCCANCGGAA	NCCNTCCTAG	TGATNTCCCN	CCCCCTCAGT	GNNNCCNCTN	GAGGTTTGGA	600
	NGGCNNNTTT	TCCNNTNGCG	GGNNTNTCTG	GNAACCNCCC	CCTNT		

1036UP

	GATCCCCTTT	GGTAACGAGA	GGTGTCGGCT	TGTATTCACC	GCACATCGTG	GGCTATTTGT	60
40	CATTAATCTG	GCCCCGTCCC	AGAGACCTAC	AGGTATAAAT	TCCCCATCAA	GTGCCACCAG	120
	AAAGATATGC	TATACTGGTT	TTGAGCTTGA	GCGACTGTTA	ACTGCAACCA	GCGGGACCGA	180
	ACGGGGTAGC	TTTTACTCAT	TTATTGAGGC	TAAATTGGAA	CCAGACATCA	CAATTCTGCT	240
	TCAGTGCGAA	ATGGACGCAT	ACAATCCAAA	ACGCCAGAAG	TATACTGAAA	TAAAATCCTC	300
	TGTGGACTTC	AATGTACGAA	ATGTCCGGCA	CCTGAGCAAA	CTGCTTAAAA	TATGGGAACA	360
	AACAGGGGTG	GTCCCATCCA	CTGATATCTT	GTAGGGGTCA	GAGACCCATC	AACCCATGTG	420
45	TTGAAACAGN	CGGCCCTTAT	GGGTGGTCAA	ATCGNAGGAA	AATCTTTTTA	GGGTGNCNGN	480
	NAGGCANCA	TTNTTTTANT	TATCCGAGTG	CAANATGGAA	ATAANCATCG	TNAATTTGGA	540
	AGGTATTTCC	CGGGGNGAAC	CANCGGNCNC	AANNNTTTTN	NGGGGTNGAA	AGANTCAAAT	600
	TAAATNGGCC	NGT					

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1037RP

	GATCATCATT	ATTTCTGCG	TTCGTGCCGA	CGATTGGAAG	GGCGGGGTG	GTTTCTTGAA	60
	GGATTTCAGG	CGTATGAATG	TTGCTCTCAC	CAGAGCAAAG	GCCAGTCTCT	GGATCCTGGG	120
5	TCACCATAAA	TCTTTATACA	AGAACAAGCT	ATGGATGCAT	TTGATTTCAG	ATGCGAAAGG	180
	GCGTGACTGC	CTCCAAATGG	CATGTCCGGG	CTTCCTTGAT	CCACGGAACA	GAGCCGCCCA	240
	GGATGCTCTT	CATAGGTTCA	AAAATCACCA	TAATTATATC	GAGAACGCAG	ATGATTATGG	300
	GCCTGAACCG	GTGATGACTA	AATCAAGAGG	ACGCAATAGA	TCATCCAGAA	AACGCAAACA	360
	TATGGAAGAT	AATCCAGATG	ATAACTACGA	TCCCCTTGCT	GAATTCAAGA	AGGAAAATCA	420
	AAGAGAAAGC	AACACAGGCA	CCGGTGGTTA	CCGTGCGGAT	ACATCTAACC	ACAGATTGGC	480
10	ACCTGCTAGG	AACGATAGCA	AGAAGGCCAA	GACGTGCTCC	AATGCCGCCG	GTATTTCCGA	540
	GGCTACTTCA	NARGATGGTG	ATCGAAGTCA	GAAAGGACAT	GGAACATAAG	AGARTCTTCC	600
	ATATTC						

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1038RP

	GATCAAAAAA	AGAAATTACA	ATTGACTGTT	GCACCCACAC	ATTCAACGGT	TGCACCCACA	60
30	CATTATGAGA	TGCTTGATTT	GGCGCGAACT	GCGCTTTCCA	ACTACAGTCC	CGAGACTTTG	120
	GGTGCCAACC	GAAGCAGACT	TCAACAGTGG	TGATAACCAT	AGTGTCGAAG	TCTAGCGAAT	180
	CTAAGGATAA	TACCAAGAGA	CAAAGCATAA	TCGTATGTGC	ACAGGATGGG	GCGAAGTGTG	240
	GTCTAGAGCT	GTCCGTGCGA	GCAGAATACG	GTGCGGGCAA	TGAGGACGCC	GCAGACGCCG	300
	AGCGTGTGGG	CAGCTCACGA	GGGCCGGAGC	GCTTCCAAGC	GGTCAGACAG	AGTACTAACG	360
	CATTGCAGAC	AAGATGGCTC	ACGAAAACGT	TTGGGGTCTC	CCACCCNNAN	AAACTACGGT	420
35	AAGGGGTCCC	CCAGTGC GCG	TGTGCGCTTC	GNCTCTTGTT	GGTCANAAAG	TACGGGTGGG	480
	ACATCTTCCC	CAATGGTTCA	NAGAGAAGGC	CACGACATTG	GTTCCCAAAT	CCCCTAAGAG	540
	GGGGGGGGCC	CTTCCCCTCT	TNCNAAATCC	GGGGGGGGTT	TGGTTTCNCG	GAGGTTTNT	600
	TATTTTTTNA	NACCCCNNTT	TTTANTTTNA	NNCNCGGTNC	CCAGNNGTTT	GGN	

40

1038UP

	GATCGGTTCT	CGGGCTTCTT	TAGCTGCCCG	TTATTCAAACG	AGTCATCGAC	TGAGAAAGAG	60
	ATAAAAGCGG	TCGATAGCGA	AAATAAGAAA	AATCTCCAAA	ATGATATGTG	GCGCCTTTAC	120
	CAGCTGGGTA	AGTCGCTGAC	CAACCCCAT	CACCCGTACC	ACAAATTCTC	TACTGGAAAC	180
	TTTGAGACTT	TATGGAGCAT	TCCGAGATCG	AAAGGCGTCA	ACGTCCGTGA	TGAGCTGCTG	240
45	AAGTTCTACA	AACGGTCATA	TTCTGCAAAT	CTCATGAAAT	TAGTGATCTT	GGGCCGCGAA	300
	GATCTAGATA	CCTTGGGTCA	GTGGGCATAT	GAGCTGTTCA	AAGACGTCCC	TAACCATGGG	360
	ACCAAAGTGG	CTGAGTATCA	CGGCCAGGGA	TTACCGGCCG	AGACCTGATG	AAGGTAATTA	420
	AAGTGAAGCG	GNTAAAATCT	TAAGAGTGTG	GAATTCATNC	GNGGGGCAGA	TTTGGTTAGN	480
	ATGGAGGCAG	CAGTCGTATG	NGGATTTATC	GCCAGAGGAA	GGTCCCTCCG	NTCTGGAGAA	540
50	AAAGTGAAN	CGNCNNCCGT	NGGNNTCCCC	TTNAAAGGAA	AATNCCCCNC	AANNGGCTTN	600
	ANNAAGGNT						

55

1039RP

5 GATCATTCTTCT CTTCAATCCC ATTGACGTGA ATGATGAACC GCATTATCTT TTTAACAGCG 60
 ACAACATGCC ACGGTATATA ATGTCTCTTA CCTCGTGATA TGCAGAACCA GGTGTTTAGA 120
 CTGGCAATAT CCCTAAACTG GTGTAATATG GTCTTCAAAA GTTTTGTGCT GTCCGAATGA 180
 GGGCAATTTA GTAAATTAAC CTCGAATTTG TCTAAAGTAT CGCCACCGGC ACATCTTTTA 240
 AACC GCACCA GCGCGCCGCT TTTTATGCG CATCGGCGCT GTGAATTAGC AAGTTGTAAA 300
 GGGCTACTGA ATACGACGCC ATGCAGCTCT TCATCGATAT TCACAACCTC GTAATCATCC 360
 AATTGGTTAG CTTGGATTTT GNGGGCATA TCTCTTATCC CTAAAAAGTG GGTGATGA 420
 TGGATAAAC TGATCTTCAT CATATAGAGA AATTTGGGCT CGCCCCAACG CAGACACAGN 480
 10 CAATGTAGTT TCTTGTTGCA NAGTTNGCTN CGCAGNATT ACTCGCANCC GGGGAGGTNT 540
 CACCCGGAG ACAAATTC CCCCTTTTCT NTGGAAATCG TNGTAGNNCC TANCAAGGAT 600
 GGGTCAAGGA CCTGGTTGCC ATTCCANTTT ACCATTTTNN CCC

1039UP

15 GATCCTTCCA ATAACGGCTA AACATCCATG TGCTGGTTTT AACTATGAGG GAGTTGGAGT 60
 AATTTTCGCGG TCTCGCAAAG TAAATTGACA GAAAACCCTC AGATCGGTAA CGAAACAGCT 120
 GAACGACGGA GATTAAGAGG AAGAGGCAAA TAAGCTATAG ATAAGATCGA TAAATATTGA 180
 GGGGGGGATG GATATATTAG AAACCTAGCTT TAGACTTGAA GATGTGCTTT CACGCTATTA 240
 TAGAGTTGAA AAGGTGGTGC GAGTCAATTA TCAACAGTTC GTACCGAGGA CTCCAGATGA 300
 20 TCAATGGTGT ATCCAATCCG AGCTTCTTAA TCCGCAAGAA GGATCCGAAA GCGCTGGTGG 360
 CGCTTTTTTC GCGGGAACTC TGGTGCTTTT AGCATCAATG ACCAGGACTT ACCCATTCCC 420
 GGGGTGGAA GGGATAGGCG AACCCCCCNC CTCGGAGAAG AAGGGCCACT TTACGGCAGG 480
 GTTTTCCAAG GCNAACCTGC AACGCCNNTG GATCTTTTTA AAGCNTGGGG GGATGNTCAA 540
 TAANAATTCN GAGGCGNAGA ACCTTTGGCA ATTGGAAAAAN NNNTTTCCCC GNAAGAAAGC 600
 NNAGGGANCC CCCCCGGNCN NATTTTGGGA ATGNC

1040RP

30 GATCCAGTGT ACCAGGTAGC GTCAGGCACT TCTAGCGCAA GGGCCGCCGT AAACCTTGGC 60
 CTCTCACAGC ATTTGGGATG AGTATGGGCC ATCTTTAGGG CACGTGAGTG ATCATGATGG 120
 GTACAAAAAG AAATGATTTT GCCCAGGATC GAACTGGGGA CGTTCTGCGT GTTAAGCAGA 180
 TGCCATAACC GACTAGACCA CGAAACCACT TTCTGCAGGC TCTTATTGGA CAGGTGATGT 240
 TAGCGCAGAA GAACATGAAC GTGATAATAA TTCAGAAACC TCTTATGCTA AAGTGAATTA 300
 CTATTGCTTA ATAACCTGAA GGGGAATAGGC ATTGCCAGTA TTGAAAATCG GGCTTTGGGT 360
 TTATTGGCTA ATTATATTAT TNNCANTATA TATATATACC AACAAGGTGA AGAATGGNTG 420
 35 TCNTGGTTT GGGGGCGATA CCCNAGAACC AAAGTAGAAG TTGACAAGTT GGTGGNAGNG 480
 GTTCAATTCA GNACTTCATG GCAACNTTTA CNATNNTTN NTNAGAACCC CCNATTANTC 540
 TTTNNCTTCG GGGGGTCTCN NCNAACCGGA AACAATNTTN CNGAACTGAG TTNGGGGGAN 600
 GTTCNTCGGT NTTTTCNCC TTTGGGTCCA AATTGGGCCG GAANCCCT

1040UP

40 GATCAGCAAC CTTCTCCGCC GTCTGTGTCC TCGCTTTACC GAGGATACGA AAATAGCCGC 60
 GGCTCTGTTT CAAATGGCGA TGCTGACGAG CAAACCACGT CTTCTGATGC AAGCAGTACT 120
 AGTTACATTA TTCTAGAGAT GGAGGCAATG CGGACAGCTC TCGTTCAGTA TTTGAGGGCA 180
 45 ATCTGCCAAG ATGCAGAGGT ATCCGCCAGT CTGTCCCTAA CGAAATTCCT ATTCAAGAGG 240
 ACGATAGACA AGCGTGCTTT TACGCCAGAA ATCCTGGAAG ATATTGAATC TCGGGAGCTT 300
 ATGGATGTAT ACAACCTCGA AAATCAAGTT AAATTCGCGT TTGGATAGAA 360
 CTGTGAAGCT ACAAGTCCTC GCTAAAGTCC CTAAAAGAAA AAATCTTGCA AGATATGACT 420
 ACATTATGAG GTTTTCCNCC AATTTAAGGA GAGGAGGATC CCAGNGACNA TTTAGCTCTC 480
 AGAGATTCTT GGNTGGGGAA AATTTTGTAG GTACCNATNC AGGTTCCCGG AATNAATGTN 540
 NATNTTTTAC ANTCGCGCNG AAATATGCTC ANAGNNNAAG TTTGGGCACC CCCCCCNCC 600
 50 ATGANGTTTT GTC

1041RP

	GATCCTCCAC	CAGAGCGTCG	GCGTCCCAT	CCTTCTGTTC	ACGCAGTGGC	GCGTTCTTGT	60
	AGAAAACGCC	CAACAGTTGT	TTGTAGGTGA	ACTCGTCCG	GAATTTCTGG	GCGCGAATTC	120
5	GCTCCAGCTC	CTCTTCGGAA	AGCTTTTCAC	GGCGCCACCA	GCTTCTCATC	CGGTTCAACC	180
	AGCGCTTTTC	GTCGAGTGCC	CGCTGTTCGG	CCGCTTCTGC	CGCAGCAATA	TCTCGGCGCA	240
	GATGCCGTAC	GCGCTCCGCC	ACTTCATGAC	GGATGACGCC	CTGCCGCTCT	TCTGTGAAGA	300
	ACTCGTAGTC	CAACCCAGCT	TCGAACAAAC	AACTGCTTCA	CGTATCGCCG	CCATACTTTC	360
	ATCGACGTCT	CGAGATAGTC	GGCCGGAGGA	GGGGCAACAA	ACAACGCGAG	CCGCCGCGGT	420
	TTGGGGCATG	TGTCANGTNG	GCTGCGCCTG	GGCCTTCACC	AACGACGAAT	AATGTTGGAT	480
10	TTNGCCCTNG	TCCCNTGGCG	GNTNCAATCA	GAATGCCGGN	TCAACCNAA	CAAAAGGGAC	540
	AATNNGCCGG	AACCAAGGCG	GTTCANGCC	GAAAGTGTTT	ATTNNCCNAC	TNTTCCGGTA	600
	NAATTTTNT	TTNTCNC	TGG	GGNTGTGNNT	NACCNCACC	CCNAAATA	

1041UP

	GATCTGCTTC	CTGAAAAATG	GCGTCTCTGT	CTTACTGGTA	CTCTCAAATA	GCTACGTCTA	60
	GGTACAGGGC	CATTTCCGGA	TCCCAGCCAC	GGGTCCACTG	CAGGAGGTAC	AACAGGATAT	120
	CGCACGTCTC	GCCCTGCGCA	CGTCACTTGG	AGCCTCCCGT	TCTCGTCCGT	ACGTCTCAAT	180
	AAGGTACGCC	GTTTCTCTTC	GCCGATGGAC	TGCGCTAACT	GTATGGCCTG	GCTACAAGTC	240
20	TGTTGGTTTC	GAGCAGCCCC	CTTCTTTATC	CACCCCTCAAG	GTTTACCGCA	ATCCAGCAAT	300
	TTTGGGTCC	GGCACAGCCG	GATATCATGT	GACTTAATTA	CGTCAACGTT	CAAGAGTTGG	360
	GGCGCGCGGC	AGCAAATTTA	ACGGGGGCGN	CGGTCTGTCC	CCCCGATCGG	GGGGGGGGGA	420
	GGGNATTANC	ANTCCANTGC	CGGCCAAATC	TTNGTTTACA	NAAAGCAAGC	ANANTCATAG	480
	TGATTTGGGG	GAANANCCCA	AGGTTNNGGC	CNCCANGGNT	CAAANTCNCC	CNTTNNTTTT	540
	TGGGTTC	NCGGAAAANN	CCATTNC	AGGGGCCNAG	GNCCGGGAAT	TTTCCCCNGT	600
25	TNNAGGGGAG	TCNNTTNGGG	GGGGANN	CCANAGGAAG	GNGGT		

1042RP

	GATCCGTGCT	GCGGACAACC	GCCAGAGCTC	GCCTACAGCC	CGTATATATA	CGCCGGCTGC	60
30	CGGCCTGCCG	CATGCGATTT	GTCCACCTC	GCTCTGCTTC	GTCCCGCCTG	CCGTTGCTCC	120
	ATGGGACCTT	TCATTTAGTG	TCTCGCGAAC	GTTTCGAATG	TACCCTATCG	TGGTACCACG	180
	TTGCCCTGCCG	TGCCGTTACT	ACATCTTCTA	GCGCGGACTG	AGTCACATGT	CTCGCCGCGC	240
	ACTCCTTTTC	TGTAGATAGT	CAGACGACAG	ATAGTCGATA	GTTGGAGATT	TGGGCAACAA	300
	TAGCGGTGGC	CATTACGCC	GCCCATTTGT	CCCATGTCTAT	TGGGAGGCTG	GGNCCCACCC	360
	ACGGGAAC	TTNCCCGTTT	AANCCTNANA	GNCCCNNGGA	ATGNAAAACN	CTTTCTTTNG	420
35	NCNGCNGCAA	ACGGGCCTNN	AGNGATTTTC	TTTGNCGATT	NGGGANGCAC	TGAGAAATCCA	480
	AGTNGGAAGG	GGGCTNNAAA	AATNGCTCCG	GGCCANNCT	NCCCAAAGGT	TTNAAAANCN	540
	GCNTAAATNA	GCCNCAGAAG	AACNCGGGA	GGAANCANAC	ANAAANTNGG	CCCCNCCTGA	600
	AGGAAAGGGG	CNGNNNTGGG	GNCGAANCCC	CNGNAACGNT	NTTTCTTAAA	GGANAACAAA	660
	NGGTNCAAAA	AAAATGGGGG	NC				

1042UP

	GATCGCGTCC	TCGAGCGACT	TGTGAGGGTG	AAGCTCGATA	CGGTGATGGT	GGTGGTGATG	60
	GTGGTGGTGA	TGGTGGTGTG	CTCTGCCCTG	CGGTATGACC	TGGGCTGTGTG	GCGTTGGGCT	120
45	GTTGCTGCCG	ACAGCAGCAC	CTGTATCCGC	AATGCCCGAT	ATGCTAGAAT	GGAGCAAATT	180
	AATGGACTGG	TCTGCATTCT	TGCAGAGCGG	AGCCTCGCAC	ATGCTGGATA	TGCTTACGAG	240
	ATCGCCGGAG	GATCTTTATG	TCTGTTTCGC	TATTCACCAC	GTGGTCTGTGG	CAGTGCTGTT	300
	GTTTCATGAC	CAGCCCGTAT	CTTCANAGGA	GTCGTAGTTC	ACGCATTGTT	GGGCAAAGCC	360
	AGTCGAAGGA	GGCCATCCTC	CACGGTCGGG	GAGTCCCCGG	GGACGTTTC	CACAAGCCAA	420
	GGTACCTAGA	AGATGAATCT	TTTTTGANTC	ANCNGTTGGG	CCNCTNGGCA	ATTTNAAGTC	480
50	GNAANTGNTG	AACTTCGGAA	AGTTGGAAAT	TGGNCCNAGG	NCTTCTTCCC	CCNCNCNCT	540
	TNGGNAAGCA	AAAANAAANA	ATTAATTGGN	CCCCCCCCCG	CAAATTTGNG	GTCNGAGAAA	600
	TTTCCAAACC	TTGGGTAAAT	AGTAAGGNCC	CCGNTGNCTG	GGCCCNCCC		

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1043RP

	GGATCGGCGA	TGGCGATAAA	AGAATTGCTC	CCTGATTGAT	TGTTGTTTCA	AGGAGATGCA	60
	GATGGATTGT	CCAGAAAAAC	CGGTTTTAAG	ACTCGTTCAT	CAAACCTGTT	AAACCATTGC	120
5	CCATCGGCTT	GCAGTATATT	GCCCAAGGTT	TCGCGGATAT	TTCTTCTGTC	TAATGATAAT	180
	CGCCCCACAG	GCTGGTCAGC	GCCTGATGCA	GAGCGCGAAG	AGGGTCGGTC	TATCATAGGA	240
	GGAAAGCTTT	CTTGATCCGG	GGAGCCGGTC	GGGCTGTCCG	TTAAAAATGG	AGGTGCGTCT	300
	AATGAAGACA	TTAGCTGGAC	AGGTCTAGGG	GCTTCAATAT	CAAATTCATC	ATCCGTTTCC	360
	TCCTGTTCTT	CTACGCACCC	TGTCCTTTATG	TTTAAGATCT	CAAGCATACC	CGCAGGaGta	420
	CCtCCAaATa	TgATAACGGT	GaGAACCACA	AcTaCCAGcA	CAGtGGCCAG	AaGAGGGGAA	480
	CTTGGANCTC	GCCCNNNNGA	CCCNtagCCA	GNGNCACTCC	AANAGNAACC	CCNAANCCCC	540
10	NCCNNNNNGG	NAACNNCCTN	NNTTTNGNNT	TGGATNTCCC	CNANNANTNN	AAAACCCCCC	600
	CCCCGGGNTN	TTNNNGGGNC	CCNNNNNCCC	NNNAANGGGN	AAAAANNNC		

1043UP

	GATCAGATTG	TCTTGTGATG	GAGAAGCTGG	CGCATCAGTA	GAGTGCAGAG	AAGACCCATG	60
	CGGAACAAC	GTACCACCCA	GGGACTGCCG	TCTTCCCGGA	ATGTTGGGAA	AAACAACAGC	120
	ACGGcCTGAG	TCACCTTACAG	TCGAGTGGG	TTGCGAGCGC	GACAGATTAA	AAGAAAAGCG	180
	CTCGGGGTTT	GTGAACAGNT	CAGACCAAAA	CCCAGGTCCT	GGCTCGCGGA	ATTCTTCGCT	240
	TACCTTCACA	TNCAACTTAG	TGTGTTCCGCT	GTCCNAAATA	TaCTCCAAAA	TCTTGATCGG	300
20	cGCACCTCTG	TGGTTCATgT	CCTGCACAAG	TTGACCACTG	TATTCCaGTT	TGaCATCAGA	360
	GGGcGAAATC	ATCAgtGTGT	GGCgttCACA	GAGCAAAATa	aCTCctTtAc	TTCctgcAC	

1044I2

	GATCTACAGA	ATGCAGGAGA	CGCTGCTTGA	CACAACACAA	ACGGCTGAGA	CGGCAGGCGC	60
	GGCCGAGCGC	GTGCAGGAGG	CGGACCCGGA	CGGACAGGGG	GCGGGCGTCG	ACTCGGGCGA	120
	GCTGCTGGAG	GTTGTGGAGC	GCCACTACGG	GGCGCGGCGG	TGCGCGCTGG	GGACGATACG	180
	GTACGAGGCC	GCGCGCGCGG	GCCGGCTGAC	GGCGCGGCGG	GGCGCGGCC	TGCCGTTTCC	240
	GTACGAGGTG	GGGCAGCAGA	CCGTGCCGGT	GCCGCTTGCT	GCCGCGCATG	GGCAGGCGAG	300
	CGATCCAACA	GGCTCGTGAC	GGTGGAGCTG	AGCGCGGAGG	ACCTTGAGAG	CGCGCTCGCG	360
30	ACGGGCGAGA	ACGCACGGGT	TGCGCAACCC	GGAGCTTTTG	TGGGTAGNCG	TGTTCAACTN	420
	AGANTCGGGA	CCCNNTTNT	NNTGCTNNNG	NACTNNNGNG	TGNTNNNACGN	NGAGCTGAGN	480
	TGCAGGNCAN	GNNAGNNNNC	CNNCNCNCGN	ACGCCCNCCA	ACCCNNNGAN	CCCNNTTTTT	540
	TAGNNNGNTT	TAANNCCNNC	CCCNNTNTNN	GNGNGGGNNT	CCCCCTTGNT	NTNNNNNNNN	600
	ANTTNTCATT	TTCCCCCCTT	CGNAGGNTTN	NT			

1044I1

	GATCTCCGAC	TGCCGCCGTC	TGTACCCGTC	ATCGCCCTCT	GTAGTCGCCG	TCATGCTCAT	60
	CCTACCCAGC	CGCACCAACC	AATGCTCGAT	GCAAGCTCAA	TGCTCGCAGC	CGGCGACTGC	120
40	TGTATACGTG	CTGGCTTAGG	GTGGGGACGT	CCCTTCACGG	CCCGGCCGCC	ATTGGAGTCC	180
	AGCAAGCGGG	GAATGCTGTT	GTGACTGTAA	CACCCATACA	TTGCAGGCCG	TACATTTCAA	240
	CGATGGGACG	CGAGTGCCTG	GGGAGCTGGA	CGGAGACCGA	ACGGGGGGAG	CCAGGCGGGC	300
	GGGCGGCAAT	CCGCAGGCCG	ACCCAGCGGC	CGACCACGCG	GGCGCTAGGC	CGAGGGCAGC	360
	AGGCCAGAGC	CGCGGGCGCG	GTTTTTCATG	AAAAATATAG	TGGCTACAAG	AGGGATAGGT	420
	TGGATATACC	AGAACTCACT	CGTAAGAGAT	AATTAAGCAG	ACGAAATGGT	TGTTTGGAGG	480
45	ACGTTGGTAT	CGCGAATCAC	AATAATTTGA	CAAAAGGTTT	TTGANTCGGG	GAGGTCGNTG	540
	TTGTTGNGGG	NGCNAGACCG	CCNTATTANA	NGAAGNGANG	GNAACNCAAG	ANNNGGGCAN	600
	GGGGTC						

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1044RP

	GATCGCGTGC	CTAGTGCAGC	CTCATGCACC	GCTTGGAAC	GCCGCCCCAC	CCATGTCAGC	60
	ATCTTTTATCT	TGCTCGACCC	TGTGACCGAG	TAAACAAGCA	CCGTTCATCCA	CGTCTCAGCC	120
5	TTCCCACATG	GATGTTCAAA	CAGCCAGGCA	TGGTCAATGC	CTCGTTTGTC	AACTATCTTG	180
	TCGTAATGTT	GTAAGTTGCT	CGAATGAAGT	AGCAGTAAGC	ACTTGGTTCGT	GCGGACGAAT	240
	ATTGTCCGCA	GCCGTTCCGA	GTACAGCAGC	TCTTCTACAC	CATAATTCCGG	GCCAAAGCAAT	300
	TCTGTATATG	TCTGAACTAG	ACGCAGGCCT	CTCTCGTCCA	TACTGGAGTA	CACCAAGGAG	360
	TCCCTATTAT	TTCGGACCAC	CACAAGTTGT	CGAACGGCAT	CAACCACAGG	GACACACTGA	420
	GCACCTTGGG	ACGGAATGGG	ATTTACTAGC	TCAGCCCTAA	GCATCTTATG	ATGAGGGCTG	480
10	CCCTTAGCTT	GCTGAGTGCT	TCGGGCTGCC	TGCTTGTGGT	TGGTGGGTCC	TTTCTTAGAA	540
	CGATTGTTC	AAACCATGAT	GATGGGGTTT	GGTCCGGCCN	GGTGATTTGA	AGATTTAAAC	600
	CGGTNCCAAG	GAATTGACCN	TGGGGG				

1044UP

	GATCTCCTTG	ACCGCGCGTG	GCGCTCTCTT	CTTGAAGGTG	ACACCGTGCA	ACTGCTACTG	60
	TTAGTATCGG	TCCGGTCTGC	GGCTCCGCTC	CACGCAGCAG	GGAGCCCTGC	TCCGCACTCA	120
	ACATACCCTC	TTGTGCAAGT	TAATGGTGTA	CTCGCGAGTA	ACAACGTCCT	TCAAACCAAGC	180
	CATTTCCGGCT	GCTTAATTAT	CTCTTACGAG	TGAGTTCTGG	TATATCCAAC	CTATCCCTCT	240
20	TGTAGCCACT	ATATTTTTCA	TGAAAAACCG	CGCCCCGCGC	TCTGGCCTGC	TGCCCTCGGC	300
	CTAGCGCCCG	CGTGGTCCGG	CGCTGGGTCC	GGCTGCGGAT	TGCCCGCCGC	CGCCTGGNTC	360
	CCCCNNCGG	CTCCNNCCAG	NTCCCCACGA	NTCGNGNCCA	TNGNNGAAAT	GTACGGNTTG	420
	AANGNTTGNT	GTNAAAGGCA	NAAAAAGAATC	CCCNNTNGGT	GGNTTNNAAN	NNNGGCNNNN	480
	NNNNAGGGAN	GNCCACCNN	ANNNAGAANT	TTAANAAGNG	NNNNTNNANA	TNNNTNGATN	540
	NANAA						

1045RP

	GTGGATCCGT	AATGTGGgTT	TGTAGGCCAG	AGGGGATTCG	ACGGTGGCTG	GGGGCCATTC	60
	TGCCCCGTAA	TTAGATGCCA	CCCAATTGTT	TTACATCCC	AGGCGAAGGT	TCGCATACCG	120
30	CCCACATACT	TGGGTAATTG	ATAATGCCGC	CACATGACGG	GATACTAAAC	AAAGCAAAGT	180
	GTCACATtCT	TATTTTCTGT	TGTGGTCAAA	AATCGGGGGG	TAGGCGATCA	ATTTGCATAT	240
	ACAACACGAA	AGGGGATCGG	AGATTTCCTAG	GTCACAGGAC	AGTTTGGGgt	TTtTATTGGG	300
	TGCTTTTGTG	AAACCATAGG	CACTTGACAT	AGGAGCCCTC	TTTAGAGTAC	AATAAGCAAC	360
	TGGCAGCAGC	CCTACAGCTT	GGGcTAAACT	TCTcCaTtAT	GtgAAACGGG	AAAGAcGAcA	420
	ATgcCTCTgA	ACGCTTTTCAC	GCCACTTTTG	GtGGcCCAat	tGcATNGNTT	CCGNAANTAN	480
35	NNTTTTNTNN	TNGGGNTTTT	TTGGNNNAAA	AAAACCNNNA	AAAAAGGGGG	GGGGGGNTNA	540
	AAACCANGNA	TNNTTTTTTT	NGGGNNGGGG	GGGGCCCCCT	TTTNTNAAAN	CCNNNCCCCC	600
	CNNNNAAANN	GGNNNTTNNN	GGNNNAAAAA	TTNNNNNTNN	NTTTTTNNGN	NNCCNNNNNT	660
	NCCCCCCNA	NNGNCCNNNC	CCNNNNTTTT	TTTTNTNNNA	NNAAANCNCC	CNNGGGNNGG	720
	CCC						

1045UP

	GATCTAATAA	CCACCCGTTG	TATATTTGGG	CGGTAACTA	TATATGGGAA	TCATATAAGT	60
	GCTTAAAAAC	ACCTCACCCT	CAAGGGGGTC	ATCTATAAAC	AAGCCATAGT	GTGtGTATCT	120
	TTGcCTACAT	AGCATCATGA	CTATGTTGCG	CACGCGTCAT	TTGCACTGTT	TTAGCATGTA	180
45	ACTGGCAGAG	CCAGCAACGA	ACAGAGCTAA	TTTTTGAGGC	TTACCATACT	GtTGTCGCTG	240
	GATGTTGAAG	CaCGGCTGTT	GTGGATAAGT	TTAGAACCCG	TCGCCAGCAC	ATTcATACCC	300
	TGAAACTACC	AGTTCCAGGG	GACATGTTCT	TCGtGGCTTT	GACAGAATTA	TTATTGTAGT	360
	CCAGTTAGAT	GtACTACCAT	TGTTGcGCTA	ACATAATCAC	CAtTgtCatC	TcTGGAAATCA	420
	CGTgTcGCCA	AGCATATTaA	TGTTTgtACT	TAAACTCGGt	aCTCCCTtta	TCGaaAGGcA	480
	TCACGGAATC	GcCCTtCACT	aT				

1046RP

	GATCGCGCGC	GCAAGCCCCGT	GCgCGAGCTC	GAgcaggTTC	TCGAGGTTCG	GGGGCAGCGC	60
	GTCACACGAG	TAgGCGTAGG	GATAGAGGAT	CTCCTCCGAG	TACGAGTGCA	GGTCCAGGTA	120
5	GGCGTAGATG	TCCAGCTCGG	CCTTCGTCTT	GTTACAGTAG	TCGTTCCAGC	TGCGCGCCTC	180
	CACGGCCTCG	AACGGCTGCT	GGCCGCTATA	GTCGCCCCGAG	CAGGGGTAGG	CGTGCTGGCC	240
	GGTCCAGtGG	TAGTCGAACG	AGTGGTCAAT	GTCGACGCCA	TCGCAGCCGG	GCATGTACGT	300
	GGGCTGCCGG	tTCTTGCGCC	ACAGGCGGTC	GTGCGTCCAC	GTGTACGCGT	AGCCGTCTGG	360
	GtTGAACACA	GGGATCACCA	GGAAGTCGAG	CGCGTCCAGG	tAGCGCGTCT	CCTTGGGCGC	420
	CCGCCCCATAC	CGCGAGAGCA	GACGCTCCAC	GACAAAGCAC	GCCGTGCTCA	CGCCAATCCA	480
10	CTCGCGAGCA	TGCACGCCGt	CCGTAATTAC	CACCG			

1046UP

	GATCCGGGAG	CTCCATcATT	AGAGGGTcTg	gACTTCGGGA	AGACACGCAG	TGGTATGTCT	60
15	GTAACTTTGC	AAATTTCAAAT	TAATTTCTCCT	TTCATCGTAG	TTCGGGCTGC	TGGGCGATCT	120
	CCGaCACAAA	CGGCTGAGTC	GCTGACACAA	ACAAAACTC	GACTACGGAA	AACGACTAAG	180
	CGTCGCAGAT	GCTATATATA	TACAACTTGG	TTCCTAATTA	GGGTTAGATC	CTTGCGAGAA	240
	ACAGACGTTG	AGCTTGTGCA	CTTCACAATT	TTAGTCCCGT	CTCCGAAGTT	TCCAGGCAAC	300
	ACGAATAACA	ACACATATTG	CCATGGCATC	GGTAACGTTT	AAAGACAATG	CGGAAGTGAT	360
	AATGATAGGT	GAGCAGGATC	GGAGAAGAGA	GCAAGGtATG	GCCAGGCCCT	GGATAACGGG	420
20	ATTTCATCGAC	GCGGATATCA	TGTGGCAAAA	GGACGGtCCG	TAACTCATAG	TAGACATCgC	480
	CAAAGAGAAC	TTCGACAGCT	TATATTGACA	TTCGTCTCTT	TGCTCTACAT	TGTTGAGGCA	540
	AAGATATAaG	AgAGTATGGt	G				

1047RP

	GATCGAGTAG	ATGTTCCGCA	GCgCTGGCAT	CTTcagGTCC	CGGTACGTCA	GGATGAACTC	60
	GCCAATGCTG	GTATCCAGCG	TGAACCCGTT	GACGCCCTGC	CCCCTCGTTA	GCATGACGTG	120
	CGTGGACGCG	CCGTACATCG	CGTAACACGC	TGCCACGATC	TCCCGGCCCG	ACCGCAGCAC	180
	ATCCTTGATT	GTCCCGCTCG	AGTCCGGAGT	CAGCTTGAAA	ATCGAAACGA	TCGTGCCAC	240
30	CGACACACCG	GCGTCCAGGT	TCGACGACCC	GTCAATCGGG	TCGCAGCACA	CCGCATACGT	300
	CCCACCGGTC	TCCGGGAACA	CGATCAGGTC	CTCCTGCTCC	TCCGACACCA	GCACCTTGAC	360
	GTTCCCGCTG	GCCTTCATCG	CATTGATGAA	GATCTCATCG	CCCAGCACAT	CCAACTTTTT	420
	CTGCTGGTCC	CCAGTCGCGT	TAGACGCGCC	GGAGAGCCCA	ATCAGGTTCA	CCAGCTCCGC	480
	GCGTCTGATC	GCTGCGGAGA	TGAACTTGAA	CGCAAACGAC	AGTGAGTTgA	GCAGCAGGTT	540
	GAACTCGCCC	GTCGCGTTTT	TGGCCGAgCT	GCgCTGCGAC	TcCAGGATGA	AACGCgCCAg	600
35	CGTAATGATA	TCCGtGTCgA	tAgCCTCTgC	GGAgTCgCGT	CTCTGTGGGT	TCACGGtAGC	660
	CATTTCTGcT	TGAGTgCGCT	GTGGT				

1047UP

	GATCACTCCC	CTCGCTTGAA	ACAATGCcgT	aTAGCGGAAT	CTGGCCGAGC	ACCAAGAAGA	60
40	TCAGCAGCGA	GACGGCTGTC	CAGATCAACT	TCTGGTTGTA	TGGCACTTTG	CGCTCGGGCG	120
	CGATCACCTC	GGGCAAAAAA	GCCTCGAAGG	GTTTGAATAG	ATCCAACAGA	CGCCCACTCA	180
	TTTCAGGCTC	ACAATGTTTG	TAGGTAGCTT	GCTGGGCTTG	GATTGGCTAC	ACAGTTGGAA	240
	CCACACAAAG	TCACTATTGG	GCGAGATGGT	ACTCTAAATG	ACTGCAAGGA	GAAGTGGTCG	300
	GTTTCGTTTT	CTGAACAGCT	TAATTGGACT	GAGTTGCAGT	AGCTGTACTG	AAAGGAACAC	360
45	GTATCTTGAA	AAAATTATAA	ATCTCAGTAC	CACGTGACCG	GATaCGAGGT	GCTATTCCAT	420
	CTCGCTAGAG	GAGCTATATG	CCTAGTCGGC	GTACCCCTGG	TGAGTAAGAA	TAGCTCTCTT	480
	GGACAATAAT	CCGtGATGAC	CTTATTATGC	TATAAAGCTA	TTTTACATAG	CAATGGATCT	540
	CCGtGtTTAG	ACCTTTGCGC	CGcCAAAAGA	CCAAGTACAT	CAGCACCGAG	AACAGcAGGC	600
	AATCGcCAGG	CGCTTGTTGA	GCTCCAgAAG	ACATgCTgGA	TGCAAACCGG	AAGAACgCCG	660
50	nTcGGAGTaC	AGTTGGCG					

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1048RP

	GATCGTCATA	GTCCGCCTCG	TCGTATTGGT	TCCTTCTGCG	CCGGCGCTGC	ACCGGCATAC	60
	CCATCGCGTC	CACCTGCATC	TTGTTCATCCG	CGTCCATCTC	GTCGTCCAGA	AACACCTGGC	120
5	TATCGTGGAG	CATCCTGTCC	CGCGCATTGA	GCTGCGCGTC	GATCCGTCCG	CGGTCCGCCA	180
	ACGACAGCTC	CTCGTGCTCC	GCGTCGTCCA	CGCCCTCATT	TTCATAGAAG	TCCTTGTTGC	240
	GATTGGCGGT	ATAGTCCGCG	TACATGTCTG	CGCCCACCAG	GTCGACCTCG	TCTATGCGCT	300
	CTTCTGCGTC	ATCCAGGTCT	TCTTGCAAAC	TCGATGCGCT	CGTCGCCGTC	GGTAATCGGG	360
	GTTCCTCGAAG	TCGATCTTCG	TCCCAGGGGAC	CCCAGGGGGG	ATTATTCCCC	CATACGGGAA	420
	GCGGGGCCCC	CTCCCAACTT	GTGGGAAGAT	AGTGGGTGCT	CCGAGGTTCT	TTTGACCTGC	480
10	TGTAATANTC	CNCTGTCTTT	TTCCGGTTCAA	CTNTAGCCCT	CNGGGCCNGG	TTNACCCCCC	540
	ATCCCGTATG	GAAGCANCCA	ATAACAAATG	CCTCCGAAAA	NTTTGTNTTT	TTCCNATTTT	600
	GGAANAAGNA	AGTTCNTANA	ANGAATTTTN	NANTTNNN			

1048UP

15	GATCGCGCTC	CTCAGCCATG	GCTTCCTCTA	ATAGTAACAC	ACGCCCTGCT	TCGTAGTCGT	60
	CGAGGTGCAC	ACCTACCCGC	GCAAATAATG	CCTCATCTGA	CAGCTGCACC	TGGTAGAACT	120
	GTGAGCACCG	GAAGTGCAGC	TTGCTGCAGA	AGCTTGTGAG	ATATTTGTAG	GGGTTGTTCT	180
	GTGTCAGAAA	GTTCCTCACC	CGTCGATTCT	CGTAGGGATC	ACGGATACGA	CCTTGGCTCT	240
	GCCCCGACAG	CGGGTACCCG	CATAGCTTGT	TTAGATTGCG	CTCATCTATC	AAGTCTGAAT	300
20	ATGTCGGCTT	GGGGAAAGAA	CCTTCCCACG	TATTTTAGTG	TCTCGGGTGT	GCATTCTTGT	360
	CTTGCGAAGA	GCAGTTCGGA	GCAATTTCGAC	CGTCAGAAGG	TCCCCCTCCT	TTAGTGAAG	420
	NNGCGATGTT	GGTGATAGGA	ACTTAAAACC	CGTTTTGGNT	TNTCNCAATA	GNAGCCANNA	480
	CCTTANGTAC	GGTNTNCCGT	TCTTAAACCC	GCCGGGTCCC	NGGGNGGTTT	CAAGTTCTTG	540
	GNGGGANAAG	GTNCCGNINC	CCGGGGGTNC	GCCTACTTAA	GNGANGCCAN	AAGGNAAGG	600
25	NCCCCNGAA	AAGTGGNTTT	T				

1049RP

30	GATCTTTCAG	CTTTGGCGTG	CTATGGCAGG	CAGCCTGCGC	CTTTATGGCC	TCAATGCCTC	60
	GCTGACGACT	CTCATGTGCC	TGTGGGCAAT	CTGGTCACGT	GGGTACTATC	CAGCGACGGG	120
	ACTCCCTATG	GCTGTGTCAG	ACAAAGCGAA	ACTCAGCATG	CTCTACGTGC	CCTACTTCCT	180
	GATTCTCTCG	CGCCTCGTCT	TTGTGTGAGG	TCTGGAGCAA	TGCAGAAGTG	CAACACTCTA	240
	TATATAATCA	CCTGACTATG	TACCTATTTT	TGGCATAGCA	CGTTACGTTT	TGTCACGATT	300
	CCAGTCAGTT	AGCTGCCTCG	AGCAACCCGG	GAGCTCCGAA	AAGGGAATTG	GCTACAAGGT	360
	CCTTAGCGCAT	AGNCCTGCAA	CTGGCTTTGG	CTAGGTCAAT	TGGTTTTCTT	GGAACCANTC	420
35	TTGGTATAGA	CTCTTGCGTA	TTGATCGGGC	TGAGGAGTGT	TTTNGNGGNA	GNCAACACCC	480

1049UP

40	GATCGTCTCC	TCGGCGACAG	CGCCTTCTAG	ACCCCTCGACG	GGCGACACCT	TGATGCTGCT	60
	CTCGCTCTCA	AACGTACCCA	GACCCTTGTA	GTAGGTGACG	CCGTTTTTCT	TGAAGAGCAT	120
	CTCAATACCG	CCAGTCAATT	GCTTCACAAC	GGTGTCTTGG	GCCTTTTGGG	ACTGGGGCAT	180
	GTTACACAGT	ACCTCGCCCT	TGACGTGCGT	ACCGCGCTGC	TTGGCATCGA	GTTGCATCTG	240
	GTGCAGCAGG	TGCGAGTTGT	TTAGCAGCGC	CTTGGATGGG	ATACACCCCA	CGTTCAAACA	300
	GGTGTACACT	AGACGGGCGG	GCTTCTCCAC	ACACGCGGGG	TCGAAAACCA	GTTTGTGCA	360
45	GCCTTCGATG	GCCGCCACNN	TTAACCACCG	GGGACCNCCA	CCCATCAACC	ACAACGTCGG	420
	GGTTTTCTTT	TGTTGGGAAT	TCAACCAGGC	CCNCTTTNNT	GGGACGACCN	CTTANNC	

1050RP

	NNNTTTNTGG	TGGGGCGTGT	AGANTAGTGG	TCGGGGNGCC	GCTCCACATT	CTCCATGCTC	60
	ACCACCACGA	CAGACTGGAA	GTACAGGAAA	AGCGACATTG	TCGTGCGAGA	GATGTGCGAC	120
5	GCGGCGTTTCG	AGTTCCCAAA	AGCAGACAGC	GTTGCGGACG	CCAGCAGTCC	AAGCCCCGCA	180
	ATTGTCGCCG	TCGCCCCACTT	CACAGGTGTT	TGGGCCACGG	TGCGGCCGTT	CGTGAAGTGC	240
	GTCTGGATGc	ACGACACCTG	GTCGTTTCGAC	TGGGTTTCGT	GTACCATCAC	CTTGAGGTAG	300
	GCGTCATTGT	CCGGCACCTG	GTACGtCACG	CCGGGAATCT	TNPTTGtGTT	CTCCGcGCTC	360
	ACATACTGcA	CGGcCTGGAT	CTgaaTGTCA	CCGGGtGTCA	CAGGAcAAAA	CTGcTTCtAG	420
10	cCGATCCCAT	ACATgTcCTT	CGc				

1050UP

	GATCCTTTTCG	TATGAAGTAT	GCAGCTGTCG	ATATGCTTAG	TTAACTTCTG	CCCAGCTATT	60
	TAAGCTGCAA	TTGAATCGGC	GGTGACTCAG	CTTGCAAAGG	GTAGCAGAGA	GGACGCGATG	120
15	GGTTTATTTCG	GAAAGGATAG	AGGTGAACGG	ATAGCTGAGT	TTCCGTGTTA	CCTGCTAGAG	180
	ACCNGAACGC	ATCTGGTGCC	GNTGNCAGGG	GATTCTATAC	AACCTTGTGA	TCGAGCGGAC	240
	ATATNGCGAG	CGGATACTAG	GGCAGNTCCC	TGGGATAGGT	GAGGCTNTAG	ACGGGGCGCT	300
	GACGGGCGCT	tttGAGGCCg	CAGAGGTACC	CCCGCGGGTt	GCGGAGGTGA	TGAAGGCGTT	360
20	CCAGGAGCGG	TACGACTCCC	GGGGACAAAA	ACGCAGGCCC			

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1052I2

	GATCTGGGTT	GCGCGTGAAG	ACCACCAATG	CGATGCACAC	GAGTATCATG	ATCAGCAAGA	60
	TTAAAGAAAA	GACAGCGTTC	AAAAATAAAA	ATACCCATGC	CATAATGGAG	CTGACGCTTG	120
5	CAGGCTGTCC	AAAGAGCCCT	GAGAAAAATA	AGAAGAGGAA	CGAATTAACA	AGAGTAACAC	180
	TGGATATCAT	AATGTTTCAGG	ATGTTAGTCG	CGCGGTCGAG	GTACGGCCTG	CATTTAGCCA	240
	GAGCTGCGAG	GTATATTATT	TCAATGACAA	ATAGAGCGAC	GGCCTGGGTT	TTACCGGAAT	300
	TGTGGGCAAA	TGCAATAAAT	ACCGCTTTCA	ACAAAAATATG	CGCGAGGATC	ATGCAGGACC	360
	ACCAGTAGTG	TGTCGCACTG	TACATTGTGT	AGAAGAAGCC	GTATTGTGT	AGCACATTTT	420
	CATTGCCGCA	TAGAATGGCA	GCTGGGTTTCG	AGTGACACACC	AATGGAAAGCC	CTTCCACNGT	480
10	AGATAGTGCG	GCAGGCAGCC	CANCCCATAA	TTGACAAGAT	AAANGTNGAG	CTAAGNCTGC	540
	CAGAACGACC	NCCGCCGGGG	ATCANCGTTC	ANTGATTCCC	CACCAGCAGA	GATCGCNAAT	600
	GANTGACCCC	GGCAGTTNTN	CGCAA				

1052I1

	GATCTCCGCT	TCAAACCAGC	TAGGGACGAC	CGGAGGTCGT	TCCAGAGAAA	GTCAACAATC	60
	AATATCCTGG	GTAAAGCTAG	CACCGCCGAA	CTACTTGCTC	TTGGCACCAC	CGCAAAGGCA	120
	CACAACGAAA	ACTGGGAAGA	TGAAC TGAAG	AAACAACAAA	CGGTCACCGT	TGATGACCAG	180
	GTTGTTTCGC	CAGAAGATTC	GCCCC TTTGCA	GAGCCAGTGC	AGGAACCAAA	GACCTCAGTG	240
20	TCCGGCTACA	TCAAGAGGAA	ACTATCCCTC	AAGCGTGATA	AATCCACAAG	ATCCAAATCGT	300
	TCGCAATATG	ATAGGTTACA	GGACTAGATA	TGGATGTTAA	GTATAGAAAA	ACTGTATATT	360
	ATTTGACGTG	CTGGGCGTTA	CGGAAACATA	TAAAGATTTA	ATTACTCATG	GGCGGATGGT	420
	ATTTTTCAT	GGGCCCCACT	GGACTCCATT	TGGGCAGTTG	GAGGACGAAG	TAGGAACCCA	480
	ATTGCTGGTT	ACAAGCGCTC	GGTTTCATGT	ACCCTATACA	CAAGTATCCA	TTATTINGGGC	540
	TTATTGATTT	GTGCTCNTGG	GCCGGACTTT	TANCTTTCTC	ACTGGGGGAN	GTCCT	

1052RP

	GATCGCGGAC	GCGTGGGCGC	AGAACCTGGC	GTGGAGCATG	GGGCTGATCC	GAGTGGAATT	60
	CATGCAACGC	ATCTTCCGGT	GGTACGTCCA	GGCGAGCGGC	GGCGAGCCGT	CGCTGCATTT	120
30	GACGTCAACG	ACCACGTCTG	TGCTTGCCCA	ACGCTCACTG	GATGCGCTAG	TGGGCCGGCC	180
	CGTGAGCAAG	GCGACACAGT	CGCTATTTGC	CAGCACACAC	ACGATGATCT	TCAGAGGGAT	240
	CCGTAGACTG	GCCTACCGTG	CGAACATAGA	GAGCTCATCG	GTTGTGTGTA	CCGGGCTAAC	300
	GTTCTTCCTT	CTGTTCGGCT	ATTTGGATTG	GCGTGGCGGT	TTACATTTGT	TCAAGCGGGG	360
	CTACTCGGAG	CTGCTTATCC	CGCATGAAGG	TCAATGAACC	CAGGTCCGGG	TCCCTAGACT	420
35	TCCAAGAAAA	ACGTGGGTGA	TTGNCTCAA	AGGTGTTCTT	TTGGGGTANA	TCTTCCCCCG	480
	NGTTCA						

1052UP

	GATCCAGCTC	TTGCGCGGTA	TGAAC TTTCC	CGCCCGCACC	GGCGCCTCGC	ACACCGAAAT	60
	CGACCGCACC	TCCGTCTGCG	TCTCGTAGTT	CCAAATTTCC	GCGCGCCCCG	AGTACAGCGT	120
	GATCAGCACC	CACGGCTCGC	TCGGGTGAAA	GTCAATGCCC	TTCAACCCTGT	CTGTCTCTCGA	180
	GACAAACGTT	TTCTACTCAC	GTTAGTACTT	GCTCCGCGCC	CTGGATAGCA	TGGTCGAGCT	240
	CTGCGGGTCC	GCCCCCTCCG	TGGGTGGCAA	AGATGGTCTT	CAAACACACC	GTAATAGGCC	300
	GTGCGCGACC	ATGCAGGCC	CATTCTGCTC	CGGACACACA	CATACCTTCG	TTTCCAAACT	360
45	TCATTGGTCC	CCACTTGGGA	TTCTTAGTAG	CTGTTCAACT	CGGCTTTTGT	GGTTCTTGTG	420
	GAAAANTAAT	ATTCCCN TGG	ATTATTTAAA	TAGGGGTCCN	TTTTNTTT		

1053RP

	GATCATAGTG	ATTGATATCG	GGAGAGGGTT	TCgTaTGTGA	CAGCCTGTAT	TCACGTATCT	60
	GGTCCTTCAC	TTCATATATT	TCTTGTGGGA	GCTGTGAATA	TATCTCCATG	CGTTCTCTGT	120
5	TCCATTTTTC	GTGCATTTTG	TGGAATGCAG	CCCCTTCTC	GTACGTTGAA	GTAGGCTTGG	180
	GTACTAACGA	TCCCTGAACA	GGGAGGAGGC	ATGTTGCCGAG	GGAGAATATT	AAGGAATCAT	240
	ATCTCATTTT	TACGTCTGAG	ATAACTAGTA	CTAACTGCAA	TGCGGCGTCC	AAATACCCGT	300
	CGTAGTAATC	GTATAGGAGC	AAAGCTTCAT	CTCTTATACG	ATGTGGAGTT	GATTCACTCC	360
	ACTGCAGCCC	TTGGTATTTA	GCCAGCATTG	CATCATATTT	GGACTGATAA	TATTCGAAGT	420
	TCTTCCACGC	GTCCTTATAC	GGATCAATTA	CTGATTTTAC	AACATCGAGT	AATATGGAAA	480
10	GATATAACTC	TGGATTGCCC	TGTATGACTT	CCAGCACGCC	ATGGAACATA	TcCCGAATGC	540
	CGTCGCGGCA	CTTGGAGACT	AACTTTGGCG	TGTATATCTG	CTCTTCGACT	GtCCCATGGt	600
	TGAgGtLAGGt	ATCTTCAGGT	agaATGAAGT	CAATGAGCGA	TAAACTGaCT	TGCTTGAATC	660
	gtcCCAAAGA	GT					

1053UP

	GATCTCGGCT	CGcTGCTCGC	GCTCGAGCCC	TACTGGGCAG	AGCGCTACCC	AATAAACAAC	60
	GCCCTAATCG	GCGGTGCAGA	TAAATTGCAC	AAGCTCTACT	CAACCGATTT	TGCGCCCATC	120
	GTGCGCGCCA	GGACTTTCGG	CTTGAACCTC	GTCGACAAGC	TTGGACCGCT	GAAAGACCTC	180
20	ATAATGGCAA	AGGTCAGCGG	CCCAAATTAA	TAGTCACGTG	TACATAAAGG	TTTTCTTAAT	240
	AGCTATACAG	CTTGCCCGCG	TCCTCAGCTT	GCAGCGCGCA	ACCGGCGTGC	AGCCATGAGC	300
	GTCCTACTGG	AAACTACCAT	TGGCGACCTT	GTAGTAGACC	TGGACTACAA	GACATGCAGC	360
	GCCGAGAGCT	ACAACCTCCT	CAAACCTGTC	AAAACCTCGT	TCTACGACTG	TCAGTGCATC	420
	TAcCGAcCTc	CATCCTgAaG	GCTCAGCACG	CCCTcGGCGA	TCCACAGGTG	GgCTTTGCAT	480
	TCCGCACGGA	TTTGCCTGTA	CACAATACCT	CGATCGAAgG	CCTGCGCGAc	ACACGGGCGG	540
25	TCACCCCGAA	GCTCATTGAA	GCCTcCGTTG	CCGCTcAACC	CGCAGAGCGC	TTcGGACAGG	600
	TCgCCTTTG						

1054RP

	GATCCGTCGC	CGGTCCGccA	ACGACAGCTC	CTCGTGCTCC	GCGTCGTCCA	CGCCCTCATT	60
30	TTCATAGAAG	TCCTTGTTCG	GATTGGCGGT	ATAGTCCGCG	TACATGTTCG	CGCCCACCAG	120
	GTGACCTCG	TCTATGCGCT	CTTCTGCGTC	ATCCAGGTG	TCTGCAAAC	CGATGCGCTC	180
	GTGCGCGTCG	TTATCGGGGT	TCTCGAAGTC	GATCTCGTCC	GGCGACCCCA	GCGGCGAATT	240
	ATTCCCCATA	CGCGAGCCGC	GCCCGCTCCC	AACTTGTGGC	GACGATGGTG	GGTGCTCGTA	300
	GCTCTGTGAC	CTGCTGTCAC	TACTCCGCTG	CTCTGTATCG	TTTTCATCTC	TAGCCCTTCT	360
35	GCGCCCGTGT	GAACCCCTCCA	TTCCGTTATG	CGAAGCCATA	CCCAAATTAC	CAAATTGCCC	420
	TTCTTGAGAT	CTTGAATACT	ATCTCCCAGA	TGTTTGACAG	ACGCGCAGCT	TCTcACGATA	480
	CGAAATATCG	TGAtTTTACG	TGAcTTTCAA	TACCTCATTT	gGATTGGATT	GGtGAAGCAT	540
	AGATTTTCAG	TcaTATTGAA	AAATTATTTT	CAAACAGGGC	AATTGGATGA	GCTG	

1054UP

	GATCGTCGCG	TTgcgCagGG	CTGCCCAACG	AAGCCTTGAC	ATGTCAAACC	GCTTGAAAGA	60
	AGAGGTGATA	TGGGCCACCC	ACGAGGCCAA	GTGGGAGCAA	CTGCTCGCTA	CTGGGACCCT	120
	TCCCCAGAT	GGGGCCAAAA	GCGACTGGAA	GCCTGGCCGA	GCATGGCTGG	AACCATATGA	180
45	GGCCGCGTTT	CGGAACCAGC	TTGCAAATCG	CAAGCGCACG	AGCCAGAAGC	TCAAGCGCTA	240
	TAGTGCCCAA	ATCAGCAAGG	TACACCTCCC	GTATTACATT	AAGTGCAAGT	CTGCTATGCA	300
	TACCCGTGCG	GCCAAACGCT	tCGAGTGTtT	CCAGAAAGAG	CTCCACACCG	TTAATCCATT	360
	CGTTCCAGGC	AGAGATCTCG	GtTCCCTACT	CTCCAAGTGG	CGAATGGTGA	ACGGaAAAAA	420
	CTACTATCGC	TGAATGTATA	TAGtTTATAG	TCCTATTTCCT	TCATcAGGtC	TCCCAGCAGA	480
50	GGCGGCCGCT	CGGTCTcAAC	TATGCGCACC	TCGCTcAGCC	ATTGCGCTGAg	GTCCTTCTGA	540
	GTTTCG						

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1055RP

	GATCCGTCGC	CGGTCCGcCA	AcGACAGCTC	CTCGTGCTCC	GCGTcgTCCA	CGCCCTCATT	60
	TTCATAGAAG	TCCTTGTTGC	GATTGGCGGT	ATAGTCCGCG	TACATGTCTGT	CGCCCACCAG	120
5	GTCGACCTCG	TCTATGCGCT	CTTCTGCGTC	ATCCAGGTCTG	TCTGCAAACT	CGATGCGCTC	180
	GTCGCCGTCG	TTATCGGGGT	TCTCGAAGTC	GATCTCGTCC	GGCGACCCCA	GCGGCGAATT	240
	ATTCCCCATA	CGCGAGCCGC	GCCCGCTCCC	AACTTGTGGC	GACGATGGTG	GGTGCTCGTA	300
	GCTCTGTGAC	CTGCTGTAC	TACTCCGCTG	CTCTGTATCG	tTTTCATCTC	TAGCCCTTCT	360
	GCGCCCGTGT	GAACCCTCCA	TTCCGTTATG	CGAAGCCATA	CCCAAATTAC	CAAATTGCCC	420
	TTCTTGAgAT	CTTGAATACT	ATCTCCCAGA	TGTTTGACAG	ACGCGCAGCT	TCTcACGATA	480
10	CGAAATATCG	tGatTTTACG	TGACTTTcAA	tACCTcAtTT	TGGAtTGGAT	TG	

1055UP

	GATCGTCGCG	TTgcGCAGGG	CTGCCCAACG	AAGCCTtGAC	ATGTCAAACC	GCTTGAAAGA	60
15	AGAGGTGATA	TGGGCCACCC	ACGAGGCCAA	GTGGGAGCAA	CTGCTCGCTA	CTGGGACCCT	120
	TCCCCCAGAT	GGGGCCAAAA	GCGACTGGAA	GCCTGGCCGA	GCATGGCTGG	AACCATATGA	180
	GGCCGCGTTT	CGGAACCAGC	TTGCAAATCG	CAAGCGCACG	AGCCAGAAGC	TCAAGCGCTA	240
	TAGTGCCCAA	ATCAGCAAGG	TACACCTCCC	GTATTACATT	AAGTGCAGTG	CTGCTATGCA	300
	TACCCGTCGC	GCCAAACGCT	TCGAGTGTTT	CCAGAAAGAG	CTCCACACCG	TTAATCCATT	360
	CGTTCCAGGC	AGAGATCTCG	GTTCCCTACT	CTCCAAGTGG	CGAATGGTGA	ACGGTAAAAA	420
20	CTACTATCGC	TGAATGTATA	TAGGTTATAG	tCCTATTcCT	TCATCAGGTC	TcCCAGCAGA	480
	GGCGGCCGCT	CGTTCTCAAC	TATGCGCACC	TcGCTCAGCC	ATTCTGCTGAG	GtCCTTCTGT	540
	AGTTCGTCAC	CCG					

1056RP

	GATCATCagC	GCGAGCTTCC	aATTtGTGGG	CTTTCTGTtG	ACATACATCC	TCCaCACCTC	60
	GCATGCGGCG	CGCCAGgGCT	CGCGCTTTTGG	CCTCGGCCTG	ACCTTCACGG	GATACGGGTa	120
	CAGCATGATT	CCTAgCGACg	TgACGAgCAA	GGTCGGcAAG	GACCGCGACa	TCgCgCGCGT	180
30	gGAGCTGGAc	GACCCCAaCG	AATTcGAAGa	TTTCGCACCTG	TACTCgCCGC	TGGCGCagCC	240
	GGCGCAGGAC	CGCTTCGAAT	CacagCTCTC	gCACGGGCTG	ATGGAaaaaAC	GGCGCAGaAT	300
	TCCGGCGCTC	GCGATCGTgC	tagAgATTTT	GGGGCTTgCa	ATTATGTGCa	aAAGCgTGTA	360
	cgACTACAtt	GTGGTcAAGC	GCATgGAGCg	CCGCATctTT	ACTGcGAgCG	ACAGCgAgAg	420
	CCcCGCATAG	ATGTTcATAT	aACTTATATa	TCCCTCATTG	ATCTTCGcTT	GGGCCCCgTC	480
	TAGGGAGCAG	AcCAGcAGTT	TCTTCGTtCG	CCCTNAaGTC	GATgCgCCA	GAGAGACCAG	540
35	ACGCCCCAGc	GCGGTa					

1056UP

	GATCCAACCC	AGGACTTCTC	GAAAGATAGA	ACTCCGAACA	CAGCCACCGG	CACGAActTC	60
40	TCATCAGCTA	GCAGCAATAC	TAAGCAGACC	TTCAGCGAAA	ATGAAGAAGA	ATCTGATGCT	120
	GAGTTcGAAG	ATGTATAGTT	GTACCCGTAT	ATTGCATTTT	TTTTTTTTTTT	TTTTTTTTTTT	180
	TTTTTTTGGa	gATGTCAAAA	GCTCATCTCA	ACTCCATGAC	CAGCCAGTAG	TGACTAAAAGC	240
	AGTGTGTCTA	GTTCTTCTAA	GTGATTTTAA	GGACTATGAG	CTTTAATGAg	AAGGTGAAGT	300
	GGGTACTAGG	CACTGCTGTT	GCGACTCTAG	TTACGATAAA	GTCTGTcGAA	GCCGTATATC	360
	GCCTCTATGC	AGCTAAGCAG	AACACTAGCA	GGAGCATTTC	TGGGGAgGAg	AAgGACGTaA	420
45	GACTGGCCAA	ACGGATTCTG	GAGTCTAGGG	CGTaCGATGA	gGAATTATaT	CgGGAGCAGT	480
	TAgCTCGGAa	CTACgCaTTT	TGGGCGaAGa	CGGTaTgGCa	CGACTACaGG	AACAGTACTC	540
	ATATgGTGGG						

1057RP

	GATCAGGGCC	AAATCACTGC	TAAGTACAAA	CACAAAGGGC	CAAGTATTAA	GGTGAGAGAG	60
	CGTTACAGGT	GCATTGATAA	TACCGCAGGT	ATATATCAAG	GCGCACAGTG	AACACATTCT	120
5	GCAGACGATA	GATATGTCTG	AGACGAAGTA	GGTTGAGATA	TTTACGCACA	AGCCTCATT	180
	GTAAGATAAA	TGGTCATTAC	TAACGTTTTT	GGGTTTAGCA	GCAGCAGGCG	GAGCAACAAC	240
	GAGGGGCAGG	AGCACGGTGG	TGGTGGACAG	GGTCCAGGAG	TCGAGGATGG	CGGGGAGCCA	300
	CGGGCCAGGG	CGAACACGCG	CAATGTGACT	GTGGCAATCC	AGTACTCGTG	GCTCCACGAC	360
	ATGAGGAATG	TCGGGGGAGA	GGGCGAGGAA	CGGGACAGGG	CCCGGGGGAG	AACGGAGATA	420
	CGTTTCGTGAT	GAGCTTCACG	GACGTGCCGG	ACTCGACGTC	GAACGATCGG	TTTCAGGAAG	480
10	TGATCGGCAT	TGCGGCGCAG	TTTGCATTGA	GCCGCGTGCG	GCGGCGGATC	AGCCTCCTGC	540
	GGGGGCTCTC	GAAGGAGTCC	TTTGAAAAC	CCCTCTCAGG	AAGCTCAGCG	AGCTGGACAG	600
	CGAGCTGTGC	AGTATATGCT	ACGACGACTT	TGAAGACGAC	ACGTCGATCG	GGT	

1057UP

	GATCTAGGGG	TTCTTCTTGC	CGCGCTACGG	GCGCCCTCG	CAGCCTCGCG	CTGGCTCCCG	60
	CGCGAGAGGG	GATCGGCAAG	GCTCCTCGCA	GCCGCACACT	GCGTCTATGC	CTGGACCGTC	120
	CGGCGAGCCG	GACAGCCGAG	GAGCAGCCCC	GCGATGTCTG	TCTCCCCGGC	GGCGCTTACT	180
	CTGGGGCTGG	TGTTGAATTT	TCCTAAAAC	GGTGAAATTG	TACGGGCTCG	CTGGAGCCCG	240
20	CGCTGTCCGA	TTGTACACGG	GAATAGCGGA	TCAATTGGAT	GGGGACGCCA	GTGTTACCCC	300
	CGAAACCGTG	CGCAGCGGCT	GGCGGGCCGA	GGGCTGAGGT	GCCGCTGCCG	CGCAAGGCGC	360
	ATTGTCTGTC	GACTGCAGAG	CTGCAGGAGC	TGTTGAAGGC	GCAGGACAAG	TTGCAGCTGT	420
	ACGTGGCGGG	GTTGTGCGAG	AGCGAGGAGA	CGCAGAAGCG	GGTGGAGCAG	CAACGAAAAC	480
	AGCTGGCTGA	AATACGGGAA	ACGTTTGCGG	GGCTGGAAGG	GGAACGACAG	CGCGTGCAGG	540
	AGCGGCTGGA	CGGGTATCAG	AGGCTAATGT	TCCGGTACCA	TGAAGCGTGG	CAGGCGGTAR	600
25	ACGGGCGTGC	CGGGCCCGTT	ACAACGACGG	GTTCTGCCGG	CGCGGCTGCA	CAAGAAATGC	660
	GCGCTGCG						

1058I2

	AAGCTTGCAT	GCCTGCAGGT	CGACTCTAGA	GGATCTTGCA	AAGTATGGCT	TGGTAGTGTG	60
30	GTGATGGTTA	TCTGCAGTTT	CAATTGCTTT	GTTAGTTAGT	GTATCACATT	CTTCTGGCTT	120
	TGGCCGATTA	GAGTGCTGGG	CCTCATGGAT	GGGGATCTCC	GGTGTATACA	CGTATATTTA	180
	TTCTCTTCGC	CCAAGTGGCG	GAGTACAATT	TTCTCTAGC	TGGACCTATT	TCGGTTGTAT	240
	TTCAGTAGTG	AAATAAAAC	ATCAATTAA	TACAGCTTCT	GTATGACTCT	GCCACAGGAT	300
	GAGAGCAGAC	ACTCTGCAAA	GTACCGGATT	TCAAATAAAT	GTTTAGGAAT	AAAATCAAAG	360
35	GCGTACAATT	ACATAATTAT	AAAATGCTCT	CGTAGCTATG	TCTTTCCGGT	CTTTTTTTTA	420
	TCTTAAAGTG	AACATCGAGT	CTTGTCCTTC	TTAGGTGTTT	AGATGACAAG	CTTACATGCC	480
	TGCNGNNGNN	AAACAGTTNG	TCGAATCCCT	CGGATCCTCN	CCANGTAGNA	AGGNANTACG	540
	NNCAGCAGAG	TCATTACCNC	NACCCACCGG	CTTGCCANCC	NANTTNCCTN	GGNNGNAGNG	600
	GGNNGGNGNT	TGNACCNANN	TTTGNCCNT	NGCC			

1058I1

	GATCTTCACA	TTCGCATGCA	GGTTCTTCTT	GTTTTTAGTA	GCACCTCCG	GCGCCTTGTT	60
	GGCCTTCAAC	TTGAGTTCAT	CCGCACTTGG	CTTGATAAGA	CCAGCTTTCA	AGTACACCAT	120
45	GATGTCGTCTG	TCATCACCGT	GCTTAAAGCA	ACAGCGCTTG	CCATAGCGGC	AGTAGCCTGT	180
	CTTACTCCAA	TTGATACATG	GCTTCGTGCG	GAATTTGTCC	GACCGCTCCT	TGAACCTTAA	240
	CTCGTGGAGA	CCATGGGCAA	ATTGGCACCT	GTTATCGTAC	TTGCAGGCCC	CCGTAGTCGC	300
	AAATGATTCTG	CATAACTCTG	TCTTGTAAG	CATCTTGTTG	ACCTTCTCCT	GCGATGGCTG	360
	TGGCTGTCTG	TGTGGGGTGG	CGGGGGCGGG	GACTGAACCC	GGCAAAAGTT	CGGCTCCGGC	420
	TGTGCGCCTG	CTCGCCCTGG	GCGCTCGGGT	CCTCCCGACG	GATGCTGCAG	GAGCGCAGGT	480
50	TTTCGGGCGT	CAGGGTAGTA	TCCCATTTGGT	AGGCCGNTAA	TGAGAGTTTA	TCGCCACCTC	540
	NAAGGTAGGT	TCCCCGTTCC	GNAGGGCCAA	GGGNAATCAN	TNGCCGCCCA	AACCGTNAAC	600
	CNCCCCCNCC	CNGC					

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1058RP

	GATCATTCTT	GAGAATGCTC	ATAGTTATGG	TTTAACGGTT	CTTCAAACGG	AAGAGTATCT	60
	TCAATTACAG	AGTAGTTTGG	AGAGAGAACA	GGTAACGTCC	TACAACATTG	CCGAGAAAAGC	120
5	AACTACAATT	GGCTACGTTG	CACTTCCAAG	AACCGAGTAC	GATGAACTTG	TAGCTTCGCA	180
	AGCTTCTACG	AAAGAACAGA	ATTTTGAGGT	ATACGCGGCG	GAAAATGGCA	AGGTCATAGT	240
	GGATAAATCT	GAGTATCACG	ATTTGAAGAT	CAAAGCTATC	CCAGTGATTT	CACCATTGCC	300
	TCAAATGAGC	AAAGAGCAGA	TGTTTGAAAA	GGCCAAGGAA	CTTGGAATGG	TAGCTTTGCT	360
	CCATTGACGA	GTATGAGAAG	TTAAAGAGCC	CTATTTCCCG	ATAACGCTTT	GGATTGCAAC	420
	AGCGAAGGAC	CGCGGAAAGG	TTGGTCTCCT	AAAGGAGGAG	TACAACCCCT	TATTG	

1058UP

	GATCTGGCGC	CCCGACAGCC	TGCCCAGGTG	CGCCTGCATC	CGCCGCTCCT	GGTCGCGCTC	60
	GTGAGCCCC	AGCTCCTGCC	GGAAGCTAGC	CCTCCAGCTC	ATGTACGACT	CATGCGTTAC	120
15	CTTCGTTCGG	CGGAATTTCT	TCTGCTCTTC	GAGCTCGCGT	TCGCGTAGCT	GCCGCTCGTG	180
	CTCCTTCTCT	CGGCGCTCAA	GCTCCTTCTG	AAACCACGAC	TCCGCGTCCT	CCTTTATTGA	240
	CGAGATCAGC	GCAAAACACA	TCTGTATTCC	CAGCAGGATG	TCCTCCTCCA	CCTGTCGCAT	300
	GGACTGGCTT	GGAAAGACCG	TCCACCTCGC	CGGTCAAAAT	GAAATGCTTG	TCCGGAATAT	360
	TCTCCAGTTT	CGCAACACAA	GGGTTCCCCC	GTGCTCGTCC	GGACTTCCTN	GTTCTCTCAAT	420
20	CCCNCTCAA	CCTGCTCGGN	TTTCGGCGGG	GAAGGTNCCA	NCGGGCTTAA	TGTCAC	

1059RP

	GATCTGTTAC	GCTGCAGCGC	GAAACCTCCA	ATGCTCTGGG	CCAAGGTTGG	CGGCTGGGAT	60
	TCTTGGGCTC	ACTGCATGCT	TCGGTTTTCA	AGGAACGACT	GGAGAATGAA	TACGGCTCGA	120
	AACTCATTAT	CACACAACCC	ACTGTTCCAT	ATGTCGTGGA	GTACTCCGAT	GGGACCCAGA	180
	TAACAGTAAC	AAATCCAGAT	GACTTTCTCT	ACCTGACACT	TCGGCGAACC	AAGATAAAGA	240
	ATTTCCAGGA	GCCATATGTA	GAAGCTATAA	TGACTCTTCC	ACAGGATTAT	CTCGGAAGGG	300
	TTATCACTCT	CTGCGACGAC	AACCGTGGCA	TACAGAAAGA	GATAACGTAC	ATTAACACCA	360
	CGGGGCAAGT	GATGCTGAAA	TATGATATCC	CATTGGCACA	TCTAGTAGAC	GACTTTTTTG	420
30	GTAAGCTCAA	GTCTGTACAG	CATGGTTATG	CTTCCCTAGA	CTACGANGAT	GCAGGCTATA	480
	AGCCGTCTGA	CATTGTCAAG	ATGGAGTTGC	TTGTAAATGG	AAAAGGTGTG	GATGCACTTG	540
	CACAAGTGAT	GCATCGCTCC	CAAACCGAAC	GARTGGCCAA	AGAATGGGTT	ANGAAGTTCA	600
	AGCAATATGT	CAAATCCAG	TTATACGAAG	TGGTTATCCA	GGCC		

1059UP

	GATCGTGGCG	GACGTGTTTG	TGCGCACCGC	GGACGTGCTG	CTGAAGATGT	CGCGGTACGA	60
	RGAAGCCAAG	GCGGCGGCGG	ARCGCGGCCT	GAGCCTGGAG	CCGGACCACA	TGAAGCTGAA	120
	GGCGCTGCAC	CTGGAGTCTG	TGCGCAAGTT	GGCCGACTAT	AACGGCGACA	TCTAGTCCGC	180
40	GCGCGCGGCC	CGCGCGGGCA	CCACGGGTAT	ATATACACAG	CCGGTCTCCG	CGCGCCATGC	240
	CGCCCGCCGG	GACCGCAGAC	ACAGGCCCCG	ATCTTGCGCG	GCGGCGGGCG	ATGAGCTGGT	300
	GCAACCTCT	TGGCCCGTAC	CCTGCTAAGG	AGGGTAATCT	CCCACCTCAG	TACTATAAAA	360
	AATTTTAAAG	TTAGCCACTT	TCGAGTTACA	ACTCCCCGCC	TGTCGGGTAA	CGGATCTCAA	420
	CTTGTAAGC	CCCTAACGCT	GCTCTACTCC	TTTTGCGCTA	AGGCAATATC	CCGCCATGTC	480
	TTCGTGGAT	ATCAATGTCA	CGGTTGATTG	GTTTATTGAT	AGGTTGAAGC	GGAAAGCAGAT	540
45	TACTGGCAGC	TACAATGTGT	CGCTGGAGAC	GTTACAAATT	CTGATGCGTT	ACGTATCTGC	600
	CATCCGGTGG	TCGACGAAGG	ACGARCTCAT	TGAACAGATC	CGTCTACTC		

1060RP

	GATCTGCTCA	TACTGAGCGG	CCAACTGGTC	GTACTCCGTA	TGCAAAACAT	CTGTGGTTTC	60
	CTGGAAGTGC	GCCACCTTGA	GCGATATCTC	ATTAAACTTG	GTAACCAGCT	CTCCCAACTG	120
5	ATGATTGACT	GCACTGGTTT	CCGTCAGCAG	GTCTCCAGT	TCGCCAGTTC	TGGTGTCCAC	180
	TTCCGCCACG	TATCCGCTGT	ACAATGTATA	CTCGTCGTTT	GCAGACCCCA	GARCAGAAGC	240
	TCGCCGCCAC	TCTGGCGCCA	GCAGCTCAAT	TACCTGAGGT	TCAATCTCTG	TTTCAACCGT	300
	TGCCAACAGA	GTGTCTACTT	TTTGGCGTAA	CGAACTATCC	CCAAAAAGCG	GAGGCAGCTC	360
	ATCGTGAGAR	GARGCACCGG	GATTTGCCGC	TACATCCTGT	ATGACTGART	TCTTCCGGCT	420
	CCTAAGCATG	GTGCAGTTGC	TGCCTCAACG	GCTTCTCTCC	TGGTGCARGT	CTGCAGTGGT	480
10	TCGTGCTTAT	GCGCAAGCAG	AATACCATGT	TGAGCCGGCG	AAATCTCATC	ACGTGATCAT	540
	CATCTTGCAA	CGGCTCGGAR	GACRCTGATG	CACGTGTCCA	TAGGCTTAGG	GCGCAATTAT	600
	ACGCTAGCTA	GTTATATTGA	TAATATGTAC	ATGATGCCTT	C		

1060UP

	GATCTTGCCG	TCCTTCTTGT	CCAGCTGTAG	GTCCGGATGA	GGGTACGCCT	CGCTCAGGTA	60
	CTCCAGCCGC	AGCTCGCCGC	TCTCCATGGA	CGCCTCCAGG	ATCGAAGGCG	CCGGCACAGC	120
	CTCGGAGGGG	AGGGGCGGCT	GCAGGAGGGG	CATCTCCTGT	CGCTCCTGGT	GCATCTGCAG	180
	CGCCGCAGCG	CTCGGCTCCA	GCGCCGGGTC	GAAGTACTTC	ACATTCGTCA	GGCCCCGACTT	240
	GTACAGATTG	AGGATGCAGC	CCTTGAGCTG	CGCACGGTGC	AACCGGTACG	CAGTCGCGAC	300
20	ATACTGGTAC	CCGCTCGTCC	CCCCTCCCGT	GAAGTGCGGC	CGCTCCGATC	CGATCGAAGA	360
	CAGTGACGCT	GTTGGCTGGT	GGCTGTATCG	CCCCTCGCGC	GCCGGCGCTG	CGCCCTGCGC	420
	CTTGTTCAAC	CACCCGAGCC	GAAACACAGT	CCCGTCGTAC	GTCTCCCCGT	TCAGCCCCGCC	480
	TCCACGTGCG	ACCGGCGARC	CCGCCGGCTG	CGARCAAGGC	GACACCTGCT	CCTCGCAGCG	540
	CGCACCCGCC	TTTATGTCTT	CACATGTCAG	CGTCCGCTTG	TGCGCTTGCC	CCGTCNGCAC	600
	CTGTTAACTG	CATCCGCGTC	TGTTGGCTGC	TGCTGCTTGC	TGCTTGCTT		

1061RP

	GATCTGCTTT	TGtAAGTaTT	CATCAGCTAA	ATACCGTAAA	GctGGTTTgA	ACGGAGGTCC	60
	TGCCTTGtGC	TCATATATTA	TAGAAGTATC	AATGACGAGG	GGATGCCGCA	TtTtCAAGAC	120
30	GTTCAAGTCG	GCCTGCAATG	AATGGCCGAT	AAGCACATCT	GtTGCGCTTA	TCATCCGCAA	180
	GAGATCCTGT	tGGACGTCTT	GCAAAGtCGT	GGTCACCCCG	ACCAACTTCT	CCTCTGTAAT	240
	ACCGCTGTAC	TtCGTCAAGT	AGtCCACAAT	GGGCTCATCT	GGCTtGACAA	ACTTGTcATA	300
	AACTAAGTTA	CAATCAAAAt	CGACGACGCT	CACACGCGTC	AACACGTATC	CGTTTTTtGa	360
	aaGGcACATC	TCACAGTCGA	TGGcAAACGT	GTGAGAACCG	tCGTGTtTGA	AACTGACAGT	420
	GTCCACCCAC	CCACTGcACT	TCTCCTtATT	CTGATACTTt	AGcAACAAAG	CCTTtTtGGGt	480
35	ACTCCTCCgA	TAAGCCAGGT	GTgTTTtAGAT	GGaTGGGGTa	CTCATTaTGc	AATAaGTCAA	540
	CAACGGGCAT	AGcAAAtCAA	GcAAGtGATT				

1062RP

	GATCTCGGTG	ACGTGGcgct	GGTATGGCTT	CATCCAGTCG	CCGtTCAACA	AGAAGTTTCT	60
	GTTAACGTCG	AAGTTACAGC	TGGTGAAGGA	ATCAACCTCT	GCGCCACGG	CCTTGATCAC	120
5	CTCTGGTGTG	TTCAAATACT	CCTCACTGTA	CTTCATGTCA	TCGTAGCAGA	GCTGGCCCTC	180
	ACACTCCTTG	CGAACGTCGT	AGACGTTCCT	ACCAGtTCTC	TGGAACGGCG	TCAACTGGTT	240
	GCCATTACAG	TACAGAGAGG	CTGGAACACA	CGACCACACG	TTCTGCAGGG	TGTAGCATGT	300
	GCGGATCAAA	CGCAAGCACC	GtGGCAAGGT	CTCGTTCAAT	GCCGAGCATT	GCTCTGGGCC	360
	AAGAATGGCG	GGTTCGCCGc	CACCACCGCA	GGCCATACGC	TCGTAGTAGG	GGTACTGTgT	420
	CAATGGGTCT	gTCAaCCCgt	tCCCaTTaG	cACAGAGcTC	AACTTaaaCG	AGCGCTCCTc	480
10	GcCTGGGTGc	GAcAAGATCT	CGGCAGcAAT	aGcAGGAaTg	Tg		

1062UP

	GATCCTGGTT	GtaTCATAGA	GAATGAACAT	ATTGATAAAA	AAATGCTACT	GTGTACAGTA	60
15	ATGTCTGAAC	ACCAACATGC	TCTTTCTTG	TATTAAATGA	TGGGATAACG	AAGTCTTGGA	120
	AGAATCCTGG	GCGGAAATAG	TAGACATGTT	TAGAGAGATT	TTTGTAATGG	CTAGAGTCGG	180
	TTTTGATGGC	CGAAAAAGAA	GTGCCAACAT	TTAATTTTCA	AGGTTTATCA	GGTAGGTCAG	240
	GGAATATACT	ATCCTCGTAT	AAACCCCTGA	TTGTACTTGC	AAGGAGCTCC	AAGTCGTCTG	300
	AGTTAGGCGA	TGGTTCATCT	TTAGTGTGAG	CATCGACGAG	GACCTCACAT	GTGATTCCTG	360
	AGTCAATTGC	ATCTATGACC	TCTCCATTCA	CAATCAAGCC	CATGGGTCCA	ACCTcCTTGA	420
20	GAGCCGCCTT	GATAAGCTCA	GTACGCAGCT	CGACCGAAGT	ATCCAACGTA	AGTGACTCCT	480
	TTATTTTCGAA	TTGCAGATAT	TCgGGCCGCa	CTGCATGTAT	AGATCCCCCA	TGAATAAAGG	540
	AGAATTGCTG	CACAGTAGTA	AACGCAAATC	CCGCGTAATT	AGTTGGTTGG	CTTCTTAGGA	600
	AGTCAGTGAA	CCGATTATTT	GCGTCCTGat	CCT			

1063RP

	GATCGACTTG	ACCGTCACCC	GGTACTGGTC	GTACTTGTCG	ATGAACTGGT	CCTGTAGTTC	60
	CCCCAGTTCC	TAGATGAGCA	CGCCAGTTT	GTCGGTCACG	TCGGACACAT	CGTCGTCGTT	120
	GTCCATGCCC	CACATCGACA	GCTGCCGCGC	AGCGGCGCGC	CGCTCATTTG	CCACCACTTC	180
30	CAGCGCACGT	AGCACCCCTT	TTTCCGTCTT	CACGAACGAA	GACAGCTTCC	GTGCCAACTC	240
	GGGGCCAAAG	TTTCCCGCTG	CATCTTTGCG	GAACGAGGAA	GCAATCCCCG	CACGCCCAAA	300
	GAACTTGGAA	CGTGTGGAAG	AGGGTGGGGG	AGGGGGTGAC	TGGAGGTCTG	ACGCAGTAGG	360
	CGCCTTCTGG	TTTCTCAAAG	AGTATGTTCT	GtGCATATTc	TCGtGCTTAG	ACTGGTCTGG	420
	CAGTCGGtAT	TTGTAGGTCC	GATaAGATTc	TcAGACGACA	GCAAGTAAAG	TACAACGGTG	480
	GTCCGtGCCC	CTcCAACGTc	TTTTT				

1063UP

	GATCTTAATA	GCaATAGTCG	ACTACAGGAA	ACACAAGCTT	TCATAATGTC	GAAATCTTTA	60
	TCATGGGATA	CACTAGACTA	TACTCTACAA	CCATGGATTc	GTACTGCTGT	TGATGCCATG	120
40	GGTTATGAGA	CCATGACACC	TGTACAGGCA	TCGACGATCC	CGCTATTTGC	CAGAAACAAA	180
	GATGTGGTTG	TAGAATCTGT	GACCGGTTCC	GGGAAGACCG	TGGCATTGTT	CATACCTGTA	240
	TTGGAGAGAG	TGATACAGGA	TGATGCCAAT	AGTTCAAAGC	TCAAAAAAGG	CCACTTCCAC	300
	ACCATAATAA	TCTCCCTTAC	GCGGGAGCTT	GCATCACAGA	TACAGGGCGT	GATTGAAGCG	360
	TTTCTGACAT	ACTATCCAGA	TGGAGAATAT	CCTATAAAAT	CACAGTTGCT	TATCGGTAGC	420
	AATACCAGTA	GTGTCAGAGA	TGATGTTGCA	GCGTTTTTGG	AACATAGACC	GCAAATTTTA	480
45	GTGGGTACgC	CTGGAaGGCT	ATTAGACTTT	CTTAAGATGC	CaaACATCAA	GACGCTTCA	540
	TGTGGCGCag	CTATTCTTGA	TGAgGCCGac	AaGTATTGGA	TATGAATTTG	AGAAGGATGt	600
	CCAGACaATA	CTGGAGATGC	TACCAAGCCA	A			

1064RP

	TAGTGGATCC	AGCATCCCCT	CTCGACCAGT	CCTGAGTTCC	GCCGGcTCTA	TCCTAGACCG	60
	CCAAAGCCCA	GcTTGAAGAC	GTACTGGGAG	ATCGTGAAGG	AACCAAACCT	CACTATATGt	120
5	TCCCTGAGcA	CAGCGCTAAT	GTTCGCCACC	TACTATGGGT	TCAGCGTCAC	GTTCGCCCCAC	180
	TACTTGAAAC	TTGACTATGG	cTTCAGTAAC	CTTGcGATCG	GCGCGTGCTA	TGCCTGTCCA	240
	GGCGTGGCCC	TAATGATGGG	CTCCCTCTTG	GGcGGtCACA	TPTCCGACCG	CTTCCGCAGG	300
	AAGTGGGTAG	CCAAGAACCC	CGGNAAGACC	TtCCCGAGcT	ACAACCGCCT	CATCTCGCAG	360
	GTGTTtGGcA	TCTGCGTCAG	cATGGCCGGc	TGTaTCGGGT	ACGGcTGGGG	AATTCAATTT	420
	CACTATCACA	TCGcTATCGc	GCTATTCTTt	TCTTTCC'TAA	TGGcGtTGGG	TATGAcCTGG	480
10	tGcTCTaAcT	CCACCATGAC	CTtCCTtAcG	GaGTCCAACC	CAAAAaGAGc	TGcCGGtacc	540
	ATTGCGtaaG	cAAcAGcTT					

1064UP

15	GATCTGTTTc	CGCCCGCCTA	TGGGCCCTGC	CTGCGGGCAG	AGGGAGATCG	TCCTGGTCCG	60
	CCTAGGCTAG	GCACGGCCCT	AGGCGGAGCT	TGTCCTGCGG	AGGCGCGGCC	GGCTGAGCCC	120
	CGCTGCGCAG	GCGCGCAGCC	CGTGAGACGG	TAGCGGcCCG	CCTAATGCCT	CCTACGCAGC	180
	GACCGCGCAG	CGGACCTGCA	CGTTAGTAAA	AAATCATTTT	TATCACCAC	CAAGATGCAG	240
	TCTgATTGAA	GTGTAAAGCT	GCAGTAGAAG	AGACAAGTAA	GCCATCATGA	AGGTATtTTA	300
20	TAGGTGCTAA	GTTCCCGATA	CAAAGCACAG	GTGGGCATTc	TAGGGCTGCA	GAGACAGGGC	360
	ATGGGCGTTT	TACGGATAGc	CCgGAGaCTC	CCcATTGGGC	GGGCTTAGCG	GGAGGGTTAG	420
	CGCGGNGTTT	GGAAACGAAT	AATGGGNTGC	CANGACGCGG	GCCACGGNGG	GACTGATGCT	480
	TGTTTTTGT	TGGGAATNAA	TCTTNATACT	AACAATCCCN	GTNGGNNGGA	CAATTCTTAC	540
	CCNGTTAAT	NGGTACGCAA	AAGACCATGN	AGGTGCGNTG	ANGACAACCN	NNTCCCNNT	600
	TTCTTNCGAN	A					

1065RP

	GATCTGTAGT	TTCCGAGTCC	CTGATGCGGT	CCGCCAGAGC	AGGCAGCGCG	GGCCAGGGTC	60
	TGCGCAAGGC	AGGCGTTGTG	TCACCGCGGA	GCCACTCTCT	GGGCAGGCAG	TTCCACGCCT	120
30	CCTGAACGAG	CGCGGGCATG	ATGGGGCCCA	GAATGCTGCG	ATAGGCATCC	AGAATGTGGA	180
	ACAGGGTCGT	CTTTATGGCC	AGACGCCTCT	TATTATGTGG	GGGTTCCTATG	TAAAGCGTGT	240
	CCTTCGAAGC	ATCAAAGTAG	AGGGACAGGT	CGTTGCTCAT	GTGGTACAGA	ACAAAGACTG	300
	ATGACATTGG	AGTAGGTCGT	GGATTCCGCA	CAGACCCTGA	CACTTGGGGG	GCAAAATTCT	360
	TTGTCTTGTC	GAGGNTTTT	CCNCTCANTC	CCNGGCAGG	TGGGGGCAGN	CTTCCCCNGG	420
	GCAAAAAGG	CTNTTCCCCA	CCNAGATNAA	CCCCTGGAAG	ANCCCGAAGG	TGNCANNAAT	480
35	TNAGNGGAAG	TNNCCTNACC	NCTCCACCNA	ATCGGAAAAA	TTGGGGANNA	ANGCCCCANC	540
	CCAACNCCCA	AANTTTTCTT	GGAAAAAAA	AGGGNGCCCC	CACCCNGGNG	GANTNANTTT	600
	TNTCCCCCCC	NATCC					

1065UP

40	GATCTCTTCC	CTTCGATCAT	CCCTCAGTTG	GGTTCTGAGT	CCATCGATGC	GTGACGCAG	60
	TTGGCCACAC	AGTTGCAGAA	CGCACAGGCT	GCAGCTCCAG	CAACCGAGGG	CCATGAGGCA	120
	GGCGAGAAGA	AGGACAACGA	CATCCCAGAG	TTGATTGAGG	GCCAGTCTTT	CGACGCGGAT	180
	GTTGAATAAG	TGCGCTGTGC	GAGGACTGTG	TTCTCGCCGC	CCATCTCAGA	ATTTGTCTAT	240
45	TTCTGCAGGG	AATATACATA	TATTGAGTGC	ACATATGGAT	ATTATGTATA	TATATGTACA	300
	TACACTATAC	CCGCCCCGTC	TTAGTCGGAC	CACATAAACC	TACGGGTCCG	CGCCCCATA	360
	TCGTTTTACA	ATAAACGCGC	CGNNCTTGCG	GGNNFNTCTC	GANAACTCTN	TTGGGGGGCC	420
	CNCCNNCCNT	TANNAGGTNC	TTCTNCCGGG	TNGGAAGTNA	AAAAGCNNNN	GTTCTNGTTGN	480
	NAGNGTCCCC	GGGGGAAANC	CNNCCCCGNG	GNNGATTTTC	NCCCAAACCG	NAGAAACNN	540
50	CNTTGCNCCA	AGTTGCCCGT	GGGAGAAAAA	AANCCNATGN	NGAAGNAAAA	TTGCCCCCTG	600
	CCCN						

1069RP

	GATCGACCCC	GGTCCCGCTC	GCATCAGCGA	GCTGCCCGTG	CCGATCAGCA	GCCCCGTCCC	60
	TAGCGACCCG	CCGATGGCTA	TCATCGACAC	ATGACGTGCC	TGCAGGTCCT	TCTTGAGCCG	120
5	GATGCCCTCG	TGCTTGCCAT	CGTAGTTCCA	GTCTACGGAC	TGCGCCTCCT	GGTCTGTGCT	180
	GCTGTGGGTA	TGCCGCAGAC	CGCGGCCCTC	ACCAGCGGCG	GCCAGCTTGG	GGCCTTTCAA	240
	CTCGTCCAGC	GTGGACGCCT	CTGATGCCCTG	TGCGAACTTC	TCTTCCGCCA	TAAGTGCGGA	300
	GCTGTTATCT	ATGCTACTCA	AGCTCCCGCC	GTATAGCCTT	GCTATATATA	CTTACGCTGC	360
	GACGCCCTAT	TCCGGACACA	GCTATATATT	GGCCCGCCGT	CTCGCGCGCT	GCTTGGGGAG	420
	CCGACTGACC	CCACCCTGAT	AGTGCCGTTG	CACCTCTGCT	GGGCCGCGCTC	AGCCCCGTTCA	480
10	GCGTCCGACT	GTGACATCGG	GCTGCGCGAG	CGCGATTAA	CACCCGACTG	GGCTGCATGC	540
	CGCACTAAAC	CTCCCCTCGC	GGCGCAGGGC	GCCCTTATCG	CCTCCGTGAT	GACGTACGTA	600
	TGTTTATCAA	AGATCCGGAG	AMCTGTTCCA	GGCTCCTACG	TTGCGATAAG	AGGC	

1069UP

15	GATCTTTCTG	CCCTTATCAG	GGATGGCACC	ACCGGTCTTC	ACCTCGTTTG	ACTTGTAGCC	60
	ACAGTGCTCG	CAGACCGTGG	ACATGATGAT	GACCTCTTTG	AAGTGTGGGA	TGTTGACCGG	120
	CTTCATATGC	GTGTACATG	GGTGAACACA	TGATGGGCAC	GTGGCAGTGA	AGGTCTGCAC	180
	CTCGTTGTGG	AAGTTCTCGA	TATCCGTAGC	GTCAGATAAG	AGACCGGCCT	GTGCCGCTTG	240
	CGATTTGTTG	CGCTCGCGCT	GCGACAGCTC	CGCGCGCTTC	TCTTGACGCC	GTGTCTCCAA	300
20	TTGGTCGCGC	GTAATGATGC	CCACCTGGAC	GTTTTGCTCA	TCTGAACGCA	GGTACTCGGT	360
	TTTGGAACAT	TTTGGCGCAG	CTTCGCCTGG	CTTGTTATTCG	ATCCAGGAAT	TGCCAGCAGG	420
	GTCGTCCAGC	GTAAGTCA	GCGGTAGAGT	GCCCCGCTCG	CACGACAGCG	CAGCGCGGAC	480
	CTTGGCAATG	AACTGCGCAA	TCTGATCGTA	CAGGTTCTCG	TCCACTTCCT	TCCGCGCCGC	540
	CTGGTCGGCG	TCCAAGTCCT	CGATCATCTC	GGTCAGCAGG	CCCTCCACAG	TCGTACGCTG	600
	GCCGCGCTTG	GGAAGAATCT	CCAGGTCCAA	TTCAACGAAG	CGGGAAGCCG	CAGTTTCGGC	660
25	CTTGATGACT	GCCTGTCAAA	ATCGGCCTTC	TCCTCAACCT	TCAGCTGA		

1071RP

30	GATCTGNNGG	GGAAACNCAG	CATTACCCGT	TGTGCAAAAA	GATTTGACTG	GTAACATCAC	60
	CAAGCTTCGC	AACAGACAAT	TGTGCGACCC	CGGTGAGTCT	GCAACCCTGC	AGGAGCTTGT	120
	GATTGCAGAG	CGTGCAACAG	GCAGCAAGAC	TGCTTCGGAA	GGGCTGCTGT	GGCTCACCAG	180
	AGGCCTGCAA	TTCACCGCGC	AAGCTCTTAG	AGAAACGCTA	GACCACTCCAG	AGCTCGAATT	240
	GTCTaAGACA	TtCACAGATG	CGTaTtGGAA	GACGTTGACG	AAGCACCATG	GTA TGCTTGT	300
	aCGTCCGGTT	TTCAAAGCTG	GCCATGAAAG	CTTGCCCTTA	CAGGAaGGAC	TTTTtTGcAG	360
	AAACTAGGCA	GcGACCAAGA	GAAGGTTGAC	ACGCAACTTT	AAGCAGtGGc	TGGcTGCACT	420
35	TGAAAAGATC	GtaGaGATTc	TgcTTCAaAT	CCCTtGGGGG	AAAcGtGcAA	AGGATTTaTG	480
	AgTaTTaTTa	TAGAAGCC					

1071UP

40	GATCGACAGC	CTCGAAGAAG	TAGCCTCCAC	AGCTTCAAAC	ACAGCGCACA	GGTCTGCATA	60
	CATCACGCTG	GTGCTTGCTG	CAGGCTTAAC	CGGAGAACTT	TGTGCGCGTG	GCACGGCGCT	120
	GGCAGaCTGT	GGCAGCACCC	CCCCCGGCGC	GGGCTTATCT	gCAAGCTCGG	GGAGGATGTT	180
	CTTCACCTCG	GCGTCCTGTT	CATGGgCTGC	CGGTGCGGCT	AGGCACTCGG	gAGACTCTAC	240
	CTTCGATTTC	TTGACCcTG	CTGTTGaCGt	CGcTCCATCT	TGAGGcCTCT	TCAGCGCAGc	300
45	GAAGAATCGG	ACCAATGTGG	CCTGCTTCTT	TGGaGtLAGAC	ATTGGcCTGA	AGTaAaACCC	360
	TACTGACCTG	CCAAATAGcT	cCACTTTGGT	CTCGCGACAG	GAGCTTCCNA	AGANTGACAT	420
	TNNNTGTNGN	NAAGGCCNNN	NNNTNNCAAA	GACGAANCIN	NTATCAAGGN	CCNNNTNCC	480
	CCAGNCNNNA	NAAGNAANAA	NNNNATNNNN	GGNATNNNNN	AAATTANGGT	TNNNNNATNN	540
	NCTTNGNAAA	TTNNNTNNGNN	TTNNNTNATTC	CCNNNGGNTT	TCNNNTNCC	NCNCNCCNTNN	600
50	GGNTTTTTTN	NANNNTNAAN	NNNCC				

1073RP

	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTTAATAATA	AATCTATTAA	TTATATAAAA	60
	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
5	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCATTTCAT	TTAATACTCC	TCTAATTCAA	180
	TCTTAAAAATA	TTCTTTAATTA	TTAAATTATA	TAATAAAAAGT	TAGTGGATAT	AGTTTAATTG	240
	GTAAACATA	TGTTTTAGGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATTAT	300
	ATCATTAAATA	TAATAACTCT	TTAATTAGAG	TGGTACCACA	AGAATGCTGA	AAGCATTAGG	360
	GGTGTGTACC	TTAGCTCTCT	AATTAAAGTT	ATAAAATTAT	CTTAACTAAT	AAAAATAATT	420
	AATTAAATAA	ATAAATAATT	AATTAAATTT	AAAATGTTTA	AAAAAAGAAA	TAAATAATAT	480
10	GTTATATTTA	AATAGATCAA	AATTTCAACA	ATTTCATT	CATTTAGTAC	TACCATCACC	540
	ATTGACCAATT	GTTACATCAT	TTAGTTTATT	AGGTTTACTA	TTAACTTTAG	CTTTTACTAT	600
	ACATGGTATT	ATTGGTAATA	TTTATCCCT	ATTATTATCT	T		

1073UP

	GATCTTAATT	TAAAATTTTA	ATTAACCTATT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAATAAAAT	TAGTAAAAATA	120
	AATAGAAAAC	CATAAGTTAA	TTGATTTCATA	AAGAAAAATG	GAATTATTTG	TGGCATCTTA	180
	ATTTTTATTA	TTTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATAAA	240
	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAATTTAA	TTTTAATATT	300
20	AAATATACCA	TTTTTATTAA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
	ATTTAATTTA	TATAAATFAT	TTAATTTACT	TCATTGATAT	ATATAATTAT	TAAATGTACC	420
	TTTCATAATA	TTTATTTTAA	TTAGTCTAGT	AATATTTCTA	TTTAATAGTC	TACCCCTTAA	480
	TTGGATATTA	CTACCTACTA	AATATTTACC	TAATAATATA	TTATTAAGAA	TACTTAAATC	540
	TAATAATTTA	TTATCTAAAG	TATATAAATT	AATTAAATCN	TTTTTTATTA	TTATTTAAAT	600
25	TATTATTAAT	TAGTAAATTA	TATTTATTTA	TTTTATTAAC	ATAATTTTTT	GNATAATAAT	660
	AT						

1074RP

	GATCTAAATA	TATATAATTT	AATTTATAAA	GATTAATATA	AACTTTTTTA	TTATAATATT	60
30	TAAGTATTAA	ATTATTTTAA	CTATTATTAT	CATTATTTAA	TAAATTAATT	ATTTGATTAT	120
	TAATACTTAT	TATATAATTA	TTATATAATT	TACTTAATTC	ATCATTATTA	ATATTTATAT	180
	AATTATAAAA	ATAATATTTA	ATATGAATAC	TATTTAGTCT	ATGTTCAAAT	TTTAAATTAG	240
	TTATTAAAAAT	ATTATTAGAT	ATTATTATTT	TCTTTAATAA	ATTATTAAAT	AGATTATCAA	300
	TAATTAATAT	ATTATTTTAT	AATTGTTTAT	TAAAATAATA	TATTTTATTA	TTATAAAGAT	360
	TTAATTTATT	TAAATATTGT	AAATTATTAT	TTTTATTATA	ATATCTATTT	TTATAAATAT	420
35	TATGTTGATT	TATATTATTT	AACTTTTTTAT	AAGAATTATT	ATTAAAATTA	ATTTTAACTT	480
	TAATTTCTTA	TTATTAAATTT	TTATATTATT	TAATAAATTA	TATTCATTTT	ATTTATTTAT	540
	TTATTTAATT	AAATTAATTA	TTTAATTAAT	ATTTTATCAT	TATTTAATTA	ATTAATAAAA	600
	TATTATAAAG	AATGT					

1074UP

	GATCTTGATA	CTAGAGCTTA	TTTTACTTCA	GCTACTATAA	TTATTCTTAT	TCCTACTAGT	60
	ATTAAAGTAT	TTAGTTGATT	ACTAACTATT	TATGGTGGTT	CATTAAGATT	ACTAACACCA	120
	ATATTATATC	TATTATCATT	TTTATTTTTA	TTTACTGTAG	GTGGTTTAAAC	TGGTGTAGTA	180
45	TTAGCTAATC	TATCATTAGA	TGTAGCATTC	CATGATACCT	ATTATGTAGT	ACTACATTTT	240
	CATTATGTAT	TAAGTTTAGG	TGCTGTATTC	TCTATGTTTG	CTGGTTATTA	TTATTGAAGT	300
	CCTCTTGTTT	TAGGTTTAAA	TTATAATGAA	AAATTATCAC	AAATTCAATT	CTGATTAAAT	360
	TTCTTAGGTC	TTAATATTAT	TTTCTTCCCT	ATGCATTTCT	TAGGTATTAA	TGGTATACCA	420
	AGAAGAATTC	CTGATTATCC	TGATCTATTC	CTAGGTTGAA	ATTTAGTATC	TTCAATTTGGT	480
	TCTATAATAA	CTATTATATC	ATTAATGTTA	TTCTTTTATA	TTATTTATGA	TCAATTAATA	540
50	AATGGTTTAA	CTAATAAAGT	TAATAATAAA	TCTATTAATT	ATATAAAACT	ACCTGATTTT	600
	ATTGAATCAA	ATAATATTTT	CTTAATGAAT	ACTACTAAAT	CATCATCTAT	TGAGTTTATA	660
	TTA						

1075RP

	GATCTATCTA	ATTACAGTAA	AGCTGCAAAG	GGTCTTTTCG	TCTTCTACA	AATACTTAGC	60
	ATCTTCACTA	AGATTTCAAT	TTCACCTAGA	TTAAAGGAGA	GACAGTTGTT	GTATCATTAC	120
5	GTCATTTCATG	CAGGACCATA	ATTAGTGGAC	AATGAATTTT	GCTACATTAT	AACCCTCATA	180
	ATAAGGCTGC	TATTTAATAA	AATTTATTAT	TATTATCTTT	ATTAAAAATAT	TAATTTTAT	240
	ATTTTATCAT	GGAGCAGAGT	TCACACTTTA	TACTTTAACT	TACGTTTCTG	CAAAGTGTG	300
	TGTTTTTAGT	AAACAGTTGT	ACAACTTTGT	TCTTATTATT	AATTATTATT	TTAATTAATA	360
	TCTCTTTATT	GACTAACGTC	AGAGCTATTT	TTGCCGAGTT	CCTTTCCTTT	AATTATCTAA	420
	TTACACCTTCA	TATACTCTAC	TAACATACCT	GAGTCGGTCT	ACATTACGGT	ATTTTATACA	480
10	TAAATATTTT	TTGAACCTAA	TAAATTTATA	AAGACATTAT	TTAAGTTAAT	TTATATATTA	540
	GATTATTTCT	ATCATATTAT	ATTTTTTAAT	ATATTACTTA	AGAACCGCTT	TTATTGTTAA	600
	ACCTTATGCT	TTAGGTGATA	AGGATTATAC	CTTATTTTC			

1075UP

	GATCCAGTTA	CTTAGTAGAA	TGATAAAATT	AATAAATATT	ATTTATTAAAT	ATTTGGTTAA	60
	CAATAAAAT	CAATAATTTA	TTTAAATAAT	GATTAAATAA	TCTCAATATA	AAATTATTAA	120
	TATAATGAGA	TATATATTTT	TAAAAAGAAT	ATATAATTAA	ATAATCCCAA	CCAAAATTTG	180
	TGCCAGCAGC	TGCGGTAAGA	CAANGGGGGT	TAGCGTTAAT	CGTAATGGCT	TANAGGGTTC	240
20	GTAGAAATGAT	TATTTAAAT	AATAATTAGA	ATTAATAAAA	ATAATTTAAG	AATTATTCAA	300
	GTAAAGATGA	AATAATAATT	ATATGAATAA	GACTTATAAA	GTGAAAATTT	AAATTATATA	360
	TTAATTGACA	TTGAGGAACG	AAGGCTAAAG	TAGCAAATCG	GATTTCGATAC	CCGAGTAGTT	420
	TTAGCAGTAA	ACAATGAATA	CCTATTTATT	TTTTATTAAAT	TAAAGAATAA	ATTAAATGAA	480
	AATTAAAGTA	TTCCGCCCTGA	TGACTACGTT	AGCAATAATA	AAAATCAAAA	CAATAGACGG	540
	TTACAGACTT	AAGCAGTGGA	ACATGTTATT	TAATTCCGAT	AATCCTCCGA	TAAATCTTAC	600
25	CATTTTTTGA	ATATTTAATT	ATAATAATTT	ATAATTAATT	ACAGGCGTTA	CATAGTTGTC	660
	TTC						

1076RP

30	GATCTTAAAA	TAAGATAGAA	TGGAATAAAA	TATCATTCAG	GTACAATAGA	TGCTGGTGTT	60
	ACTAAAGGAT	TACCTGGAAT	ATAATTATCA	GGATGTCCTA	AAGTATTAGG	TGAAAAGAAT	120
	ACAAATAATG	AAAAGAAAAT	TATAAATACA	AATACTGTTA	CTAAATCTTT	AAAAATAAAA	180
	TAACCATGCA	TTGGTAATCT	ATCTAAATTA	CCTGTAATAC	CTAATGGATT	TGATGAACCA	240
	TGTACATGTA	ATAGCATTAA	ATGCATAATT	ACTATTGCTG	CAATAATAAA	TGGTACTAAA	300
	TAATGAAATA	GAAAGAATCT	TATAATAGTA	GGATTACTAA	CACATAATGA	TCCTCATAAT	360
35	CATAGTACAA	TATCATTTCC	AATAAATGGA	ATAGCACTAA	ATAAATTAGT	AATAACAGTA	420
	GCACCTCAAT	GTGACATTTG	TCCATATACT	AAACAATAAC	CTAAGAAAGC	TGCTGCTATA	480
	GTTAAAATAA	AGATAATAAC	ACCAACTGTT	CATACAATAA	CTCTAGGTGA	TTTATAAGAA	540
	CCATAATATA	AACCTTTACC	AATATGAATA	TACATACCAA	TAAAGAAGAA	TGAAGCACCA	600
	TTAAGATGCA	TATATCTAAT	TAATCAACCT	AGTTGTTTCAT	CTCTCATAAT		

1076UP

	GATCTAGAAT	TATTAAGTCA	ACTATTAACT	AATATCTATA	ATAATAATGG	TTTATCATTA	60
	AAATCATTA	AGATAATTAT	TAATAAATTA	CCATTTAATA	ATGATATATT	ATTATCAAAA	120
45	AATTATGTTA	ATAAAATAAA	TAAATATAAT	TTACTAATTA	ATAATAATTT	AAATAATAAT	180
	AAAAAGATT	TAATTAATTT	ATATACTTTA	GATAATAAAT	TATTAGATTT	AAGTATTCTT	240
	AATAATATAT	TATTAGGTAA	ATATTTAGTA	GGTAGTAATA	TCCAATTARR	GGGTAGACTA	300
	TTAAATAGAA	ATATTACTAG	ACTAATAAAA	ATAAATATTA	TGAAAGGTAC	ATTTAATAAT	360
	TATATATATC	AATGAAGTAA	ATTAAATAAT	TTATATAAAT	TAAATTTATAT	ATCACTTAAT	420
	ATTAATAAAC	TTAATAATCT	ATTTATTAAAT	AAAAATGGTA	TATTTAATAT	TAAAATTTAA	480
	TTAAATATA	TTTAAATAAT	ATCTATAAAG	TAATTTCTTA	TTTATTTTAT	AACATTTTAA	540
50	AATGTTTTAT	GTAAATAGAA	TAATAATCAA	TTAAATAATA	AAAATTAAGA	TGCCACAAAT	600
	AATCCATTTT	CCTTTATGAA	TCAATTAACCT	TATGGTTTNC	TATTTATTTT	ACTAATTTTA	660
	TCT						

1077RP

	GATCCAGTTA	CTTAGTAGAA	TGATAAAATT	AATAAATATT	ATTTATTAAT	ATTTGGTTAA	60
	CAATAAAATT	CAATAATTTA	TTTAAATAAT	GATTAAATAA	TCTCAATATA	AAATTATTAA	120
5	TATAATGAGA	TATATATTTT	TAAAAAGAAT	ATATAATTAA	ATAATCCCAA	CCAAAATTTG	180
	TGCCAGCAGC	TGCGGTAAGA	CAAAGGGGGT	TAGCGTTAAT	CGTAATGGCT	TAAAGGGTTC	240
	GTAGAATGAT	TATTTAAAAAT	AATAATTAGA	ATTAATAAAA	ATAATTTAAG	AATTATTCAA	300
	GTAAAGATGA	AATAATAATT	ATATGAATAA	GACTTATAAA	GTGAAAATTT	AAATTATATA	360
	TTAATTGACA	TTGAGGAACG	AAGGCTAAAG	TAGCAAATCG	GATTCGATAC	CCGAGTAGTT	420
	TTAGCAGTAA	ACAATGAATA	CCTATTTATT	TTTTATTAAAT	TAAAGAATAA	ATTAAATGAA	480
10	AATTAAAGTA	TTCCGCCTGA	TGACTACGTT	AGCAATAATA	AAAATCAAAA	CAATAGACGG	540
	TTACAGACTT	AAGCAGTGGG	ACATGTTATT	TAATTCGATA	ATCCTCGATA	AATCTTACCA	600
	TTTTTTGAAT	ATTTAATTAT	AATAATTTAT	AATTAATTAC	AG		

1077UP

	GATCCGTGTA	TTTTTTATTT	ACATTATTTA	ATTAAAAATA	ATGATTTAAA	TAAATATTTT	60
	TTATAAAAAA	TAATTAGTGC	ATTGTTACAT	GTTCAATAAA	GAATGATTAT	TATCAAAAACC	120
	ATCAACTAAT	TGTTATATAT	TTATTAAATA	TTAATTTTAC	TTAATTAAGA	ATTAGGAACT	180
	TTATCTATTA	GTCTGGGCTG	TTTCCCTTTT	GATTATTAAC	CTTATCGCTA	ATAATCTGAA	240
20	ATATTTAATT	TTAGATTAAT	AATATATTCT	GAGATTTAAT	ATTTTTAATA	AAATAAATAA	300
	TTATPCCCTA	AATAATATTA	ATAACTATAC	CATATATATC	TAATATTTAA	ATAATCATAC	360
	TAACATATGT	TTCTAGAAAA	ACCAGCTATT	TGCAAAATCAG	ATTTGACTTT	CTCTACTTAC	420
	CATTATTCAAT	CAGATAATAT	TGCTACATTA	ACCTGTTCAA	TCGTTTATTT	ATTTTATTAT	480
	ATTTTAAATA	TAATAAATAT	ATATTTTAAT	CATTTGATAA	TAGTAAGATC	ATCTGCTTTC	540
	GGGTTAATTA	ATATTAACTA	AATTTAATTT	ATTTTAATTA	ATTTTAACAT	TGTTAAATAT	600
25	TTATATTATT	TTTAATATCA	TTTTTTATTT	TAATATTATG	CTAATATTAA	TTACTTGC	

1078RP

	GATCAGGATG	GCGATGAGAT	ACTACCTTGA	AGCAGCAGCC	TTGACCTCAG	CTAACTCCGC	60
30	AAATTCCCTT	CATTTTTCGA	AAGCAGATTA	TAATTGCTTC	TAAGCCATTC	AATTGCTTTA	120
	CTTTTCCGTT	AATCAATGCT	CTATTTTACC	ATCATTCGAA	GTAAGAGTAT	GTCGATATGT	180
	CTGACCTAAG	CTACAGATTA	TCTAATCACA	TAGTTATGTA	CGAACCAATA	AGATTATCGA	240
	ATTTCTGTTG	AAAACCTCAGG	CGAACGGCAC	AGCGTTGCTT	GCGCCTATTA	GATGCTTTTG	300
	CCATAGCATA	TCACGAAGTG	ACCTCACAGT	TTTTAAGTAA	CCGGAATAGT	CTGTAGATAT	360
	GGTATTGTGA	AAAGTTTATT	NGCTGGTTTT	ACCCCTGGG	AATCTNGGNG	CTGGNCTGGG	420
35	TTCTTAGGTG	GGGAATCCGG	NCCCCCNNT	C			

1078UP

	GATCTCCTTC	CTTCTGGTG	TCTTGCCAAG	CCCTTATTTG	TTGACCAAAG	TATTCTTCAC	60
40	CGTTGCCCTG	TACTCTGTTC	TCATAAATTT	CCGCGGTAGG	ACACCTCTGG	GCTTTCTCTT	120
	GGCGATCTAT	GAGGGCTTTG	CAATCATCTT	CACCGCCGCT	AAAGTTTTC	CACCATTTTT	180
	GTATGAGCAG	CTACTTCAGT	AAGCCCCCGT	ATTAGGATTG	TTAAAAGAAG	TAGGATCGAT	240
	ACCCTTCAAT	TCCAGATGAT	CGTTGCGGTG	GGCTATTAAT	TTGTTAGCCA	CCTAATACTG	300
	AAATTTACAT	ATTATTGCAC	TAGTTAATTA	ATATTTATGA	TGCAATGGGA	ATCTATATCG	360
	GTTCTCCGTT	CCATCTTCTC	GTAATTAGAT	CACGTCGGAT	ATNGTNGCCC	CGTACCGAGG	420
45	AGGGACCCGA	TTGGGNTTAT	CTTTATGGTC	CCGAGAANTN	ATAGAGNGCC	NNAANATAGA	480

PAG1078i1

1 GATCTAGTTC GTTAACTTCC GCAAAACACC TGTCAAGCGC TTCAACAAAC

5 51 GTCTGGATCA GATCCAAGAT GGCCAGTTCT GACTCCTGGT CGTCGACAAT

101 GAAAGTAAAA TAGAGTGTTG CATAGTTCTT GTAGATTATT TGGATATCTT

10 151 CGTTAATGGT TCACTACCA CTCGATAGTA GCGAGGGCGG CGTAATTAAG

201 AATGAAGACT GAATTGAACT GTTGCGCTGG CTGATCAGCT CGTAAACCTG

15 251 CTCCAGTAGT AGCTTCTGCT TCGGGAGATC GACAGGAGTA TAGTACTTTA

301 CAAGCCTAGG TTGGCACTTC TTGTAACTT CATGTGTTAG TAGGATAATT

20 351 TAAGTACTGC GGCTGCGCGG TGGCAAAGGG GTTCACCCAT ATCAGGACGG

401 CGNCGNNTCA TCCNCGTCC CCACCACGGN TACNCGCCNC NCGCA

Pag1078i2.

25 1 GATCTAATAT TCAATTGGCA AACTCTTGAG AGTGTCTTGG AGGAAATTAT

51 TCAAGGGGGT ATGGTAATTG AAACGAACGT GAAGAAAATT GTGGAGACCG

30 101 TCGACGAGCT CAATAGAACT TCTAACCAGG AAGCCAGGTT TGGGAATGGA

151 CTAGGAAACG CTTTTCAGGC CATCACCATG GGTGGCTTTT CAAATTGGGG

35 201 TGC GCGGCAG TGAATATTAG CACACACTGT CTTGAAACCC CATAATAAAT

251 GAAATAAATA CTCCTTGCTA GTGTCTAAGT ACGAAACAAC GCCAAGGCTT

40 301 TTGGATCATC TATGTACGCA TTCAGTTCGG CAGCACTCAC CATGGGCACC

351 AACTCTTCTT ACTTGCTATT TCCTGTGTCT TCATTGCGC TTCGGCTGCC

45 401 TGATGGTCTC AAAGCTCCTC CCTAATCCTC TGTAATTCTC CTG

50

55

1079/RP

1	GATCGCTCAT	TATTTTTGGT	CGGAGCCTGG	GCCCTCTTCT	GCTTCTTCTC
51	AAATACCTTC	AAATTTTCGT	CTATATAGGT	CTGCAGCTCT	TCCTTCTTCG
101	AACATTCCGC	CTTGTGAAGC	TGGTTGAAAT	ACTGCAGGGC	CTCTGCACTC
151	ATGCGATTCA	CCATTGAATT	GCGCTCTTGT	ATCTCTTGCT	GGAAGTGTTC
201	TTGTTTGCQA	ATGGCGTTTT	GCCGCAGTTG	AGCTTGCAAA	CTGGTTGTAT
251	CAGACTCGTC	CACTTCATCT	TCCACGTCCA	GTGGATCCAT	CCCTGCAGCT
301	AGTCTAGGTG	GAGTGGTCTA	TGTACAGTGC	TGCTGTGCGT	GTTAGCGCGC
351	TCACCTTCTG	CGACTGTTCA	AAGATGTGCG	TTTCCAGCAA	GAAAAGAGAC
401	AACCGGAAGT	ATAAGTACAG	CACGCGAGCC	TAATTTTGTC	AGCTTGCGGA
451	TTTAGCTCAG	TTGGGAGAGC	GCCAGACTGA	AGAGAAACTT	CGGTCAATCG
501	TAATCTGGAA	GTCTGTGTT	CGATCCACAG	AATTCGCATA	TTTTTTGCTC
551	ACGTACCCCA	CCGGGTANGA	ACTGGCATTG	CCTACCTAAT	GGCCAGCAGT
601	GGAAAGCGCT	CTTGTGATAT	ATATATATCA	AGTAACACAT	CTATGTAAAC
651	TTTGTACACA	GTCCCAAGGT	GAATCTTGCC	TCGGATCTGC	CTCATCTGAR
701	TCC				

1079/UP

1	GATCAGCGAG	CTAGGTACCC	GGACGAACAT	GCCGTTGCGC	AGCTTCCCAT
51	ACTTCAGCGA	CCGTGTGTGT	AGCGCAGAGC	TTCCGTCCCTG	GAATAGCGAC
101	TGCACCTCTG	CGTTCAGCAG	ATCGCCCTCT	TTCAGAAAGC	TGCGCATCTG
151	CAGCTCATCG	CTCTCAGACT	TCCGCCGCAG	CACGCCGCCG	GGCAGGTTCA
201	CAGAACCCAG	CATGAGCACT	GCGTGTGCT	TTCCGCCAAT	ATCCACCTTC
251	CATCGTTTGT	TGCCGACCTC	CACGATCCTG	CCGACAATGT	GGTCGCCCGT
301	CTCTGGCGTG	TACCGCCCCG	GCCAAGGAAT	CACCGACAGG	AGTCGGTTCA
351	CCCTGGAAC	GGTGCCCGCC	ACCGACGAGT	ACGTTTTGTT	CTCCAGGAAG
401	TATGTGCCGT	GGCCTCGCAT	CCACACAGGA	TCATCTGTAA	TCAGCTCTCC
451	TGGCGTCATA	ATCACCGACG	AATCCGCTCC	TTCCATCTCC	ACGTCCAAAT
501	CAAACCTCTC	TTCTTCATCG	TCCAGGTACT	GGCTCCGATG	GAAGTGAAC
551	CCACGCCGCT	TGCGGATCGT	TATTACCTCG	CTCATTACTG	CTGAGACGAC
601	ACGTTTCARA	ACTTCAGAGG	CTCGCTAGGC	CAGGCGAAAC	AGTGTTGARG
651	ATACGCTTTG	TTACTTCTTG	AAG		

1080UP

	GATCCGGCCA	CGCATGTATT	CCACTATGTA	CGCTATATCG	CGGCCTCGCC	TCCGTGCGGG	60
5	GCACCGCCTT	ACACCTCAAA	GCCGCAGCCT	TTCATGCAGC	CCTTGTAATT	TTGCACCAGT	120
	TCCTGGCACT	TGACCGCATC	CACGCCGTTG	AACAGCAGAC	AGCTGTCTCT	CGCTTCCTTC	180
	TCGGGCTTGC	ACACACAGCA	TGGCTTTGGC	TTGTCCGTAC	TACTACCTTG	TGAAACACCT	240
	GGCACAGAAG	AGGATTCAGG	CATGATTAAT	GCTACAGTTC	TTGGAGATCT	TCCAACACCG	300
	CCCGCTCCTT	GGGGTTTTTC	TCACTTTATT	TTTGCTTCAA	CGCGCAAAA	TTGTTGTCTGA	360
	ATTACAATAT	ACAGAGGCGC	AGTAACCCCT	TTAGTGGCTT	TTTGGCTTCT	TGGGCTGGAA	420
10	ANTTNGACCC	CCCAACNTNC	C				

1081RP

	GATCTTTTCGC	AGTGACTAGT	GCATGCGGCT	ATTTAAAAAG	TATCGAGTTA	CCCTTGGAAG	60
15	TTTCAGCATT	TATAGTACTG	ACGGAGCCGC	TACAAAGCCA	AGGCTTTGAA	GGTACTAGGA	120
	GACATATTCA	GGCGCATAAA	TCACCGCAAG	CTGGATTGAG	CGATGTTTTG	GGTTGTGTTT	180
	ACAGGAGCCA	GCGCGGTGGC	ATGCGTTTTT	GCGTATGGGA	TGGTGGACCG	ATATCTCTCC	240
	TTCAAGCTGC	ACAGGCATAC	GCACCCGTTT	GTGTTGGTAA	CACTTTTTCGC	AAATATGACA	300
	CTGTTGCTCT	CGATCACATA	CCTGCTTCCA	CTCGATGTGT	TTTACTCAAA	CCAGACAAGC	360
	GGGCGGGAAG	ACGAGCGGCC	AGAGCTGCCG	AACCTCGCGT	TGTTCTGGGC	GGTGATCTAC	420
20	TGGGCGGAGT	TTGTGATATG	CTGGTTGGTG	TTCCCGGTGC	TGATTTCTGA	CGTGGATCTC	480
	AAGTACTTGT	ATCCGCGCGA	GCCACAGGAG	CCGGGGCGGC	GCAGCGTGCT	TCGGCGACTG	540
	CGANGCGCCG	TTATATGCAA	TCTCAAGTTC	TATGGTCTTT	GTCTACTGGG	GGTGATCTGC	600
	NGGCTGGTAT	ATCTCAAGAC	GACGACCGAT	CGCGGGCGTC	AGAC		

1081UP

	GATCCAAGAC	GAGCTGCGCC	AGGGGAGAAA	ACCCCCCAC	ATATGTCCAG	CGATACGCTC	60
	AGCATGGAAA	ACCCAACCGT	GGACTTGCGC	TCGTAGTTGT	GCTTGGCCTG	TGCGATATAC	120
30	TTCAGCACAG	ACATGATGAT	TTTTATAAAG	TACAGCACAT	GGCAGTAGAA	CAGTGTCCGAC	180
	TGATTGTTCA	ACCCTGTTTG	CGTAATGCTA	ACCACATATT	GCACTGTGCC	AATGCAAAAA	240
	AGCCCGATGA	ACAACATGAT	CATCTTCCGG	TGCGCTGTGC	TCATCCTATT	CGCCGGCTCT	300
	CCGGTGAAGC	CCCATAGTCT	GGTGCCCCAT	AGCACCTGCG	ACGCCAGCAG	TCCGTTAAGA	360
	AGCCAGCTAT	GCATGGCATA	CCAGTAGTCC	GACCAACCTA	CCGACGGCCT	CACCGCGCTG	420
	GACGTGTGCG	CTTCATTCTG	CCAGAGCACG	TCTGCACAAC	CAGCGAGAGT	ACTAGCGCTG	480
	TATACCCGAT	GCAATTAAAC	ACCACGTAGC	CTTTCCGACAA	TGCTCTTGCG	CTCTGCCGCT	540
35	TCCAGTTGAT	CCATAGTGGC	GGATACATCG	ACACCGACCA	ACATGTCCGG	TACAAGTATC	600
	CGAGCAACTG	TCTCTTCCTC	ATTCCAGCCT	CGTTCCAAGT	GCTTCTACGC	CGGTCTTCTG	660
	GCGTCAGAT						

1082RP

	GATCCACGAG	CAAACCTATTA	TTAGGCGCCC	CCCACCCAG	TCTGCAGCAT	TCGAAAGCCT	60
	TCCTAGCCTT	TGTGCGATGT	CCCAAGGTAC	AATTTTCTCG	CAGCTGAAAA	TACGAAAGAA	120
5	GCGCCAAGAA	GTGGCCTTCT	TTGAATCCAA	CGCCGACGCC	AATGATGTCG	AGGCGGGCGA	180
	ACATTTTATA	ACAGAGCTCG	ATAAGGGCGA	TAAGCGGCTC	GGCCTGTTTT	CTTCGATCGG	240
	CTTGATATGC	AATANAATGC	TCGGGACAGG	TATCTTTGTC	GTTCCCGCGA	ANATCTTCCA	300
	GTTGACTGGC	TCAGTATACT	TTGCGCTAGG	GTTATGGGTA	CTAGGAGCTT	TAATTGCTCT	360
	AGCAGGTCTT	TATGTTTACA	TGGAATTTGG	AACTGCAATA	CCGCGGAACG	GTGGCGAGAA	420
	GAACCTACCTT	GAGTTCATCT	TCAAGAAACC	GAAATTCTTC	ATTACGTCAA	TGTACTCAGC	480
10	ATATGTCATC	TTTTTAGGCT	GGGCCGCGAG	TAACCTCTGT	ATGGCAGCTG	CAATGTTCCCT	540
	TGATGCTGGA	AAGGTCGAAG	CAACACGTTG	GCGTTGAACG	CCGTCTTGGA	GTTGCGGTCA	600
	TTTTCTTCTG	CTTCCTTGTC	AACTCTCTCA	GTGTCAAAGC	TGGGTTGTTA	CTTC	

1082UP

	GATCCGACGC	TTCCGCAAGC	GCCGCTTCTC	CTCCGTGTAC	TCCTCGTCGT	CGTCGTAATC	60
	CGGCACCATC	GACGCCTCCG	GCTCCTCCTC	ATCCGCCGTC	GCGTCCCTCT	CCTCGTCCAC	120
	CGTCTCCGGC	AGCAGCGAGT	CGTCCCTTCG	CCCCGTCTCG	TCGTCTCGTC	GCTCCAGCAG	180
	TGCGCCCGGA	AGCGGCTGCT	CGTCCGGGAG	CGGCCCGAGG	TACGGGTACT	TCACCGGCCC	240
20	CATCTCCCGC	TCAATCCGCG	GGATCACCAC	CTCCCGCACG	TACCGGTCCA	TGATCTGCGC	300
	ATAGTGGTAG	ATTTCCGACT	CCTTCGTGTT	GTACATCCGC	GCGTCCACG	TGATCCGCAC	360
	CAAGTCGTTT	ACGAACTCCT	GGGCCGCTT	GTAGTGGTTG	AGCTTCTTTT	TCACCGTCGC	420
	GAGGCTGAGC	GGCTTCTTGA	TGATCCGGTA	GTAGTCGGGA	TAATCCTTCC	TCAGCGGCAA	480
	AGTGTAGAAA	ATCGGCAAAA	TCTCAATACC	ATTTTCCTCC	TTTAAGTCAA	ACACGCCATC	540
	CAACAAAAC	TTGAGCTGGT	CCCGTAGCAA	CATCGTTAGC	CCTCGCCACC	TGAAAAGCTG	600
25	AAGACTTTGG	TAGTGTACTA	TGTGTTCGGA	AACAACATCC	CACGCGTCGT	TTCTGCCCGT	660
	TCACAGCCTT	GCTTCAAGTT					

1083RP

30	GATCATCAAT	TTCTTTTTTG	CTGTTTTCTT	ATTTACAGCC	TCTATTTCTG	AGCGAACATG	60
	CGACGCCACA	GCAGTCCTAA	TGAGCTCATC	TGTTAGTTTC	GTTGCAACCG	CGTTACGCAG	120
	TTCATTCCCT	TCTATTGCTT	TGGAGCCAGA	ATCTCTAGCT	TCATCTTGAG	CGCTAGCTTC	180
	AGTTTGGGCT	CCCAGTTTTA	AAGCTGTTTT	GTTAAAATGA	AAAGTATTTT	CCTCTTTTAG	240
	CTGGGAATG	CCAGCAAATG	GTTTTCTGTG	CGATGACTCA	AACGGTACAT	CTTTTTTAGT	300
	TTTTGTTTTCC	TCTAAAATAT	GCGGTGAGGT	TGTAGAGCCG	ACACTAGACA	TAAATGGTGC	360
35	CGTAAACTGT	TTGCTGGACT	GCAGATCAGA	CTGTTGCTGT	GGCTTGAAC	GCATGCTAGA	420
	TTTCACTTCA	CTTCCAGCGC	GGGATTGGGT	AGTGGGTTTC	GTAGTCTTAT	AATCTCCACT	480
	ATCGAAGTTG	AAAGTTTTAG	ATATATCCTG	GTGTTCTCCG	TGCAAGGAAG	AcCCCTGCTC	540
	AATGATGCTT	TCCGAATATG	TGGGTAGATT	TGAATCATTC	CTCCCTAGNA	GCAGCATCAT	600
	CCTCCGAAAG	AGA					

1083UP

	GATCCTGAGC	GGTGCGGACG	AGGAGGAGCG	CGAGGAGGAG	CCGGAGGCGG	TTGTGGGGGA	60
	AACCGTGAGC	CGCAGCGCGA	CGGGCGGGAC	GAAGCGGCGC	TTTGCGGATG	AGGAGGCGGA	120
45	GAAGGCGGAA	GAGGCGGCGA	CGGCCGCCCTC	GGACGACGAG	GAGGCGCCCA	AGAAGGCGCG	180
	GAAGTAGCGT	AGATAGAAGG	ATATAACTGT	ACAGTACCAT	GCAAGACGAA	TCTGAGGCCG	240
	GCGGACGCGC	GCTGGCGCGG	CGCCGCGGTA	GCTGCGGAGG	GCAGAAAAAA	TCGCCGTCGA	300
	CAATCTCTGC	GTCATCATCC	CGGCCAGAGG	ACAAGATGGC	TGGCAAGAAG	ATTGCGGGTG	360
	TGCTAGGCGC	GACGGGCTCC	GTGGGGCAGC	GGTTTATCCT	GCTGTTGGCG	GACCACCCTG	420
	ACTTTGAGCT	GAAGGTGCTT	GGGGCATCGC	CGCGATCCGC	TGGCAAGCGG	TATGCGGACG	480
50	CGGTGAATTG	GAAGCAGACC	GAGCTGATGC	CGGCGTTTGC	CGAAGACATC	GTGGTGAGCG	540
	AGTGCAAGGC	TGAAGCATTG	TGCGGCTGCG	ACGTTGTGTT	CTCTGGGCTC	GATGCGGACT	600
	ACGCAGGCCC	CATCCAAGCG	GGAATTTGCC	GACGCCSGAC	TGGCTGTTGT	CTCGAA	

1201RP

	GATCTTTCGAG	ATGAACCCAA	TATGGAACAC	GGGCTTCGCC	AGCTCGATGT	GCCCGAAGTG	60
	GCCCGGGCAG	TCGTTTCATGC	CCTCGCCACA	CGTCTGACAC	TTGAAGTTCC	GGTCGATGGA	120
5	GCCCGAGCCGG	GGGTTCGTTCA	GCCCTCCCAC	CTTTGCGCGC	ATCTGCGTCT	CGTCCATCGT	180
	CTCTGGAAAC	TCAATCTTGG	CCACCGAAAT	CGCCCGCACC	TCCTCGGGCG	AGAACAGCCC	240
	AAACTGCACC	TCCTTGATGG	TCCGCAGAGG	CGCGCTCGAA	TACGGAAAGT	CCACCATCGC	300
	TGTGTCGTAC	TACCGCTCCC	GGAGATACAC	CCGTTTGCAA	GTTCGTGTGT	GCACCTGACG	360
	CCCAGCCGCC	ACTCGCAATC	CTCGTTTACG	CCGACCGCTT	TGTTTCGCTC	CCTTGCCGCA	420
	ACAACGAAGC	TCTGTTATAT	GTGCCCGCTC	GAGACCCTAA	GCCTGCTCCT	GTGGAACACA	480
10	CGCTCACGCC	CAGAAACTCG	TGTCTTTACC	TTGCAGCTCT	GGAATTGGTN	CGCGCCAAAC	540
	CNGCTTATTG	CTTGGGCGAA	CNCCTATGCT	CCGTGTNATC	TCAGCTGGAA	TNCACCANAA	600
	ACNGACCCCC	CACCTACCCC	NCAACTCTGG	TTATTGGATT	TTGCCGGGAA	TAAACNCANT	660
	GTTNCCAATC	CTTNCACCCC	CAACTGTTGT	NTCCNCTGTT	CNGTNCNCTN	TTACTCNTNA	720
	CCCTCCNACN	CCAATTTTTT	TTNCCCGTTG	CCCT			
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1201UP

	GATCCTCCGA	TTAGCCTCGT	CTTAAAACTC	AACCAAGCTG	CTCTGAAACA	AACAACACGT	60
	ACCACTTCTG	TGTTGTTTCT	CTGCGCTTGT	TGACCGTCCC	GCAACTACTA	TGTCGTTACG	120
20	TGTGTTTTTT	CGGGAAACTT	GCCACCGTCT	CAGAATCAGA	GGCTGTGAGA	TTCTTCTGTC	180
	GAATATCGCT	CTGGACGTTT	GCTTACGTGC	GCCCGGCCAG	TGCTCTTAAC	CGGCGCCGTA	240
	GCCCGCGGCC	CTGGCCGGTA	CCAACAAGCA	TGGCAGGAGA	CACAGAGTAC	TACAAGCAGG	300
	CGGTGGAGGA	GTACGCGGCG	CTCAAGCAGG	ACACGGACCC	GGAGGAGTGG	GACAGGCGGA	360
	TCGCGCAGAC	GGGCTGCTAA	GTCGAGAATA	TGGCGCTGCA	GCTGTGCCAC	GCGGAGACCG	420
	GGGACTGGCG	GGCGTGCGCG	GCGGACATGG	CGCGGTTCAA	GGCGTGCTGG	GCGGCGCAGG	480
25	CAACCGCGAG	CGCGTGACGC	ACCGTGAGCG	GTGAGCTGCG	GGCTGTAAAT	AGGTGTATCT	540
	GGAGGCGTGT	CACGTTGACA	CTGGACACGT	TACGAANCAT	TNTCNGGNTN	GGCCNCCGGA	600
	ATGGCCANCC	CCNATCTNAN	NACCCAAACN	GGGGTATGAT	NTN		
30							

1202RP

	GATCGAAAAC	GCTGCCACCG	AAAGCTTGAC	ACTGAAGGGA	TTTGAGTATT	CTCTTGCAAT	60
	TTCCAAGGCG	AATACCAGCT	TGTCCCAGGC	TGCCGATCCA	ACCTTCCCCT	CCTTCAGGGC	120
	CTGCTTGATC	CTGTGCTCTA	TCTGCAGCTG	AGGTAGCAGC	TCTGTGATCA	GCATGACGAC	180
	GGCCAGCGCA	GAGGTAAAAC	CTTTTCAGAA	GGCCTTTGAG	ATTGCATTGT	CGATGAAACC	240
35	GAGCCTGAAG	ATGCCCATGG	CGAACACCAG	GACCCCTGAT	ATGCATCCGA	TAACCCGAAC	300
	GGTCATCAAC	GGTTCAAGCG	ACTTGTGCGC	CCATGCATCG	CAGCTCTGGC	CCACCACAAG	360
	GGACGCAACC	GTCTGCGGCC	CTACAACCAT	CGTCGGGACG	CTGCCGAAGA	CTGCATATAT	420
	CAGTGGGGGG	ATCACCAGTG	CGTACAGCCC	TGCGTATGGT	GACACATGTG	CCATAGTGGT	480
	CAGCGAAATG	GCCAGCGGTA	TCTGGAATGA	CGTCAGCGTC	AGCCCAGCAA	GCATGTCTCT	540
	CGCATTTCCC	CAGAATACTC	TGGCAGCCAG	CGTATAATGG	GCCGTAGTAA	GACNCATAAA	600
40	ATTTNTTTCC	TNCCATACCGT	TGTCNNTTTA	TNGNCTGTAC	CCCNATACGAC	TTGTCANAAG	660
	CAGNTNCCCC	CCGCCCGGAG	ACTTCCANCC	CNTCCCTACT	CCCAATTTGG	ACCANGACCC	720
	GGTTCTCTGGT	GCTTN					
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1202UP

	GATCGCCGCC	GCGCCCCAGG	ACTACGTGCA	CTTTCTCTCG	CTCACACACG	TACTGGACGA	60
	CCCGCAGCAG	CCCGAAGCGG	ACTGCGTCGA	GCACAGCTAC	ACGCCCCGATC	CGCTGCAGCT	120
	CGCCGTCTAC	GCGCACGCCC	AATGAGAGCT	CATCGCTCCC	GCGCAGTGCG	ATTTTTTTTCG	180
	CGGCCGCCCG	CAGCGCTCCG	CCTGGCCGTC	ACCGAAGCCC	CAGCGATGAC	AGCCAGCGTC	240
50	CAGGATATCG	TGGTGGCCAC	CGCCGGCGAC	AGCGCCGGCG	GGCGCGACGG	GCGCCCCAAC	300
	CAGGCGGTCA	CCCTCCCCGT	CGCGCTCGAC	AGCGCGACCG	GCGAGGTGCT	CGTGCGCAAG	360
	GCCACCGGCA	AGACCCGCGT	GCGCAAGGGC	CAGACAGAAG	AGCAGTACTG	CGAGCAGCTG	420
	CAGCAGTACT	TCGAGCGTGA	CGGCGGTCCC	GAGTGCACGG	ACGAGGGCTG	GCTCGACCGC	480
	GCGGCGCCCC	CGGCCGCGCG	GCGCACCAAG	CAGGAGCGCC	AGCGCCTCGC	CCGCCGTCTA	540
	CCAACGCCTC	TACTTCTCTG	GCCGCCGTGC	CGAANCCGCC	GCNNTCGCCC	GCCACTGCTG	600
55	TATACGTTCC	CNGNTCNGGG	CNCCTNCCNA	TTNGCGCCCC	AANTNCTCNA	NCTCNNNNCT	660
	NNTNCTNNCN	GACCCNNNNN	CCCTTAATTT	TTNNTTNNNN	NNTTTNTCTT	TTCCCCCTCC	720

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NCTGTTACCC TCNCTNCNTC CNTGGTNNTT CCNTTTGGTG NGCTNTCTTC CNTNCTC

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1203RP

	GATCAAAACAG	CTGCAGTTGT	TGAAAAGGTT	GCTTGAATCC	AAACCAAGGA	AGGACGTATT	60
	TTCGTTTCTA	GGCCTGGATA	ACTAATCTCT	TCTCCACTCT	AGCTGGGGAT	AACACCTGCA	120
5	GGACGTGAAC	TAACAAGTTG	ACTACTATAC	AGCAAAATAA	CTCGAACAAG	TTATACAGAA	180
	TTTTGTAAAT	ATATTATAGC	AGCCCTATTA	CTATAATTCC	ATCATTGTGT	AACGCTTTAG	240
	CCTTCGTTCT	CAGACTCGTC	GTCATTTTCT	TCATGATAGT	TGATATTTTT	GCGTTGCCTT	300
	GAGCTTTTCC	TTACTGGGCC	TGCATTGAGG	CTCCTACTCT	TTGGCCTGTA	GTCACCTGCA	360
	GAGCTTGGTG	TATCTTCGTC	CTCGCTTCCC	TCATCGACAA	CTTTGCGCTT	CTTCTTAGTT	420
	TTAGATGAGG	CTGATGATGG	CCGTTGCGCT	TCTTGAATTC	TCTTCCTCTG	CCCTTGGCGA	480
10	TGTTGAATTG	GCGCGATTAG	AGAAGCGCGA	TACTTTGGCC	CTTATATTTA	CTGTCAGTGT	540
	TTCAACATGC	TGGTCTGATA	TATAGCTCAT	GAACGCGTTT	CTTTGCGCCT	CTTCCCATAT	600
	TGGGGAATGG	CTGATAAAGT	TCAGAAGGCA	GATTAGCTCC	CAGGTAGACT	GGTAGATTCC	660
	ACCCCGTTG	GTTTTAGCTC	AAANATNATC	AATTGGCAAC	CNGCTAGANA	TAATNTNTGA	720
	ACATATGCTC	CGTGTNGGAT	CCGNTGCGAT	CTCCCC			

1203UP

	GATCATTGGC	TCGCTGCTCG	GGGAGACCAT	CTCGGAATGC	GACACTGTGT	CGATGTCTGT	60
	GCTGCGGAAG	ATCTTCAACA	AGTTTCTGAC	ACACGATTTT	GGCCCCGCTG	GCTCCCTGCA	120
20	GGCCTCCGCG	CGCGACCCGG	CCTTTGATTT	TTCTCTGACG	ATCTGCCAGT	CGTACAGTAA	180
	CCGACTCGGG	CGGCAATTCA	CGAAGTTCTA	CTCCGAGATC	CTGTACGGGA	TTACGAACCC	240
	TGGCTCGGCC	GGCTCAGGCG	AGACCGCGGG	CCTGCAGTCG	ACACTTGACT	CGGAGTTCAA	300
	GACTCTTCTG	AAACTGCATA	AACTTACGGC	CAACATATGG	GAGCATGTGC	CGGAACCTGT	360
	GGGCTCCGTC	GTCCGATTTG	TGCATCAGGA	GTTATGCTCA	GACAATGTGC	CGCTGCGAAT	420
	TGGGGCTACG	CGACTTGTAG	GTGATTTGTT	AGCCGCACCC	TCCGCTGCCA	ACTTCGTCAC	480
25	GATGCATACG	GACACATATA	ATGCCTGGAT	GTCGAAGATA	GCGGACATAG	ACGCCACGGT	540
	GAGGCGCGAA	TGGGTGAAAG	CCATACCTAA	GATACTGGAT	AACAGTCTGA	TTTGGCAACA	600
	GATATCTGCA	AAGGCTCAAC	AAGACACTAA	TGGATACCGA	CGATGTGGTT	AGACTATGCA	660
	GCTTAGAAGC	GCCTGAAAGA	ACTACAGTCC	CCACGATTCT	GGGANATCTC	AAAATTCCAC	720
	TTNTTCCNAA	TTGTTGCGCC	TACCCAAANA	AAACNAANCT	TAGGAACTTT	TCATTTGTAC	780
	C						

1204RP

	GATCCGCTTG	GCTAGGTCCT	CAGCCGGCAT	GTCGTCACGG	TATAGGGCCT	CGGAGCCAAC	60
	TAGGAAGCCG	CGCACCCTGT	CCGACTTGAT	CCATGGCAAG	TAGGTCCTGA	GCGCATCCCT	120
35	CTCCATCGAA	AAGTGAGCGT	CGTCGTCTGG	CCAGACACCG	ACCCATAGCT	TGAAGCCAGC	180
	ACGGTCCGCA	GCAGGACCCA	AGAACTGCAA	CGTGTTCAG	TCAGAGGTAG	AGTAGACTTT	240
	GACCGTGTCC	GTGTAGGGGC	GCAAGGCCCT	GAAGTCGTCG	AGGTAGTCCT	GAGTGTACTT	300
	GCAGGTACCG	TCGTGCTTCT	TCACACCTAG	GTTGAAGGCC	AAATCGCCCA	TAGCGTGTAC	360
	AGACGAGGCA	CCAAGCAGAG	CTGCGGAAAC	AGTGGCAGAG	AAACGCATAG	CTAACGAATT	420
	GATGGTGAGT	TAGTCTGGCT	AAAGTGCGCT	GTACTGGAGA	AACGACAGAG	AGGGACAAAT	480
40	ATATGTTAAT	ACCAGGTCAG	CGCCATCTGC	CGGAGGAAAA	AGAAATGTGC	CGCGTGTTC	540
	CGGCACCTTC	CTTAATTTAG	AAGCATATAT	TATCACGTGA	ATATCACGTG	AAACACGTTA	600
	AGCCTACAGA	GAGCTATTGA	CGGTGGCTCG	GAACACGTTA	GCACCTGAGT	ATGTACTAAG	660
	GTGGCCACGC	ACCATGCAGC	TGTCCCTCGAT	GCAATATAAC	CCCCCGGGCC	CCGGCAGTCA	720
	ACCGCCATCA	AAAGTNCTGN	CCCCGAGNNC	CCTCAAATGT	CCNTG		

1204UP

	GATCAGGAAG	CAATAGGTAC	TCAATTGCGG	AAGATTTCAGA	GACAGCAAAG	GTCAAGTGCA	60
	GTTCAGCAAC	ATCGAATCCA	CACAAGTTAT	GTCGTACAGA	GGCCATAACT	ACAACGCAAT	120
50	GGCACCCGGG	GGGCAGACGT	TCTCCAACAG	TCCATATACG	AGCAATATGG	GGTCCACGGG	180
	GGCTCGCGGG	CGCAGCTCAG	AGCTGTTCCT	GAAGTTCGAG	CGATTTGCGA	AGCGCATAGA	240
	GGACGTGACG	GACCACCCGC	TGGTGCAGCG	GTTTCGTGCCG	TACACACCGC	TGATTGCGCG	300
	GTTTTTTTATT	GTGGCCACGT	TCTACGAAGA	CTCGATCCGG	ATTCTGTGCG	AATGGCCGGA	360
	GCAGGTGTCTG	TTTCTATCCT	ACTACCGGCG	CTACCCCGCA	GTTTTTCGTAG	TGCTGTTTTT	420
	GATGGTGGTC	GCGGTGCTGA	TGATGGTGGG	GGCCACGATG	ATCCTGCTGC	GCAAGCAGCA	480
55	GCTGTATGCG	ACTGCGATCC	TATGCGCGTG	TATCATCTCC	CAGGATTTGT	GTACGGGCTG	540

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TTCTCCGGCA	CTCCTTCGTG	TTTGCGGAAT	TTCAGCGTAA	TCGGCGGTTG	CTGATTACTT	600
CCGTGACTCC	ATCCGTGCAG	AAGCGCATCA	CATTCCGGCAT	GCTGCCGGAG	CTAACAGCAG	660
GAAGGCGCAC	CAAGGCTACA	TCCTGCTTGC	GGCCGCATAT	CATAGTCTTA	GTTTGTGACT	720
TTACCTCCGC	AAACTGGTGA	CGNTTCCTCN	CCTCGCGNAC	GGTNCTCCCC	TCGGTN	

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1205RP

	GATCGCACTT	CAACCCATT	AAGAAGACGC	ACGGCAGTCC	GGAGGACGAG	AACCGTCACG	60
	TGGGCGACAT	GGGCAACGTG	CTCGCGGACG	CAAACGGCGT	GGCCGTAGGA	TCGGCGAAGG	120
5	ACCCTCTAAT	CAAGATTTT	GGTCTTACGT	CGATTCTGGG	CCGTACGGTC	GTGTGCCACG	180
	CCGGCAAGGA	CGACTTAGGC	CGCGGCGGCA	ACGAGGAGTC	GCTAAAGACG	GGCAATGCGG	240
	GCCCCAGACC	TGCTTGCGGC	GTGATTGGCA	TTGCCAACTG	AGCTGGCTGC	TGCCGCGTGC	300
	CGGAAGCTCT	GGAAGGTTGC	CAACTAGAAG	CTCTGATGAC	TATGTTAGCA	GAATAAACGT	360
	TTTATGGTTC	GCTGTGTTGG	CGCTGTATGT	TACAATTGCA	GCAATTAGAA	GTCTGCTCTC	420
	GCGCCCGACG	GCACGCTCGG	CAGCGAGTAG	CTTGGTAGGA	TGTTTGCGGC	CGCCAGCAAC	480
10	AAGCCGAGGA	AGGGCTGCGA	AGGGTTCTAG	CACCTTGGAC	ATGTTACTCT	GGTTGGTACT	540
	GCGTGCGGAC	GTTAGTAGGG	TTGGTTCGACG	AGCTCGAGAA	TCTCGCACCG	GTGCCGTCTC	600
	GTCTCTGCCC	CCNAATTACG	CCAGCNCCTG	ATTTCTGCNC	ACTTTGGTTG	ATCCCNATCN	660
	ATGAAATNTT	CCNCCCAAAG	AGCCTGCCGT	TATTTCTNAN	ATGACATCGG	TTCCCCCGAA	720
	AAGTGTCTAA	ACATCCCTGT	CCCCCN				

1205UP

	GATCTTCAGG	TTCCGCGACA	TGATTATCAG	CGAGATGGGG	TGGCTGCGCC	GGCGCCCCGG	60
	CTCCTGCACA	CGCTGCGTGA	ACTGCTCCCG	CTCCGGCAGG	TCCTCGGGCA	GCACCGCAGA	120
20	GATCATCTTG	TCCAGCAGGA	TGTCAATGAA	GTGCTCCTGC	TCCTGTACCT	GAGACACCGC	180
	GCGCAACTTG	GCCGCGCGCT	GCTCCTCCGT	ATCCTCCTCG	TCCGACATAC	CGGCGCCATT	240
	GTCGCTGGTC	TCCCTCTGCC	AGAAGCTGTC	CGCGCTGCTC	TCCAGCTCGT	GCCGCAACGC	300
	GAACTCGTCG	AACTGTGTTT	CGATTGTTT	GCGCTGCTGG	TCTTTGCCCG	TCCGCGAGCCG	360
	CTCCCATGTC	GCGTCGAACA	GTGAGCACGC	GATGTTGGTC	ACCAGCTCCC	GGTTCGTGAC	420
	GCACGGCCCG	GCTTTTCAT	CGTCTGCCAC	CCTCTCCTCT	GCCTCCATGA	TGCGTTCATA	480
25	CTTGCGCGCC	AGGAATPCCC	CCAGCAGCGA	ACGCGCTTC	TTGCTGCCAA	TTGCAACGCT	540
	CTCAAGCGCC	TTGGTCTATC	GTCTCTCTTC	ATCGGTCTTC	CGCCCCCAGG	TCATATAGAT	600
	TGCGGCTCGC	GGTAGCACAC	TGGCGAAGGC	TGCCTTGGTT	ATATGCCGCT	AGAAGCAGTC	660
	TCGGCGGTCA	GTTAGTCTTT	TCGTGATGAT	GACGTGTTCA	CGATGACTCG	GATATAGAAC	720
	AGTCATCTAT	CGATTGAGAA	CATAGCTATA	TAGAAATGAT	TTACTGTAAT	ATATCGA	

1206RP

	GATCGCGTCC	GTCGTCTGTCG	GCTCCTCGTC	CTCGTTGAAC	TCCGTCCACA	GCTTGAACGG	60
	CCGCGCCGAC	AGGTCCACCT	TCGCCACCGT	CTCCGTCAAC	ACCTCGGTTT	CGAACTTCAC	120
35	GGACTGCGCC	TTCATCCGCT	CCATGAGGTC	GCTGCCCGTT	AGCCCGTCGG	GGAACCCCGG	180
	GAAGTTCCTCA	ATCTCCGTCG	TTGTCTGTCAG	TTGCCCGCCT	GCAGCCACTC	CGTTCGCGAA	240
	CATGCCCTCG	TACAGCGTCG	GCTTGATCTC	CGCGCGCGCT	AGGTAAATGG	CCGCAGTGTG	300
	TGCGCGAGGG	CCGGAGCCAA	TGATCGTAAC	TTTGTGATGC	ACCATTCTGT	TCTGCAAAAGC	360
	TTGTCCCAAC	CGGTATCTTG	TTGCTGCTGC	TAGCATCAAC	TGTGCACCGC	TAAGTTTCGC	420
	TCGCGCTTGC	TGGTPTTATA	CCTCTGGGCT	TCACCATCGG	TGAACCTTGA	TCCGCCGTTAC	480
	TATTTCCGAC	GCTTATGTCC	GCACCTGACA	AATTCCGGCT	CGCGGGTGCG	CGACTGCGGT	540
40	CAGTGCGGGG	TGCAGTACAA	GATACGCACC	GCGGGCCTNT	NGNNNTCNC	GGCCCTCTCN	600
	GNGGCCCGCC	GNCCCTTCNC	AGGATCNTTN	CCTCANCTAN	AACNNGGCC	GGNGNNNTCT	660
	TTTTTTTGTN	CNGCNAACGA	AGGCAATMNA	ATNTTTNNTN	GGNCNTNNGT	TNGAANTGTC	720
	CNNCNGTGGG	CATCGCNGCT	TATNAACACN	C			

1206UP

	GATCCGCTGC	TCGTGCACCA	CCTGCTGCAG	GTAGGTTGCT	ACTCCACGCG	CGAGATATGG	60
	GTCTTGGTCA	ACATCTTACA	GCTGACCTGC	TTTAACGAGA	CAACCAAGGA	CAAGTACGAC	120
	CGCCGCATCA	TCAGTTCGCG	CGGAACGGTT	TCGACGGCCC	TGTCTGCAGA	TAAGACCTTC	180
50	GCTCAGGAGT	TTAACTCCAA	ATGTCTCAAC	TTTACGACCT	GGTGGCACCT	CATGGCCCGC	240
	CTAGACCACG	CTGTTTTTCAT	GTGGTGTCTA	GACATTATCG	TGGCCGAGAA	CTCACAACCC	300
	TTCAAAAGCA	ACCCCATCAT	CCGCGATAAG	CTCAACGGCA	AGGACTGGGA	CTACTACCGT	360
	GATCTACACG	TTGTTGTTCAN	CTATAGGATT	ATCTGCGCCC	TGACTCTTAC	AGTGCTTCTC	420
	AGCTATCATT	TTGGCTTCAA	TAATCTCTAC	GACCTCTCTT	TTGTCGACCC	AGCCTTCCAG	480
	ATAATAGGGG	CCGAACAAGC	GACTTGGGGG	ACGTGCATGC	AACCTTTATC	AAGAAATGGC	540
55	ATCACAACCTA	TAAAAAGTTC	TAGTTGCTCG	ACTTGTAATC	TCATCTCTAA	ACATAATATT	600

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CTTTTATATG CTTGTATTAC TTANCCTCAA CATGATNACN TATGCCTGGA AGATTTCCNC
 GNIGGCCGTN AGAACNGATT TGTGTCAACT TNTATAAAAC TGACCCCGTC GCCCCTCCCG
 TAACCCGANA TTTCCTGATN CNTGATCCTA TGANGATGCC GGCNCATTNN CANTATTC

660
 720

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1207RP

	GATCTGTTTC	AAAAATTGGA	AACGCTTACC	ACCTCACCAA	CACACCAGGA	CTTTATTTTCG	60
	TAGAAACAGG	CGATCGGCCT	GAACAACAGT	CACTAGAAAC	GGTGCACCAA	GGCAGCTTGG	120
5	CAACGAGGAG	GCACCCTAGG	GCTCAATGCG	TTGATAGTAA	AGCATGTACA	CGAGCTTTGT	180
	CTCCGAGAGA	AGGAACGACG	TCTTGCACTC	CGACACGTAC	GAGTCTGAGA	TACACCACCA	240
	CGGGTGCGTA	GTGGTGCGAC	GTAAGCCTT	CAGTTTGCGG	GGACGGCCCT	GGGGACGGGG	300
	GAGTACCTTC	GTGGCAGCCG	AAGATACGCC	CGATGAGCTC	GCAGAGCTGG	CTCCGGAGCT	360
	GTCTGTCTCG	GCTGACGCGT	CGGGCTTGGA	GACGGGTCT	TCCGTTAGTA	GTGACTGTTG	420
	ATGGAAGCTC	CCCAGTAACG	GTCTTGAGCA	AGCGGCCATC	GGCCCAGGCG	GAAGGCTTCC	480
10	AGCTGGCGTA	GGGCACAGGC	ATTCGAGGGG	CTGGCTGCGG	GACGGCGTCC	GACGAGATCA	540
	CATCTGAGCG	AATGATATCT	CGCCCGTCC	TGGTCTTCC	TAAGTCAGTT	TGTTGGCGAA	600
	CATGCGTTAT	GCCCTGAGAA	TGGTTGCCAT	GTGCTTGATT	CATGCGCCAA	CAGCTTATAG	660
	CGAATGCCAA	ACCCCCACCA	TTGTTNTCCC	CNACACTGCT	CNTGAGACAC	CCCCCCCCGA	720
	AANTNAATGC	GGTTTNTTTG	TTAAACCNCN	TNAAAA			

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1207UP

	GATCTAATGA	GCGATAAGTC	ACCGGTTATA	GAAAGTTTCG	CGAATCCTAC	AACTGACTCC	60
	AACTCGCCAC	AGGAGATATC	TCTATTAGAA	AAGAATATCA	AGGATGTCAT	GCGTTCACTA	120
	AAGGGCGTTG	ACACGCACCT	ATGTGAACAG	ATCATTAACG	AAATTCCTGT	GGTTGATTAC	180
20	GATGTTTCGAT	GGGAAGATAT	AGCTGGTCTT	ACAATAGCAA	AGAAGTGTTT	GAAGGAAACA	240
	GTTGTTTACC	CATTTTTCGG	GCCAGACCTT	TTTCGGGGTC	TCCGGGAACC	TATCTCCGGG	300
	ATGTTGTTAT	TTGGACCTCC	AGGAACAGGT	AAAACGATGA	TTGCCAGGGC	CGTTGCGACT	360
	GAAATCGAAT	CAACTTTCCT	TTGCATCAGT	GCTTCCTCTT	TGTTATCGAA	ATACTTGGGT	420
	GAGTCGGAAA	AACCTGTCAA	GGCCTTATTT	TACCTAGCCA	AACGGCTTTC	CCCCCAATT	480
	ATATTCATTG	ACGAAATCGA	CTCTCTACTA	ACTACCGTTC	AGATAATGAG	AACGAATCAT	540
25	CCAGAAGATT	AGACGAGCTC	TTGGTCCAAT	GTCCCTCCCTA	ACGAGCGCCA	CGGCTAGGAA	600
	CAGAGAGGCG	AAGAGGCCAG	ACGCGTACTG	TCTTGCGCCG	AACCACTTAC	CGTGGGCAAN	660
	AANGANGCTG	CNATAAACTT	TTTCACGGGT	CTATNATCCC	TTGCCGGAAT	ACAACNAAAT	720
	GTTCTTTGAA	AACTTNTTGG	CTCCAAAAAG	AATTTTCGAAC	TNATTCNNCN	T	

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1208RP

	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTTAATAATA	AATCTATTAA	TTATATAAAA	60
	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCAATCAT	TTAATACTCC	TCTAATTCAA	180
35	TCTTAAATA	TTCTTAATTA	TTAAATTATA	TAATAAAAGT	TAGTGGATAT	AGTTTAATTG	240
	GTAACACATA	TGTTTTAGGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATTAT	300
	ATCATTAAATA	TAATAACTCT	TTAATTAGAG	TTGGTACCAC	AAGAAATGCTG	AAAGCATTAG	360
	GGGTGTGTAC	CTTAGCTCTC	CTAATTAAAG	TTTATAAAAT	TATCCTTAAC	TAATAAAAAT	420
	AATTAATTAA	ATAAATAAAT	AATTAATTAA	ATTTAAATG	TTTTAAAAAA	AGAAATAAAT	480
	AATATGTTTA	TATTTAAATA	GATTCAAATT	TCCAACAATT	CCCATTCAAT	TAGTACTACC	540
	ATCACCATGA	ACAATTGTTA	CATCATTAGT	TTATAGTTTA	CTATACTTAG	CTACTAACA	600
40	TGGTATATGG	TATAATANCC	CTAATAAACC	TTATANANTT	TTTACCNAAC	TTNGATTAAA	660
	AAAAGGGCGA	NCNNCTTTGG	NGGACCCCTA	CCCNTAAAG	GNGTAATGGT	TCCCCAATTG	720
	GTGGCCGAAA	TAANTTGGCC					

1208UP

	GATCTTAATT	TAAAATTTTA	ATTAACATTT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAATAAAAT	TAGTAAATA	120
	AATAGAAAAAC	CATAAGTTAA	TTGATTCTAT	AAGAAAAATG	GAATTATTTG	TGGCATCTTA	180
	ATTTTATTA	TTTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATAAA	240
50	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAATTTAA	TTTTAATATT	300
	AAATATACCA	TTTTTATTAA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
	ATTTAATTTA	TATAAATTAT	TTAATTTACT	TCCCCTGATA	TATATAATTA	TTAAATGTTT	420
	CTTTCATAAT	ATTTATTTT	ATTAGTCTAG	TAATATTTCT	ATTTAATAGT	CTACCCCTTT	480
	AATTGGATAT	TACTACCTAC	TAAATATTTA	CCCTAATAAT	ATATTATTAA	GAATACTTAA	540
	TCCTAATAAT	TTATTATCT	AAGTTATATA	AATTAATTAA	TCCTTTTTAT	TATTATTATA	600

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ATTATTATTA	ATTAGTAATT	ATATTTATTA	TTTTATTAAC	ATAATTTTGT	ATAATATATA	660
TCCATATAAT	GGTATTTTAT	ATATACNTN	ATGAATTAAT	GANAACCTA	TATATGANAT	720
TAGTTATAGT	GACTTAATCC	CNATCTCAAT	ATATATAATT	ATTATAGAAN	ANATACTTTT	780
TC						

1209RP

GATCAGCCTA	TGTAGCAACT	GATCGGCGCT	GGTCCGTGTC	AAACGCCGAA	AACACCCAC	60
CAGATTACGC	AGACACTCCC	ATATTTTGAC	CGACTGGAAC	TTTGTGTACA	CAAAGCTATT	120
CAGCTTGTC	CTGGCCACCG	TCAGCGGCAT	GTTGTTTACG	CGAGTCGCTA	GCGCCGCACT	180
GCTGTTGCCC	TGCGCCAGCG	ATGGCTCCTT	AAGATCCTGC	GTTTCGCATAT	ATTGCGCAAA	240
CTTCGATAGG	TCTCGACTGA	GCGAATTACC	GACATGGTCC	AGTAATAACA	ACACCCACAG	300
GCAGCCCCC	CAGCTGTAAT	TCACCGTTTT	GACCAGCAGA	AAGTGCAATT	GTAAAAGAAT	360
GTACCAGTAA	TGCCAGTAAA	ATGTGGAAAA	GACCTGGTCC	TTCTGAAGAT	ACGAAATCAT	420
CACCTGAAGA	TTCTTCAGTC	TTCTCCGTCC	CGAACATCTT	GGAAAAATCT	GCNGNTCGTC	480
GCTTCTCTTC	CACTCGAACC	GCAGGGCTTC	CAAGGACACT	CCTTGCAATT	GAA	

1210RP

GATCTAAATT	TATCAGCCCA	TGGACGGATG	GATTTACGGC	AGCGTGTGCG	CGCAGCACGG	60
GGCACGCCAG	ACTGCGAGGT	GGCAAATAAT	TCACATAGCA	ACCTGCATTA	TAAACATCCC	120
AAGTCATTAA	ACTTACTAAA	TATTGTTGCG	TAACCAAAAAG	CACCGTGTAT	CATCATCTTC	180
ATAGTCTTAG	CTGAACCTAC	TGTCGCACCA	GCCCTTTACT	ACGTATTGTA	TCTCCCTTTT	240
ACAAATGCTTG	CCCACTGCCA	GTTTTCCGCA	CGGGCGTTAG	CATGAAGTCT	TTGCCCGCCT	300
TGTACCACGG	CTTGACGTCT	GACTCTACGC	GGACCAACGA	GGTTAGACGG	AGTGCACCCG	360
GGACCGAGTC	ATCCTCGCTC	GCGTGTTCCT	AGAGACAATT	TGAGGTTCCA	CGGAGCATCC	420
ACGCCCCATGC	AATCCTGCCC	GTAAAAGTTT	GCACANTTCA	TCCACACTT	GGGGGGTTNT	480
TATCACNCCA	NCTGATCTG	GTACGNAAAA	NTTTTCNTN	TTTGGTGAGG	AAATCAGGTT	540
CCCAATA						

1210UP

GATCGAGAAG	ATGCGGCGCC	GCAACGAGGC	CGCCACGCCC	GAGGCGGGCG	GCNACGAGCT	60
CCTGACGCCG	GCGGAGCGCT	ACGCGCTGGA	GCAGGGGCG	GGCTTCCTGG	CGCCTGTGCT	120
CCCTGTGCGN	GAGCCGGCNC	GGCCCCGTGG	CGTGCCCTGC	AACGAGCTTC	CCGATGAATA	180
CTGCATCACC	AAGACTGACT	TCGACCGGCT	CGCTAGCCAC	GGCATCCCGG	TCGAGGACGT	240
CCACGAGGAC	AGCAAGGACT	GGTACTTCCA	GTGCCCTGT	GGAGTAGAGG	AGGTTAGCCC	300
GGGCCTAGAG	AGCCCCGCGC	TGCAGCAGGC	CCTGGTCTGC	TGCGACCAAT	GCCTCCGCGT	360
GGCAGCAGCT	GGGACTGCCA	GCACCCCGCA	GCGATTGAGC	TTGCTGGCCN	GCGGGCAAGA	420
CTCCTCACTA	TTTTGGCCCTC	CNTGCCCCCT	TGGCCTGCCC	CACGCGCCCG	CGCCCTCAGC	480
GGCGGNGNCG	GGCGCNAAAC	CCCTACCAGA	ACCAAANNAA	CNACGCCNCC	GCCGCCCNTC	540
GGTGAAGCGA	ACCCTTTTTTN	NCTCCTGTCT	TCCNCCCTG	AAAGACCTAN	TTCTCCTTCA	600

1211RP

	GATCTCCTCC	AGTAATGGCG	TCAGAGCACA	CTGGTAGCGG	ACCCCTGCCA	GGTAGCTCAT	60
	CGGCAAAAAG	ATAGCACGCG	TATGTACCCA	CCAGCGAGCC	GGGTGATAAG	GAAACTGGTA	120
5	CGGCAGCAGC	CATAGCTCTG	GTGGCGCTGG	GTTACAGCCC	TCCCACCTGT	ATAAATTGAG	180
	CACGAAAGC	CACACTTTAC	CCCAGTACGG	CGAGCCAATA	GCACCCCCCA	TGCGCAGCAG	240
	GGTCTTCCGC	GCCCCGTGCA	TCACGATGTG	TTCGCGCTCC	ATCCCTAAGA	GCCGCAGCAG	300
	AACGTAGTTC	AGCGCGGTGC	CCATCGACAG	TCGACTTGTC	CTCCGAATGC	AATCCCCACC	360
	CGCCGTCGAC	AGGTGTGCCG	TGTTCAACAC	GTTAGCGCAC	TAGTCCCGC	CGCTGAGGCT	420
	CAGGAATACC	ACCCCGCCCA	CATGCATCGC	CACCACATAC	CCATATCATN	ACATCNGGCC	480
10	CCCTGTTACA	ACAGGAAANT	GCCCNAACTT	CCTCCTGCAG	ANGGCCCAA	CCGCCCCCG	

1211UP

	GATCTACATC	ATGGGAGGCT	AGGAAGAGCA	AGGCACCGCG	TGCATTTGTA	GA CTACACGC	60
15	TATAATATGC	AAATGGCCAA	TACCTTTGCC	CCGGATCCAA	AGAAGGGCAC	TGTCAAGCAT	120
	ATGGTTATCG	AGACGAGCTT	CAACCACTTG	GCTCTAGGCA	TGGTCAGCCA	GATATTTCCG	180
	CACTAAACAA	CGTCTAGAAA	ATGACTTGAC	CTATGACGTG	CCGGGCTTGA	CTCATCTTAC	240
	TATCCTCAGG	CCCGGCCCTC	TTCTTGCGCA	GCATGGCTCT	AAACCCGTAA	TAAGCCCTAC	300
	CAACCTGAT	ACAGGAAACA	TGCTTACGCG	CTGTTACACT	TATAAGAAGA	ATGTTATGCG	360
	CACGCAATTT	AATTGGCTTG	CGCCAGTTTA	AGAAGTTGGG	CCAACACTAA	GTCACCCGAA	420
20	CTATCCGCGA	AGGCTACCTA	TCATTTACCC	TGGAAGTGGG	TTGTTTGGCT	ACTCANTCCC	480
	CAGCNTGAAA	ATTGCCCCNA	ATTGCCGCTC	CAGAANCCTG	ATCCAACGGA	ACTACTCGAC	540
	CAAATCTAAT	TTCCCTTATA	ATGTGAATTA	CACTGTNAAT	TCAGAANTGA	ACN	

1212RP

	GAGATCTCCC	AGTACGTCTT	CAAGCTGGGC	TTTGGCGGTC	TAGGATAGAG	CCGGCGGAAC	60
	TCAGGACTGG	TCGAGACGGG	ATGCTGGATC	CCGAAGCTCT	TCATAAGCAA	CAACCGCGGT	120
	TGCCGCGTGT	AGTCATCGAA	CCGTCCCTCA	GCGAATCCTG	CGAGTCTCCA	CCTGACATCA	180
	CCATTGCCCA	CGATGCACCG	AAGCGTTTCT	GGAAGGAACA	CGCAAACTAG	CAAGAAGCCG	240
30	ATGCCGGCCA	TGATGCTAGT	GAAACCAAAC	AACCATCTCC	AACGGTCATT	ATCGAATAGG	300
	ATCAAGCCAG	CAATAATGGG	CGCCCCAAAT	CGGGCCACN	TTTAGGGCCC	CAACATNAAT	360
	TACGCAATTG	CCTTGCCGGG	GTPTTTCGGN	GGTGTGATT	TCNCTTACCG	TACGGGCCCC	420
	TGAGAAAACG	AGAACTCNGA	GGAAATGCTG	CNCCCTNTT	AAAAAAATAC	NCCCATCGNG	480
	CAGGNTGAAA	GCANTTACNC	TTGACTATAA	ATCANCCCCC	GANAAANTTA	NACTCG	

1212UP

	GATCAGCAGT	GTCTTCCGGG	ACGTCAACGG	CTTGACGGTC	TTGCGTACCG	TGGCCAGCGT	60
	CCGCACGCCA	TGAAATGCCT	GCACTGCCTG	CCGCAGTCCA	CAGTTGCGCA	GCGATGCCAG	120
	ACACGAAAAC	ATCCTCGTTA	ATGCAGCTTG	GGTCTTCCG	TCGTCACTGT	GCGTCTCGAT	180
40	TAAGCCCAGG	TTATCAGTAA	CATCAAAAT	TTACATAACT	GCCACGTGAT	ATACACGTGA	240
	TAAAGATCTA	CACCCATGCC	CCCTGATTGT	GTAAAAAAGC	AACTTTTGAA	AAATTTTCTA	300
	CGGTTCCATC	CGATGAGATG	AGCTTAGCCT	AGTGCGAGTC	CAATATCAGT	GCACTAAGTT	360
	TATCCAGTGA	TACTTGTTCT	CGAGCTTTCA	GCAACAGCAT	CAGTTTACAA	ATCGCACCAG	420
	CAGTTATCCC	TGGAAAGAAA	TCCTACGGTC	CGAACTCCCA	TGATAGTTTG	ATACGGCCCT	480
	TACAGACGCC	AGCGAAAATC	CCACATCTCC	NGGNGGCTTC	AAATNNNCTT	CCGNGGTTCT	540
45	AAAGCTTAGG	GGNATTCCCA	TGCANGGGTT	TATNAAATTT	GANAAAT		

EP 0 866 129 A2

1213RP

	GATCTTTTTT	AGAGAGTTCA	GTGTCCGAC	CAACACGGTC	GGAGGCCCTT	CAGCTACTTC	60
	CAGAAGGTCG	TAAAGAGTCT	CCAGTAGCCC	CAGGGTGCGC	TCGTGGTCAT	AACAGTCCAT	120
5	CTGAGGTAGC	GTGTTAATAA	CCGCTTTCAG	CATGCTCGTA	GAGGACTTCT	TTACTAGGGC	180
	AGAACTTATA	AACTTAAATG	TCTCGTCTAT	GCATTTCAGG	GTACGAAGAG	CTGCCAGTGT	240
	CCGAATGTCA	TCAGCCGATC	TGCTCGTTTT	ACTTTGCTCA	GAATCGCGCC	ATAGTTTAAC	300
	TNCNGTTCCC	AAATTAACCC	GGTTTCCCN	GACCCTTTTN	AACAAAAAGG	AAAAAAAATT	360
	CCGTTTCCCC	CCCNCNCCC	NNNNTGGCN	AAAAATTTTT	TNCCNCGGN	AAAATTTTANC	420
	CCCCCNCTT	AAGNCCCATT	AAAAAAAAN	NNNNNTTTT	TTTTTTTTNT	NGGNGCCCN	480
10	NAAAAANNTN	CCCCNNTTTN	NAAAAANNNG	NGGNTTNNNG	NNNNANANNN	NANNN	

1213UP

	GATCGCCAC	TTCACGAACT	CCAGCTCCGC	AGGCCGAAAC	GTCGTCCGCCA	GCTCCGCCTC	60
15	GCGCGACGCC	CCCACGTTCA	CATACACGTA	GAAGCGCCCG	CCCTCCGCGC	CTGCCCTGCTC	120
	CCCCCGGTAC	CGCCGCCCA	GCGCGTGAGT	CACCCGCTTC	ACCTGGTACC	CCAGCCCCCG	180
	CAACCGCACG	TTCATCTCCG	TTACGTATGT	CCCCAGCTCT	CCCCCGTCGC	CGCCAGCGC	240
	GCCCAGGCAC	TGTGCCAGCA	CTTGCTCGTG	CACCGCCCCC	CGCGCCCGCA	GGATGCACTG	300
	CAGCAGCAGC	CGCCGTCTAT	CGTCGCGCGT	CGTCTCCGTC	ATTGCTCTCC	TGCGCCCCCG	360
	ATGCACGCAA	ATCCGCTCTC	GAATGCCTTT	GGCTGCCCC	GGCTTGCGGT	GTCTGGGGTT	420
20	GATTGCCACG	AATGCTGAAC	CAAACTGACA	CATTTTGCCA	AAAGAAACGC	CAATGTCTCT	480
	CGAACGAATT	TCNCGNTCTC	GTTGAACTAA	CCGCCGCGCC	CAGTTGGGTG	AAGCCGCTGC	540
	TGTTCCCACT	TATCCGGTAG	GGTTCAGCCT	TCCTGTGNTT	CCACTANTGG	NAAACNCCTG	600
	CTT						

1214RP

	GATCGTTCAC	GTCAGCCAAT	TCTGTGTGCT	AGCCCACTAC	ATTGTAGAGC	TTATAGATTA	60
	AACCTCGAAT	GCAATCATTG	GGGTAAGCCA	CAGCTTCTGT	AGTCTGCCTA	TAGCAGAACT	120
	TTTCATCTTC	AAGGGTATGT	CTTGAAGGCG	GCTTTAAGGA	ACCCTTCATC	GAAGTACTGG	180
30	GTCTTTCTAC	CCCTCCGCGG	GAGCAGGATG	TTAGCCGGAG	CTTCTGAATC	AAACTCTTGC	240
	ACTTCAAAC	CTTGTCGTGG	ACCGAACGCA	ACTTTAGCTG	CGCCTTCAGG	TTTTGTTTTCT	300
	TTACTGCCAG	AACCTGTGGG	CGGTGATGGT	AGGAATTTTC	TCCCATCTGG	GTTAAGTTCC	360
	TTCCATATCN	ATTGACACTG	CACGCCCAAA	CATTCAATTT	TCCANANCCC	CTACCCCCC	420
	NANATGTTAA	TTTTTTCNGGT	TTAAAGGACT	TATCNNCCCT	NTCAATTTTTT	CTTNAATNAA	480
	CTCCATTTGT	CCCNAACNAA	CAATTNAATT	CCCCGTGTCC	TTCCCA		

1214UP

	GATCAAGACC	TGACGGCTTC	CTAAAATCGC	TAAGTTTAGT	ACATAAATTG	CGGCAAGAAT	60
	TACCCAAATC	ACCTGCTGTG	GAGATACGAG	GCAAGCTGAG	CGGGTGGAATG	TGCCCCATTCC	120
40	ACACCAAGTAA	CTCTTTGGTG	TGTGGCTGTC	ATGGTACTGC	TCGCTACCGC	CGTGTTCACG	180
	GCCTTGCTTA	ACGGGAAGCG	ATGCCGGTAA	AGCCAAATCA	TGTAACACCC	AGCGATAAGT	240
	CCACGAGCAG	ATGCTGAGAG	GCTCGACCAG	AACGACGTCG	CATGGGTGAT	GCTACAGATG	300
	CCTATGCGTG	TGACAGGTG	AAGCAACTGT	GTTCTGCTTC	AAGTAATAGC	CAAACTTGGC	360
	GCGGTAGAGA	ATGACACTGC	GGTGCTGTG	CATATGTTGG	CACTATGCAA	GGTTACAGAT	420
	TCGCAAGCTG	CCCGAATGTT	GGCCCAATTT	CGAACCAACCA	GCCAGCTATT	GGTATGGAAT	480
45	TATATACAAC	TTGGTNGGGG	AGGAATTCCG	GTGAAAAACG	GCGCACCAGG	NAACTTTACT	540
	GGAACGGGAA	NCGGGNAATT	TCCCCCCCNC	CCCGGGTTTT	TGGAACCGGC	CCCNNTTG	

1215RP

	GATCAGAGCA	AAGTGATTCA	AAGCGATTTT	GGACGACGCG	TAAGCTGCCA	GCGCAGGATG	60
	GCCCATCTGA	CTGAGCCCCG	AGGTTACGGC	AATGAAAGCG	CCCTGCGACT	TACGTAGCAG	120
5	TGGAAGCGCC	TTGCTGGCCA	GATTACAGAC	GCTAAACAGA	TTAATCTCGA	ATAGGCGTCT	180
	CCATTCCCTT	ATGTCCGCCT	CCGCGATGCG	TTGTTGGTAC	GAGACACCCG	CGTTCGCTAC	240
	GACAGCGTCT	AGCCGCCCAT	ACTCCGAGGA	CACCTTATCG	ATCACGGCCT	GCACCACACG	300
	CTCGTCAGTG	ACGTCTCCGA	CAACATAGTC	GAATTTCTTG	CCATGTCTCG	CCTTCAGCTC	360
	CTGCAATTTG	TTTCCGCCC	GTGCAACCC	TACTACAACC	ACGTCGGGGG	TTGAGCACAA	420
	TCTGTCAACG	GTTGCCGCGC	CAATGCCACG	CGATGCACCT	GTCACAATTA	TAACCTTCAT	480
10	TCTTGCTTGG	TACTTTATCT	TCAATGGGCC	ACGAACGCTC	CCGCTGTTAG	TTTATATATG	540
	ACTTCAGGGG	CTGTTGGCAC	AGCTCACTAG	CACACTACCC	TTACATGTTC	ACACCAGTTC	600
	GAGAATGAAT	GGCACAGTTC	CATTTGTAAT	CATGATTATC	AATACAATAT	GTGTTGTAAT	660
	TATTGATTTG	TAATATGCAT	AATATAGATG	GTTATGATTT	GTAATACAGT	AAATATACGG	720
	TAAATATAAA	GTATTTTAAG	GAATATTTAT	AATT			

1215UP

	GATCGCCCCG	GGCCTACGTC	ACTGCAGATT	GGCGCAAGCC	AGGAACAAGA	CGGACACTAA	60
	GTCAATCTGT	TTATGTAGAT	TGGGTGCGCA	GCAGCGCAGC	CGGCGCCGCT	GATCTAGCCG	120
20	TACCGCACCA	ACGGCGGGAC	GCATGCGGGC	CCGGCGCGCT	AAACCACGAC	CGTCGTGCCC	180
	GGTGCCAATG	GACCGCGCGG	TCATCCACCC	CGCTCAGCCG	GAATGTAGAC	CAAAAAAAGA	240
	GTGTGGTTCC	AGCTCTCAAA	TTGGGCTGGT	CTCAAGGGGT	CGCGGCCCCG	CAATCGCCTA	300
	TATAAACGGA	CAGCGGAGAC	AGTCCGTGCA	CTGTGAGGGA	CAGGCACACC	GATGGTGAGG	360
	GTTATCATTG	TGACAGGCGC	GTCGCGCGGC	ATCGGTGAGG	CAACCGTTGA	AAAGTTGTGC	420
	ACAGCCCCCG	ACGTTGTGGT	GGTGGGAGTT	GCGCGGGCGG	AAAAGACTTG	AAGGTGCTGA	480
	AAGAGAGATA	TGGCAGTAAA	TTGCACTACG	TTGCTGGAGA	CGTCACCGAT	GAAAGCGTGG	540
25	TGCAGGCGGT	GCTCGACAAG	GTGTCTCTCG	ATTATGGGCG	GCTAGACGCC	ATCATAGCGA	600
	ACGCAGGCGT	CTCGCGCTTC	GAACGCATCG	CCGAGGCAGA	CATCCAGCAG	TGGAAGCGCA	660
	CGTTTGAGAT	CAATTGTTTA	GCGCGGTAAG	CCTGGTGAGC	AAGGCGCTCC	GATGCTAANG	720
	AATCCCAGGG	TTACGGTGAN	TGTGGTTACC	TCNNGANTCA	ACNAGGTAGN	TANCCG	

1216RP

	GATCAAGTCT	TTTATCACTA	CAAATGAGCA	GCGCTTAAAT	TTCCAGAATC	GTTTACAGCT	60
	GGGTACGCTT	GCAAGCAAAAT	TTGGCCTTTT	TGAGCTAGCG	GAGGAACAGT	TCGCTCACGC	120
	CAAGCGCCTC	ATGCGGCCCT	CAGAGCGCCG	CGAGCTTTAC	ATGTATTACA	AATCTCTCAG	180
35	CGCGTTCTAT	TCCTTAGCCA	AAATGCCGAC	CTGCTTAATA	GATACTCTGC	GTGCCTTTAA	240
	TAACGAGCCG	CACCTCGTCC	TCCGTAACAC	ACTACTGGCT	GCGCTCTATC	CGAACACATA	300
	TCCACTGGCT	CCGCCGCAAT	AATGCAGAAG	AAGAGGTCCA	TAGATGAGCT	GAACCAGCCA	360
	GCGCCANACG	AATGTACTCC	CACTTATGCG	AACTCCNANA	NTGGAAGGCC	CTGCATACAT	420
	TTCCGGTCCC	ACCNACTTCT	GCGTTCTTGT	GCTTACCAC	CTTGTGAACC	GAATNGTGCG	480
	GCATGCCTTG	CCCCAAAACC	CCTGGAATTC	CATAAATACC	TCNCGGGGGT	TANCTGCGCT	540
40	CCCCCG						

1216UP

	GATCTGTGAA	TATATGCTTG	GGGTGCGATTG	GTTTGCCAGT	GCTATAGAGA	GCGGTCACCG	60
45	GCGTACGCAC	GGCAACTCTT	CGAGTTGTCA	GCCCCAAGTAG	CCTGATCATA	TACAGGTGAT	120
	GGATGGCTCC	TGTATACCTT	CCCACACTGC	AAGCCCCCTGA	GTTGCTCAGG	TGTTACTGCG	180
	GCAGATGGTC	ACATCGCTTC	GGAGTATATA	GTCTGCGCTT	TGAGCCACTT	AAAAGGGGCT	240
	CGCCGGCTAG	CCCCGCCGCG	TGGTCACGTG	ATTGCCATCT	GCCCCGAACG	GAACCGTAAC	300
	AGGCCGTTGT	AACGTGGTGC	TCATCCGTCA	GCAGGCCGGT	CTCCCCAATGT	ACTTCGCATA	360
	TGTTATTTTA	CGTTTATGTT	ACCTATCGAG	GGTCGCTCAG	GGTTATGCCC	GCGGTGCTGC	420
	CCTGCCACGG	AACCCGCAGC	CTGCAANCC	CCCTAATTGC	CCATGGTGAA	TTGAACTCNC	480
50	AAGCTTATAT	CTCCTTGCC	GATCCCCAT	NATGCATTTG	AAGTTTCNCCA	NAGGACAAGA	540
	AACANACNCA	AAAAACNAAA	TGGTTAAGTA	AAATTGATTT	GGTGTTCCTC	CCT	

1218RP

	GATCTTTGTG	GGCCACGACG	ACCACCGGAG	TACCGCCCGT	GGCTTGGACG	TACCACTGAA	60
5	AAATGTTCTG	CATGAATCCC	ACCTTGATAA	TACCCATGGA	CCACTGGAAG	TTCTGCGACC	120
	ACGCAGCAGC	GATGGGTGGC	ACACGAGCCA	CTCCCATCAT	AGACGTGATC	GCCAAATTTT	180
	GGAAGTACGA	GAAAAAGAGAG	ATCGAGTTCC	AAGCGATGTG	CGCGGCAGTG	GTTGAGTGCC	240
	CGATCACAGA	CACAAACCCG	GAAGTCCAGG	ACACCCACAC	CAGCTATCGC	GGCGAATCGG	300
	CCACGAATGC	ATACTTCGTC	TGCACCGTCT	TGCCGTGCCG	ACAGCACCCG	CCCTGCAACA	360
	CAGGCCCATT	GGATGCTCCG	TACTGGTGTG	TCAGCTTTCC	GCNAAGGCCT	TTACACCATC	420
10	CGTGCTTCCC	AGTTCCCNCG	AAAATATACC	CCNCCTTGGT	ATCTTCCCNT	GAAAAATCAC	480
	CGCCGAAATT	TCCAGTTGA	ANCCTCTTTG	ATCCCCCCCC	CNTGCCCTCC	CCCAGNNCGG	540
	GANATTCACA	ACNAATNC					

1218UP

	GATCCACAGT	TTCCGCACTG	AACTTACTAT	CCCTCAGCAA	CCGCAGGTCA	TCGTCAAGCG	60
15	TTGTGACATC	AGGCTTCACC	CCGTAGCTCA	TAATGCCCTG	GACGGATGCC	TTGGTAGAGT	120
	AACAACCAAA	AAGGCATGTT	GGATCAGCTG	CATAAGCTAG	TAAAAAAGAG	CAGACGCCGC	180
	CTGAGCCACT	AAAGGCAACG	ACCCGCCAAT	ATATGATAAA	TAGAGAATAT	AGAATGTTGC	240
	CAC TAGGCCA	AGATGACCTG	CATTGAGATC	CAGCGACAAA	GTGCCAGGAA	TTAAGGGATC	300
20	TTCAACATTC	CTGATCATAT	GAGAAGAGCA	ATACAGGGTT	AAAACGGCGG	CGTTTAAAT	360
	TTACAGACT	CAATCAAATG	TTTCACAATA	CCTGGTTTGG	ACAAGTCCGA	GACATCCCCC	420
	TAAGTATCT	GCCTCCCCCA	GCCAAGGATT	TTGCGCCATA	TACGGGCCAT	ATTTTGCCTG	480
	ACGATTCTTT	TGCATTCCCT	CCCGAACCAC	AAANACCTTA	GGGGCACNAA	CGGCCCATTT	540
	CCCNANNGAA	AAAAAAAATA	GGTGCTTTGN	ATNNCCCGNA	CCCCCCCCCC	CCCCTNTTTC	600
25	CCNG						

1219RP

	GATCCTGATA	TTGTACCGGC	TCATAAATAC	TTTGGATATC	TTCCGACAAT	GTATCGTACC	60
30	CGATACCTTT	CAGCACATGG	ATCAGTATAT	CATGCTTCTT	CCTAAATGCA	GCAACAGTAT	120
	TGAGGACTTC	CTTCAGACTG	TCCGTCTGAG	TATCTATCTT	CATAAAGATG	AACCTTTTCGG	180
	ACCTCTTCCT	CATCAGCTCT	CTGATGAGTG	ACGTTGAATT	CTTTTAATAG	CGCTTCCCAC	240
	TGGTTTGATA	ATCTTGATAC	AGTGGTCCAT	AGTCCTCCCT	GGAAAGAAAT	GAAGTCGGAA	300
	GAAATCAGTT	TTGGCAGCAC	TCTCTCAGTT	TCTGATTCAA	CTCCCGTTAG	ATATTTCCCTC	360
	CCACAAATGT	TTACGGCCCT	ACAGTTGGTT	TCTTTTGAN	CCTTCACTTC	CNTCCNAAGC	420
35	CATGAAAATG	ANTCCATCNC	CNCCCCCCCA	CTTTGTNAAA	NTTCCCATTC	GCAAATTCNC	480
	CAGTTGAATT	CCCCCANCCG	GGTGTTCCTC	GCGTTCCCCC	NAAAAAANAC	NGAGGGGGGT	540
	TTTAAAAAAN						

1219UP

	GATCGCGGCG	CTGCCGCCGG	CGTCGGAGTG	GCGCCACGTG	GGCCGGCCCT	TTTGGCCAAA	60
	TCCCAGCGGT	GGGCGGGTTT	CGAGCTGCTT	GACCTTCCGC	GGCATGTCAA	AGTGCGGCGT	120
5	TAGTTTGGTC	CTGTAGGCGA	ACTGTAGCGG	CGATGCGACC	GTCTCGCCGA	CGGTGGGGAG	180
	CAGGCCCTCG	GCCAGCAGCT	GGGGAGCAAA	GAAC TTGAAC	GCATTTGACA	CGGTTCGCTG	240
	TTTGAGCTGC	AGCTGCTGGT	CATACGTCAG	GAAC TGATAC	TGGCAACCGG	AGCACTTCCC	300
	GAAGTACTTG	CAGTTGATGA	GGTCGTCGTG	GCGCATTTCA	GCAGAGGTCT	GCACCTCCAG	360
	CAGAGACGCT	TCGGCGTAGT	GCGGTGTGTC	TTGTGCACTT	GGATGGTGAC	CACGTCGCCC	420
	TGGCCAGCCC	AAATTTGGCAC	CCAGCACTAC	TGTTTCCCTG	TTTGCTATCC	TCCCGGGCTG	480
10	TCCAACAANA	CCCATCCCTC	CCCATCCACT	TTACNTCCAC	ACATCACTTT	CATCAGCNCC	540
	GGTTGTTCCT	CTGCTGCATC	GCCCCCGAA	TTTNTTCAGA	ATGATTACTC	CTCCNCNG	

1220RP

15	GATCGCGCAG	TTGTGCGCCT	CAGCCAGCCG	CTTTT TGGGC	ACGCGCGGGA	GCGTGTCCAT	60
	GTACCCGTCG	GGCACGCCCC	CGTCGCCCTC	GCCGATCAGC	TGCAAGTGCT	GCTGTAGCTC	120
	CTCCGGGCATC	AGTCTCACGA	TCACATTTAG	TAGCGCGGTG	CTGTGCGCAT	CTGCCTCCTG	180
	GAACATGTCA	GCCAGCTGCC	TGCGAAGTTC	GGACCGTGTC	CCCTGGTTCGT	CTGTGAGAGT	240
	TAGTATTCCT	GGCCGCAGTC	GGTCGCACAT	TGGCATCACT	TACTATTGTC	GCTGGGCATT	300
	CACCTCCCTG	GATCACTGGT	GCTCCCGGTG	GCGGTAAGGG	GCAACAGACA	GGCTTTTTTTT	360
20	ATTTTCCCTCT	ATAATACGCT	GCTCTATGTA	GCGTATACTA	TACAAGTCTT	AACTAAGGTG	420
	AAGTGAGAAG	TCATTATTTA	GCTGCGTTTC	GGCCGGTTCAT	GCAGCCGGCT	ACCATATTAG	480
	CATGCCGCTG	GCCTTGACGG	CTTTGGACGT	GGGGGAATTG	TTGATGCCCA	AGGACCTTAT	540
	GGAGTTCAAC	CTCACGGAGA	GGTTTCCGAG	ATCGAAAATG	TCACTTTCGG	CAAATTGCGA	600
	CACACCGTAA	TACTCGGCAA	ACGAGTTCTC	GACACCGCTG	AGCTCGTCGT	CGACGTCGTC	660
	GACATAGGAC	AGAAGAGGCT	TCGTTCCGGC	TGGCGGGCGC	GCGCGCGCAA	CCGGAAGNGC	720
25	CCCCCANAG	CTGGCGCCNG	GCCGCC				

1220UP

30	GATCCAGAAT	ACTCGTCGCA	CCACTTCTTG	AACCGCGGGT	ACAGCGCGGG	GTCCGTGCGG	60
	TCCAGCGCGG	CCTTGTGCGC	CGCGTGGAAC	AGCCGCGCGT	CCTCCTCGTA	CAGGTAGCTT	120
	GGCGTCAGGT	CCGAGCCGCC	GCCGAACCAC	CACGTCTGCG	GCTTGCCCGC	CGCGTCCCAC	180
	GTCTCAAAAGT	AGCGGTAGTT	GAGGTGCACG	GTCGGCGCGT	GGGGGTTCAC	GGGGTGCATC	240
	ACCAGAGAAA	TGCCGCAGGC	GAAGAAGCGC	ACGCGGGCCG	CCGGCTGCCC	GGTCACGGGG	300
	TCCGTGGGGA	GGTGCAGGTT	TTTGTCGTCG	GCCCCGATGG	CACTGACGGC	TGCCGGCGAC	360
	AGCTCGCCGT	GGACTACCGA	GACGTTAACG	CCGGCCTTTT	CGAACGTGGT	GCCGTGCTGC	420
35	AGCACGCACG	ACGTGCCGCC	GCCACCCCTC	TTGCGCTCCC	AGGAGTCGGC	CTTGAACCTG	480
	ACCGTGTGCA	TCGCCCTCGAA	CGCGGCTGTA	ATCTCGCGCT	GCTTGCGGCG	CACGAGCTCT	540
	TCCATGCGCT	CGCGCATGTG	GGGGGTGTGG	GCGGATGCCA	TTGCTGGGGC	GCCGCAAGAG	600
	GCGAAATNAN	CNGTGCGCC	GGCGGCTTAT	ATAAAAAGCGT	GGCACGGGTG	TTTGTCCCAC	660
	GNCACCANGG	GCTGCNAACG	TCCGCGCCAA	NANANCCAGG	GTCCCGGCCA	NAACACNTCG	720
	GCGGGCGGCC	NAACGCCGCC	NCNCACAATC	ACNCCGACAA	TCGCGCNCNG	GGATTCC	

1221RP

45	GATCTCTGCT	GTTTGGGCTT	GCAAGCATCT	TCCTCGCTAA	CTCGTTCCGC	GTTTACGTTT	60
	GAGGTTCGGG	GGACGTATGC	TANACCAGAG	GCATTGCGGG	GTTGAGGGGA	AGAGGTGAG	120
	ATTATGAATG	ATATATACTG	TTATACCGGC	TGCGGGTGGC	TGTGCGCGTC	ATCACGAGGG	180
	ACTTACAAGT	TCAAAAGGTC	TTCATCGATA	TTTACCAACT	TGTAATAACG	CTCTGTGAG	240
	TCTGAGTTGG	AGGAGCCGGG	CTGGTCGCCA	TACTCCATCA	ACGTGTTTAC	CATTGCGCGT	300
	GTATAGCTGA	TCAGGTTTTT	GAGGGATGAC	TCGCTCTCCT	CCTTTAGGAA	CATCAAAATG	360
	GTGGTGTTC	ACAANCNGGA	AAACCTATCC	TGTTAGTNNA	GAAGGGTTGA	GAACACCGCT	420
	AATCCCTTAG	GCACTCCACC	ATGGTTTTAT	CCGTACCCCA	TTACCCAAAT	TTCCCCCAAG	480
50	TGCCCTTNA	CTTTGNCGAA	CCCCCGCNAA	ATNCCCGTTT	TTAAAACCCN	AAAAANG	

1221UP

	GATCGACCCT	ATCAACGCCT	TGCAGGCTGC	TATGGAGGGC	TATCAGGTCA	CCACTATGGA	60
	CCAGTGCGCC	AGCTACGGCC	AGGTTTTTGT	CACCACCACC	GGCTGCAGAN	ACATCATCAA	120
5	GAAGGAGCAC	TTCTTGGCCA	TGCCTGAGGA	CGCCATTGTG	TGCAACATCG	GCCACTTCGA	180
	CATCGAGATC	GACGTCGCCT	GGCTAAAGGC	CAACGCCGTC	GANGCCGTCA	ACATTAAGCC	240
	ACAAGTCGAC	CGCTACTTGC	TTTCCTCCGG	CAGACACGTC	ATCCTGCTTG	CCGATGGTTA	300
	GACTAGTCAA	CCTAAGCTGT	GCCACTGGCC	ACTCCTCCGT	TTGTCTATGTC	TTGCTCTTTC	360
	TCCAACCAGT	CTTTGGCACA	GATGGTCTCN	TTCAAGGGCA	ATNAAAAGGC	CTTCAAANAA	420
	ATTNNTTNNT	TTCCCAAAAA	ACGGCCNTCA	AANCGGGNTT	CATTCTNNC	CNAAAATTGN	480
10	AAAGGCGCNC	CCATTTCCCC	CTAAATTTGG	GTTTTNTTTT	AAAAACATTCC	CCCCCCCCCA	540
	TTTCCGGGTT	CCCAAAAGGG	TNTTTTNGGG	NCCCTTAAAT	NTTA		

1222RP

15	GATCGAATAA	TAAAAGTGGC	TAATACTTGG	TAATAATATA	ATAGAAAGGG	AAATAGAAGA	60
	GAAGTCAAAT	GGGAAATAGT	CAACGGCGTA	CTAGGTGAGT	GTTCAAGTGC	ATGGAATCGT	120
	AGTCAGAGAG	GTTTATCAAA	AACGGCAGTC	GTCTGATGAT	AGCAGTATCA	CGAAGTGCTC	180
	ATGCGCCCTG	CATACAATGG	CAGGCTCAGC	GCAGGATCAA	ATGGATAGCA	GCGGGCGTAC	240
	CCGCGAACGG	ACTCAGTGGG	TGGAGTGGCC	CCGGTGGTAC	TTGAGGCCGT	TGAGGTTCTT	300
	GTAACGTTTT	CCACAGACCT	CGCACC GGTA	AGGCTTGTCC	TTCTCGAACC	CATGCCCGTC	360
20	TGGATAGGGC	TCGTTGGACT	CCGGGTCCAT	GATGCTAAAA	GTGCCCCGTC	GGGTTTTTCAT	420
	GAAGCTTTTG	ATTCTGGTGG	CCGTGGTTTT	ATGGTACTTG	AGTCCCCTTT	GATCCTGGTT	480
	AGTCTTATCG	CAGCCCCATGA	GGGACNNTTG	AAGGCTTNTC	CCNCCTTGT	CCNCN	

1222UP

25	GATCTCGCTC	AGACCGTCAC	CCACGTTGTC	TGCAAGGGCC	TCCGCCGCTT	TANCTGCCTG	60
	CCACGGCTTG	GAGCACGCTA	GCTGCACGCC	AAACCCGGGC	AGCTCCGAGC	AGTGCGCCTT	120
	GGGCAGCGCC	CACTCCGAGT	TGGTGCCCTG	GATCAGCGGC	ACAGCGAGCG	CCATCTCACT	180
	GTACGTCACG	TCGGCGCCCA	ATTGGCGCAT	CAGGCGCCGG	AACGGCAGGT	TCCCCGACGGT	240
30	GGTCAGCGGA	GAAACGATCT	TCTTGTGATG	CAGGTCCAGC	GGCTTCTTCT	CCTGTGCAAA	300
	GTAGCGTGTC	TCGTGATACT	GGGCGTACAG	CTCGCGCTGC	CGGGCGCGCT	TGTTGCTCAA	360
	TTGCTCCTCC	CGCTGCTGCA	CCTGCGGCAC	CTCTGCGACC	GCGCCTCCGG	GGCCGCCGCG	420
	GCCCCCTGCA	TCTCGTCGCC	GGAACCTCTG	CTGGATGGCG	TCAAAAATTC	ACNATTTCTC	480
	CCTGCNCNGG	AAGGGCCCCA	NTTTTCCCCA	ATNANCNCCA	ATGAACCATT	GNTNCCCCCN	540
	TGGTTNCAAA	ACNAATTTTG	CCCCCCCCCG	AGATTNTCCC	A		

1223RP

40	GATCGGTTTT	CACCTCAATT	CGTTTCTGGT	CGCGCAGTTG	GTGATGCTGC	TGATGCTGAA	60
	GCTGTAATTG	CTGTTTCTGC	TGAGCAAAC	GCTGCTGCTG	TTTCATCCAG	GGATTCTCCG	120
	GAGGAGCTGA	GTCCGGTTTG	CGCCGTCTCT	GCTTGTCGTT	CAACAAGTTG	TTATATAGCT	180
	GGTTCATACC	TTGGGAGGTC	AGGAACTGAC	TGACATTGCG	GTGCCCCGTC	GGGTGGTCTA	240
	GCAAACGGAG	CATGGCCTCT	CTCTCCTGTA	GAGTTTTCTT	TGCCGCCATC	TCAAACCTCC	300
	TAGATTCCAT	TATCAGCGCT	TCTTCTCAG	CAATCTCAGC	CGCCGACCTC	GAAAGCAGCC	360
	TCCGTCAAAT	ACTTCTTCCG	CTGTATTTCC	CTGGTCTTTG	GAATACGCTA	GGATGGTAGT	420
45	AGCGGTTTCC	CCGGGTCTTT	CGCCCTGAAA	TTATTTTTTG	CATACGNGGT	TAAAAATCTC	480
	CCCGTANTTC	CTCCAACGGT	CCTNNANNCG	NCNTAAANAN	ACNGGTCNGT	AAATNATAGC	540
	NNCC						

1223UP

	GATCGCGCGC	TTGAACATGG	ACGTGGACAC	GGCGAAGTGG	CGCTGGAGCG	CGCGCACCGC	60
	TGCGTCTTGG	AGCTCTGTGT	GTGCCATGGT	GCGCTCTGTC	TTGAGCTGGC	GCACAACCGC	120
5	GGCGGATATG	GCCTGGACCC	TACTGGCGGC	GAGGACATCT	GGTAGCGCGG	CCGCCTGCTC	180
	GGACTTGACC	ACGACAGTGG	CGACGCGGAC	CTTGGTGGTC	GGCGCCGTGA	ACGCCGTGTT	240
	GACTGCAAAG	TGGTCCGAGG	GCGCGATGGT	GCCGGGAGGG	AGGGGTTTTG	GTGAGGATGC	300
	GTGTGCGCGG	CGCGACGGCG	AGCGAGATGA	GCTGGCGCTG	CAGCTCGGCA	TCTGGATTGC	360
	GGTCAGGTCC	TGAATCTGCT	CGGTGGTCAG	TTCTGCGTAG	TCTCCGAAA	AACAGGAAAA	420
	ATGGTTGGCG	GCATNGTTCA	ACATCCTTGG	CNCCCTGGGT	TAAAAATGGC	CGAACTGGNN	480
10	GCCGATTTCC	CCGAGAACCC	ATTTGTATT	CCCCCTTCCT	TCTGCNTNCC	GATTTTTTTG	540
	CAAAANTNAA	AACCCCCCCT	AAGAAGANN	CGGGGNNGCC	CNCGGCGGN	TTTTTTTTTC	600
	CNCCCCCA						

1224RP

	GATCAGTAAC	AACCATAGCA	GCCGCACCTA	CGAAAGCATT	CGATACATTT	TTAATAAATT	60
	CGACAGCAGG	TAGTAGTCTT	CTTCCGATT	GCTTTACAGG	CTCGCTAAAG	ATGTGTTTCGT	120
	AGCTCTTCCA	AAGAGAAATT	TGTGTAACCT	CAGAGTCAGC	AGCGGACTCA	AAACAGCACC	180
	TCAACCAAGC	GGTTGACCGC	ATAGGTTTAT	TCAAGCCCAA	TAGTTTTTGG	AATAGATCAG	240
	GGGGAAGAGT	TGGAACATGC	GTAGGGGGTC	TCGGTTTAC	TCGCCTAAC	AGTTTTATCT	300
20	CTACTTTTGA	AAGTAGTTCG	TAGTCCGGAA	GCTCAAACAT	GTAAGTCAAC	AAGCTAGGCA	360
	AAACTGTAGT	CAAGATTGAG	TTCCGCTCAG	GGTTTTGACA	ACAGAGTAGT	TATTCTCTCA	420
	CTCCCCAGGC	AAGATGTACT	GGTATAGAAA	ATCCAGTTGA	AGCCATAACC	AGCTCGTTGT	480
	CACAGTCCAC	CAGAAGATAG	GANACATCAG	GTTGAAGAAT	TCCTCATCTA	GGTTATCTGC	540
	TGCCTTTCCT	GTTCTGCTTT	GGACCAACCC	ACAACCCNAA	AACCAACGCN	AAATCAAANA	600
	CCNGGTTTCT	TCCTTGNTCC	CCCNAAATGA	AANAGGTTTT	GAAANGGTTN	TCCCTCTTGC	660
25	CGGGCCAANT	AAAAAAAAGG	CCCNACAGNT	CNACNATATT	ANCANTCCCC	NAAAAAGGCC	720
	TTCTGNTCTA	A					

1224UP

	GATCGGGTGC	GGCACATGCC	TCATCGGGCA	GGTGGGGTGG	CGGAGGCATA	AACCCACCCC	60
	TGGTTGTTGC	AGTGAATAGG	TATGGGTACA	GCCTTGGCGG	CCACGAATGT	GCGGAGACGT	120
	TTCAGCTGCC	AGAGGGACCC	GACCGCACCG	GTGGACTGTT	GGCTTGGTTG	GACGCTCCAG	180
	GGTTACGAGC	CGGCGCCCTG	CGGAGCACAT	GATGTCGAGC	TGTGCATTGG	TCCAGGTGCG	240
	CACTAACCAT	GCCAAGGGCA	TCCGGCCAAG	GCGGATGGGG	CTGGACGGCG	CCAGGGCGGG	300
	ACGACTATCA	CTAAGAAATC	ATCGATTAAA	ATATAAACTA	CATAAAGTAA	AGGGCGGACT	360
35	GAGTGCACCT	TCAGCGCACT	AGCAGCGAGT	AGCCGTAGTT	GAACCACTTG	CNTGCGATCC	420
	GTGGCACGAA	GCGGAAGTAA	CCGGAACCTC	GATAGTTTCA	AACGAAGAAC	CGAAAAAGCC	480
	TTAAAAATGG	TTACNCCCTA	GGTCCCCCAA	CNGGTCTCTC	TGTTTGGAA	TAGGGTGGGC	540
	GGAAACCCAA	ATGCCCCANT	TGTTNTCCAA	TTCCCCGGNG	GCCCCAATTT	NAATTTCCAA	600
	ACCNATCNEN	ATCTCGGCTG	NATCCCCCCC	NTTGCCCCCC	TCAATGGCCC	CGAACCTTTT	660
	NTGNCCCCCC	CCCAAGGGCC	CTTGNGNATT	TTTTTTCCNG	CCCNCCCGNT	TNTCTTAAAA	720
40	NAAAGCNGCA	TTTTTCAATT	CCCCNGGAAC	NCTTTTTTGT	TT		

1225RP

	GATCCTTTTC	TTTCTTCTTC	CCTCCTCCGA	GGATTCCCTT	TTTGAGCTTG	CCCCTGCGC	60
	CCAACCCACC	GCCTATGACA	CTAGTACCGG	CGGACAGACC	AGCGGATAAG	CCCTTATTGG	120
	CAAAATCGCC	AACCTTTGTC	TCCACCTTGG	TAACAGAGAC	AGTGTAACCTA	GGAGAAAAAT	180
	TGAAGTTCAA	GTAAAGAATA	CCACCGTCCT	CGCCGTTAGG	ACCAGTTAGC	TGGACTTCCA	240
	TTGGGGTTTC	ACTGTCTGGG	TCCACCTCAG	CTAGAGCGAT	GGTTGCGGTG	CCAATGAGAT	300
	CGTCACTGTT	TCCGGCATCC	CAGTCCATGA	CCTTGATGCG	CAGGTAGTTG	TTAATCCGGT	360
50	TATTCACATG	CAGGGATGTG	TTCTCGTTCC	AAACAGGTTT	AAGCGTCTTC	TTCTGGGTTT	420
	TGGTCTTGT	ATATTACCTC	ATCTGAATTG	TCGAGGTTAG	AATTTGACAT	AAGGTCGGAC	480
	TTGCCGTTCC	GGTCAGCAGG	TAGAGCCTGA	CTGCATTTAG	AACCTCCAGT	GTTAGGTCGC	540
	AGTGTTCTGT	TCAGTTTGTG	TGTNGCATCT	CNAACCCAAA	AAGGAACCAC	AACCGTTANN	600
	TCCTTTTNG	ACCCAACCTT	NTTTACAANN	AGGTTTAAAT	TACANTTTCN	ATTTNTTTGN	660
	TGGAANGAAC	CCCNAAAGNGT	CCNCCTGTTT	TACTGANCNT	NPTCCCNAAAT		

1225UP

	GATCCTACTG	GAACCACCCA	CTCAGGAGCA	GGTTAAAAAA	CCAGCCAAAG	TAAAGACAGA	60
	GACAAACGTA	AGCATCCCAA	AGCAGACCCC	TACTCCAAAG	TCTAAGTCGG	CTTCAGCTTC	120
5	GTCTTCTAAA	GTGCCTACAC	CCCTGTCAAA	GCAGGAGCCC	GAAGCGCCGT	CTACCATTMT	180
	TGACGCTCCT	TCTTCTTCCT	CCTCCACTCC	GGTGCCTGGG	CACCTGGATA	TCTTTAGCAA	240
	ATTTAGGAAA	GCATCCAGTG	ACTTTGACAA	GCCCTTTGTG	GCCGAGTCGA	ATGAAGTTGC	300
	CGAGAAGCCG	TCCGGGAAGG	CCAAACGGCA	AACTACTCCC	GCTGCCAGCA	AATTAAGGCC	360
	CGCTGCAAAG	AAAATAAAGA	CGCCCGCGCT	CGATGAAAGC	GAATCTGATT	TTGACCTTGA	420
	CCTCAGCGAC	TCCCAGCCCC	CCATCGCCCC	TAGAAGTAGA	GCCTCGCGAG	CTGTGCGCAA	480
10	AAAGCCAACC	TACGTAGTTG	ACCTTTCCGA	TGACAGTTTT	GTTGATGGAG	ACGCCCAGAG	540
	ATGTTGAGGA	ACCGATACTG	ACGAATCCTT	CCAGCTCTGA	CTAGCACTCT	AGCTCGCGCA	600
	TTGACAGTNC	NCTACCTTAT	GGAGGNTTCC	GAAATCCNTT	GAATACCCCC	CGTTTTTTTAC	660
	TAAAACCCCC	NCTTTCTTTT	TCACCCCCCA	ACCCCCAGGG	GACGAATACT	TTTTTCTTTA	720
	CTTTCTATCA	NGGGGTTTCGT	CNCCNCCCN				

1226RP

	GATCGTCCTC	GCATGGGAGC	ATCAGATGTC	ATATCGGCGA	AGCCTTTCCA	TATGGCGGCT	60
	ACGAACGATA	CGAGTTCGCG	TCTGTCTTGC	GCTGTGTTGG	TCTGTGAGCG	TGCTGTCTATT	120
20	GCTGTGCGTG	ACGCCACACA	TGTGGCCTGG	ATGGCCATCT	CCGGCAGCAC	GGGAGGTCCC	180
	GGCTTCACCA	GAGTCACAGG	CCCCGGCTTC	ACCAGAGTTA	CAGGCCCCGG	CTTCAACACA	240
	GCCACAGTCC	CCAGCAGGGT	CTAAGACGCT	ACTGCAAGAC	TTACTGCTAG	ATAGCAAAAA	300
	ACCGGAGGGG	GCCTCTACGC	CACAGATGCA	GTGCAAGCGC	TACTTTGAGG	GCACATATCT	360
	CCGGGAGCCT	TCTTGGGCAA	ATAGCGTGTT	GCGCATGGCA	GACGACTTTC	TTACGGCTAC	420
	GCAATACACA	GCGAGGCTGT	TGGAGCGGTG	GCGCATATTT	GCTGATTGTT	TCGTTATTCA	480
	GATTTCCGAT	TTTCAAATAC	NCTATCCAAA	CAAAAAAATC	TGCCCAANTT	CCATCAGCGA	540
25	ANTTCCCTTT	TCNTNGGCAA	AAAAAAAAN	NGAGGANATT	TTGCCNTTCC	CCNGAATTC	600
	NCCCGGGAAA	ATTTTTAAGG	NGGNTTTTTT	GNAANGGGC	CCCACCAAAA	NANAAAAGGN	660
	GCCTTTTTTG	GAAAACGGGC	CCTTTTCCCC	GGNGNGAACA	AATTNNTNNN	GGGGACGCC	720
	NGAATTTTC						

1226UP

	GATCGCTTCA	AATTTCCAGC	CGTTGATATT	CAAAGAGTGG	TCACGTTCCG	AAAGATGGTC	60
	CTTCTGTTCC	TCTGTACGTT	TGGAGGGCCG	GCCTACCGGG	GCGTTCGGCG	TTGTCTCCAC	120
	GGTGC GG TGC	TGTCTATGSG	GGACATCCTG	GATGTGTGTC	TGCAACGCAT	TAGCAAATGA	180
35	GTTTTGTAG	TGGTACTTAG	GAAGTTTATA	ATTTAGGCTC	AGTTCTATAC	TGCCGCTAAT	240
	ACTTTGACCT	GGAACAATCA	TCGTTATGTG	CTCACCCTCG	GCGTGTCTC	TAGCGTATTC	300
	CCGCCGTGCT	TCAGCATTTG	GTTGTTCTCT	GATCGTTGGG	TATGGATCCT	CCCACCTCTG	360
	TAGCCAGTTG	GTATCCAGCT	TCTCACCTCG	CTGATGCGAT	TCTGGACGCG	GGGGTTTCAG	420
	CAGGCGTTAG	CAATGAAGTT	GGCGTTGCCG	GTTCAAAAAA	AAANACCGGN	GGGGGCTTGG	480
	TAANCCCGNC	CCTTTAAGGG	CGGCCCCATA	TTNCNCNATN	CCNNNACCGC	NCCCCCATN	540
40	ACGCCCCCAA	AANATNTTTG	AAAAAATTGC	CNTACCTTTT	TGNGGGAGCC	CACNCNCTTA	600
	NATAACCCAT	TTTTTGAAAN	ANGCCNNTCT	TTTNTTTAAC	NCCNCGGTTT	NCNANTATGC	660
	NGGGGCAAAA	TTAAACCNC	CCCCCNAAAT	GNAATCNNTT	TCCCTCNAA	NACAAAAAAT	720
	ATTTTNTNTT	NGGGCNGGGA	AT				

1227RP

	GATCGATGAA	CAGACTGGAG	AACAGAGAAA	GGTGGTGCCC	CTCGAACTCG	AACGGTTTTT	60
	CCCCTCGAT	TTTGATGAGA	TATTACTCCG	GGATACGATG	CAGAGGAACG	CAGCTATGGA	120
	AGAGGAGGAC	TACAGGGAGC	TGGGGAAG	AGATATTGAG	GTGGCGTTCC	AGAACACCGG	180
	CGTGACGCTG	GATGACAGGC	TCCAGTCGTT	GCCGGCCATA	TCGCTCTTCG	GGAGGTATGT	240
50	ACGGGATATC	GACGGGATGT	CGGAAGCGCT	TGCGGACGGG	GACAGGCACA	TCATGGTGTT	300
	TGCGCCGACA	AATGACGCCA	TTACGGCGAT	GCCCAAGAAG	CCGTGGGAGT	ATCCACGGAA	360
	CATCGACAAG	TTGGAGCAGG	CAGGCGCGTC	TGCGAGCGAA	ATCCACGACG	CCATCCAGGC	420
	GAATGTGAGA	CGCTTTGTGC	TAACCCACGT	GGTTTCCGAC	ATCGACCTCT	CTAAGGTGGT	480
	TCGGGAAGAT	TGCTCCAGCC	GTGTTTGACA	AGCGACTTCA	TCCCAAGAGC	ATGCAGGGGA	540
	TATTCTTTTG	CGCCAGGAT	GGCAANGGTT	TTACAGTNTC	NTCCAANANN	GGGCGGACCT	600

TGCCGTTNAG	ANGTTACCCC	CCGCTCTAAC	GGTTTATTTT	GGTINTCACN	CCCCCTTGGN	660
TGCGAATTNG	AAAACCCCTCC	NCCTGNCCCN	NCCCAATNAN	TCNCTTGAAT	CCCNTTTNG	720
GAACCNNCNN	TTNCCCCCAN	CNCC				

1227UP

GATCATTTGC	CGGACCAAGA	AATATTTTCA	CTCCTCGAAG	AGCTGGCCAC	TAAACTTCGT	60
GTCTGGTTAG	GTTCGGCTCC	AGCTGATGTG	CTAGATATCG	AGGTGAGAGG	TAAGCTTATT	120
GAATACTGCA	TGAATACTGC	ACTTTATTGC	GGTGGGAAAA	TAGAACATCC	TACATCGACG	180
ACTTTGATGA	CTGACCATGA	TGAAGACGAA	TCTGAAAGCT	CTGATTCCGA	ATAGTCCAGG	240
CAAGTTAATA	CCCAATGCTC	GGCTTTAGCC	TCAAGGGAGA	TATCGGTAAC	AGCTCTATCT	300
ATGCTGCCAG	CACGTACGAG	TTTTTACTAA	ATTTGGCATA	CAGTTCATGG	TATTTGACAT	360
AAGCTTAATG	TTTCATTTCG	AACACAAGGC	TTGCCGATGT	GTAAAGTGCG	CCGCGTCTCT	420
GCATTCAAGA	CAGCATACAT	GAACCTTCAG	TTTTATACGC	CGATCATGTT	GATTTCTAAT	480
AGGGCTAGTC	CATGGCCCCCT	ACCTATAATA	TACTACCATC	CAGCCCNCCG	AACCGNAACN	540
NNATTTTTTA	TTTTAATNAA	ATTTTGGGGG	NATNCCACAC	NNNCCCTANC	NNGGANNTCC	600
AATGTTTATT	TAANTNAAAA	ANCAGTTTGA	AGGGTATTCC	NNCNCCCCNC	CCCACNGNT	660
TCAAAACCAA	ACNANACCGT	GAAGCNGTN	NTCCCCCNCA	AGGAGNGCCC	CCCCGCTTCN	720
AAAAACGGTN	NCCTTTNCCN	CCCTTGCNCA	ANATTCCCCC	CGCTGCCC		

1228RP

GATCCATTGG	GCCCAACGAT	GCTAATGAAG	TTCTTGCCCTC	CAAAACCCAC	ATTGTGCACA	60
CCCTTGATCG	ACTTGAAGTT	CTTCACCTCT	AAGCCAATCA	GCCTCCCCAT	CTTTTTGAGA	120
CACCTGAAGCT	CAGTCTAACT	GCTCTCGATG	TTGTTAGTGC	GCTGTTAATA	TGTCCAAACA	180
AACGCGATCA	TGGTTGTGAA	GAACGCGCG	TTCCGCATACA	GCGTCAGCAC	GTAGCCCAGC	240
GGCCCCGCGG	GCCCCGAAGAT	CACTGAGATC	GGCAGGAACA	GCGGCGTCCA	CAACAGCACC	300
AGAAATACCA	AAATCGCCGC	AAACGTTATG	ATGTACAGGA	TCACCAGAGT	CACCGCCTGA	360
ACCCAGATCT	GCCCCGTGGCC	CATCCCGACC	ACCATCGACT	GCCTGAATTA	GTATATTCCG	420
TCCACCTGCT	TGTTTTCATAC	ATACCACCCC	AGGGCACACC	AGGCGGTAAC	AACCCCAAAG	480
GNGTCCCTAG	GGAGCGCATG	CAAAATATCC	ACNCTCCGCA	TGGCATCTCC	CNNTTGGA	540
GGGGNCCCCC	NAAATTTGGG	CCNAAANCCC	TTAAAGGNC	CCTGTGNCCN	CAANNACTTC	600
NAATTTCCCG	NTTNGGCCCC	CCCCCCCCTC	CAACGGGATT	TAAAACAGGN	GGGNGNGGGA	660
AAAACCCNCG	AGGGGNTTTT	TTTNGCCCCCT	TTCCGAAANA	ANCCNCCCCC	CCNGGGAAAA	720
AAATATTTTT	TTTTTNGGG					

1228UP

GATCATGCCA	TTCTTACGCT	TTGCCACAT	GGACGCCCAA	ATGAATTTCT	GTGTATGCGA	60
GGATGCTGAC	GATGCAGCTG	AAGCAGGAGA	CGACAGCGAT	GTGACGCCTG	GTTGTATGAC	120
GCCTACTATT	TCACCTGTGA	ATACTGTTC	TTGGCCCTCT	GTAGACATAA	TCTTGTTAAG	180
GACAAAGCTC	CTGCTGTGCG	TGTGTATCAG	GTCAAGTAAA	GTAAGCGCCT	TAAATGCCAA	240
TTTGAGAGATA	CCGAAGATTA	AGCATGCCAA	ATCGTTAGCC	GCCCTAAACT	GCCATGGGTG	300
ATGCTGGGAA	CAGGTAAATA	TGGCCTGAGG	TGCTGTGTAC	TTACCTGATA	TAAAAGTATG	360
CAGTATGCGG	GGCGCTTCGT	ACGTTCTGCT	GTAGTCTATC	GGATCCTGGA	TAGATGTTAG	420
TTTCATCGGTA	AATGGTTGGA	GATAATTTTC	GTCTTGCGAG	GCCTGTATAG	TAGTTTCCCTG	480
TGTTTGAATA	TTTCATGAAAT	GGTTGGGCTA	GCTTTTCAGCA	GCTGCTTCTT	TAGTTCTTGC	540
TCATACTGAC	TTCTTTCGAG	ATCTACNCCA	CCGCNTTGGG	GCTGACCCCA	GCACACTTAT	600
GATTTTANA	AGGAATCCCC	GTAATCCAAN	GCCCTTNCNT	ACCCNGTCCC	AATNGTTNCA	660
TCAAAAANGTC	ANNCCCTCNA	TTTCCNCTTT	TCTCNCCAAA	ACNCCCACNT	TAATTGAANA	720
NGNCCNTTTC	ACCGCGAGAG	GTGGCGNC				

1230RP

	GATCCC	GGCGTCTGGC	GGCATAATGT	CTGCCGTATA	GGTGGACTCT	GGCTGTATTG	60
	TCCGCAGGGG	AATGGCATGC	TTCTTGTAGA	AATACAACCG	ATCATAGGGC	GAGCTCATAT	120
5	CCACCGTACG	TCGCTGGGAC	ACGTACTTTT	TGACTGAGCC	ATCATTCGCG	CTGTTTCATTG	180
	CGACTCTAAT	CTGATTGAGA	ACCCTGACCT	CTAGTGCTAT	AGCGCAGGGC	GTACCTGTCT	240
	GATGATGCGC	TTTTCAATGC	TCGAGCGTGC	GCAGTGTTAC	ATCGATCGTC	GCGGACGATG	300
	TTTAAGCAGG	ATGCTGAGCT	AATATGTATC	GGTATAGGCT	ATTGGCAGTA	GACCTGGGTA	360
	TATACGCCTA	GATATGGACA	AGATGCTGCG	CCTAGACATC	CAGAACTTAA	CCAGGCTCGG	420
10	GTTAAAGCCA	CCCAGATAAC	ATTTGAACAT	TAGAACAATT	ACCACCGCGA	ATGGAGGGGA	480
	ACCCAGTCTGA	AACCCACCGG	CATCCAATAG	TTTCCCCCAA	CNGCGAAANG	GCAGAAATGCA	540
	CCGCCCAATG	CTGCCCCAAC	GCCCCACGGC	ACCCTGACCC	CATTGACCTN	GAAGCCCTGG	600
	GGCNAAAACG	CATTTTACCC	CCCCCATTN	GGAAAAANTG	ACCGAATAAA	ANNCCCCCCN	660
	AAAAANAAAN	GGCCNCCCCC	AATTACTTTT	TNNCCNNGGG	CCCCNAACCC	CNGGGCINNAA	720
	AAAANNANTG	GGGGGGGGTT	TCCGNNNTTT	AAAAGG			

1230UP

	GATCTTCCGC	TCCACTTGGT	TGGGCTGGCG	CATGTCAAAG	GTTAGTAAAA	GCCCCGAATC	60
	GTGTACTGAC	GCGAACTTGT	TGGATCTTCC	GGAAGAACAC	AAGGACGTAT	CCGCGCCCAA	120
20	GGACGCGAAA	TCATAGGTCG	GCATCCACTT	TACATCACGG	ACGGAATCTG	AGCCTGAATT	180
	GAAATTCAGG	TCGCTGCGGT	TCACCTTGTA	AGAGTGCGAC	CGCAAGTCCC	ACACCTTGAT	240
	GCAGCCGTCC	TGGCCACCGC	TGATAAGGAG	ATGCGTCTGG	CCCATGTTGA	AGTCCACGCT	300
	GTGATGGAA	CGCGAGTGCT	CCGACAGGGT	CCGTGATCAG	CGCGGAATCC	TTTGCCGACG	360
	CGCGGTTGAT	ATCGTAGATG	GAAACCGAGG	TCGACGTCCC	GCATATGGCG	ATGTAATTCT	420
	TGTGGTGGTG	GAACCCCGCC	CTTGACGTCC	CGAAATCCGT	GCTAATCTTG	CGCCATGTTT	480
25	CCGGCGCCAT	GCTGCTCGAA	GAACCTCGTC	CCCGCCCGCC	AAGGNTCCCC	NGTTGTTTNT	540
	GTTATTCGGT	GCACCTGCT	GCTCCCTGTA	CCCTCCGTCN	AACCTGTTCA	GCCCCAATGG	600
	TCCTTCCCCN	CCCCCNCAAC	CATGCCCCCT	ANCTTCTTTG	ATTTTTTTCC	AACCCCTGCCA	660
	CCCCCGGTTG	CCTGGAGGGG	GGGTACCCCC	CCCCAAAACC	CNCGCCCCCC	CAATTNTCCC	720
	ACGCCCNCCC	GAATTTGGTT	TNCCTNNGGG	NCCCCCNNGG	GNCCNNAAAA	CCTCCCCCTAA	780
30	AGNA						

1231RP

	GATCATCTGC	GTGAAGGGCG	ACAGAAGCCT	GGCGATGGAA	ACATTGGAAT	TGATGCATTA	60
	ACGCAAAACAC	ATGGGTCAAT	TCCTCAAACCT	CAACAGAAAG	GGGACGAAGC	TGCGCACACA	120
35	GTGCTGCAA	ATCTTTAGCC	GAGTTCTGAA	AATTCAAAGT	CGGTAGTTCT	CGTATGTTGA	180
	AGCCAGATCC	ATAAACTATC	TTCTCACTCG	CCGGATGCAA	AGTATCAAGG	AATAGGCGAC	240
	AATCGGTAAT	GATTGGCTCG	AGCTCACGCA	GATATTGGCG	CACCTCTGAT	ATCCGTGGGT	300
	TGTTTCGATG	ATGATGCACA	TGAATAAAAG	GAAGAAGCTT	CGAAAGAGGT	ACACGGCCCCG	360
	GGTAGCCGTG	TGATGAGAGC	TGTTAGTTTCG	GCTTCAACAT	CAGCAAGTTT	CTCTATAGGG	420
	GACGCAGGGT	CGTCAACATC	ATTTATTAGA	CACCTCCAGC	ATTTGTTCTT	GAAAAAAAGT	480
40	NGTGATGNA	CAATNGCNCC	CCCCCTTTT	GAAANGCCGG	AGAAAAATTC	CCTNNAANAC	540
	NAATNTCTNG	GTNNAANTGC	TTNNAANCC	CCTTNAATTA	AACCCCTTNNN	GCCNCAAAAA	600
	AATNTNTTAA	ANCCCTTTNA	ACNCCCCGGG	AAACANAAAC	CCCCCCCCCA	AAAAAAAACA	660
	NGTTTTNTCC	NCCCCCCCCC	CCCCCGANNT	TTTNAAAACC	TTTNAAAAT	CCCCCCCCCC	720
	CNAAAAANCC	CNCNAATTTT	TTTTTTAANC	C			

1231UP

	GATCGTCAGC	GTGCATCGAC	TTGGCATTGC	AAAGGGATGT	GATCCCTGAG	GGGAGGCTTG	60
	CAGCAGGCGC	GCTCCTTGTT	TCACATCATA	GGCTGTGAG	GCCGGACTGA	TTCAGCTCTC	120
5	AAGGCGAGCA	CCCTCCCAAC	GCCCAATAGG	GGCCCCCTCC	TGGGCTGTGC	ACGGGAATAC	180
	CTCAGACACT	GCGTTAAGAT	ATATGTATTT	AAGAGGGCAC	CAGCTGGCTA	TCAATTGCCC	240
	TCTCTGCTCT	TGTTCCAACA	CCAGGCAAGT	ATCATGATGT	CTGCTGCAGG	AAAAATGTTT	300
	AAGAACAACG	GCCAGAAGGA	TGAGCGGAAG	AATGCGGGCC	AGAGAGAGGA	GCGCCAGTAC	360
	AGGGTCGGCG	ATGAGCAGGG	CTTGGGCGCG	CAACAGCAGG	CTGACTTGGG	CGCCCCAGTA	420
	CCAGCAGGCG	CCACGCTCGC	AGCAGTTCGA	CGACACTTGG	NGCTTCCCN	CATTTGGGCC	480
10	CCCCACCAAT	TGGGNCCCCA	GCAAAATNGG	CCCCNCNNCT	TTNATTTTNG	GGGCGAATGG	540
	GCCNAAACCT	ATCCCCAANT	TGNNGGNAAC	TCCCCCCCCA	GNANGAGAAC	NCATTTTTCG	600
	ATTGGAACAC	NCACCTTNNN	TTTGNNAACG	CCCCCCCCNA	AAAGCCANGG	GACTGTNTTT	660
	TTTNGAAAAAC	GNCCCCCTTT	NTGTCNCNNN	ANAAATTTT	CTANAAATTTG	CGNGGATTCC	720
	TCCCTTGGGG	CCATTCCNTT	TTTACCCTTT	TAACCCCCC	CC		

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1232RP

	GATCTTATTA	ATGAATTTTT	CCCCACGAAG	CTTGTGCAAT	TTTGATTCTA	TGCTTTGCAA	60
	GCACTCAACT	TGGGCTGTGG	TCATGCGAAA	CTAACACGCC	GCGAAACAGA	TACTGCCCAA	120
20	GCGTTAGCAC	TCGCTCTTTG	CGGTGCTACA	AACAAGTGTC	GAGCATTAGC	GTGTGACTTA	180
	TTTAGGGTTG	GAATATACAA	AAGTAAGGCG	TACATGCCGA	TATCTCTCTT	GTGTTGCTCT	240
	CTCTTACCTA	CATCTAGATG	TATTCAAGGA	ACTTCCCCGC	GAGATTACAG	GCCAAGGCCG	300
	TCCAGCCCGT	AAAGTGCTGC	ACCCGTTGAC	CTTTCCATCG	TTCTGGTTGT	ATTGTTCCGGT	360
	AACAAAAACC	ACCTTTCCCC	AAANTCNAAT	AATTGNITCA	ACAGGTTGTT	CCCCCCATTG	420
	AAAGGGATAN	NCGTTTAAAC	CCGGNCNAAA	CAANNAANGG	GNNGNTTTTT	TTGGGCANAA	480
	ACCCCCCCCC	NAATTNAACC	GCGTGGGGCC	CTNCNCNAAA	TTNTTTTTTT	CCCCCCTTGG	540
25	GGNCCCCNCC	NAANAACCCC	CGNNGTTNNA	ATATATCCCN	CTTTTNCCAG	AAGNGANTCC	600
	CCCNNAACCC	GNNGNGATNT	TTTTGTGNTT	TAAAAANNCC	CCCCCCCCC	CCNGGGAGGG	660
	NNTTCCNCNC	CCCANCATTT	NNACCNAGGN	GAGTTTTTTT	TCCCTCCCGG	GGGAAAAAAC	720
	ANTGTNNNTT	TTNNNNCCNA	AAAAAA				

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1232UP

	GATCAGTTTG	CCGTAATTGA	TACAAAAGGC	AAGTGGTGCG	TGGGCGACGT	TGCGAGGAGT	60
	AAAAAGAAGT	CCCGGCGACT	GCGCTTGTTA	AGGAAGTTTA	GCGGGACTAT	TTTTGACCCA	120
	GAGGAGTACT	CCAATTGGAA	TATGATAGAA	TGGTCACATA	TTCACACAAG	ATTGCTTGTG	180
35	ATGAATAGGT	CAACTTTTAT	GGAAATTGAC	TTTGTAGACG	GATGGCAGCA	GGAAATTGTC	240
	CAAGCAAAGA	CGTGGTCTAA	CTTGCGCGAT	TTTAAACGCC	TTTCCGATGA	GAGCAGTGTC	300
	CTACTCACCT	GCAAAGAGAT	TATATTCTTA	GACCACAAGC	AGCAGGGAAC	AAAGAGGGCG	360
	CTATCTTGGA	AACACAATTG	GGATAGCAAA	GATTCATCTC	TAAAGCTTGC	TATACACATT	420
	TCTGGCAGCC	ATATGAAACA	ATATTTACAT	GCATTCTCTA	TTCCACCATG	ACTCCCTGCA	480
	GTGCTTATGT	GTCTTCTTTC	CCGGTCCGAA	AACACTTTCC	ATTTTTCCAG	CCATCCCCC	540
40	GCTGNTTGTT	TTTTNCCATT	TACACNCCNG	NTTTTACCGA	AATTACCTCC	CCNTGTNCC	600
	NAGAAACCGA	GTTTNANAGA	ACCACACCCC	CTTTTCAATTC	CCTANNTGTG	CCCGCCCCC	660
	CCAGGGCGAG	AGTTTTGGGN	CCCCCTTTT	NTGNACCATN	TTNCCCCNCC	CCNCNAGGGT	720
	TCCCCACCNT	AAAANCCCTG	AAACCCCTTT	TCCCCCCAC	ATTTTNGGTN	GGGGATN	

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1233RP

	GATCACAGTG	CTGTGGGCAT	TGCTGCTCGT	CGTGCTCTTG	TGCCCCCTCAA	GCGCCGAAGT	60
	AGACAAGCTG	CCAGCAAGCA	CTGATTGGTA	CAGGAGCTTT	TTGTTTACGT	TCTTAAGCAG	120
	GTTTCGCGTC	GAGTCCGCGT	TGTTCAAAAC	AGCGCCCGGC	TGCACGCTCG	AGCTCGACTC	180
	CCCCGCCGGC	GACGAGCCCG	TGGAATACAC	CTCTGATCCC	GGGTGCGCAT	CCCTCGCTCT	240
50	CGCAGTCCCC	CCGGAAGCAA	AAAATTCCTC	CACGGATGTA	TTCCCGTGGT	TGCCCAGCTG	300
	CGCACCGGGC	GTACCCGAG	CGCTGTTGAC	ATTGGACGTG	ATATTCTCCA	TCAGCAGCTG	360
	CGAGCTGATG	CCCCCTCGGG	CGCCTGTCTT	GCTCGCATCT	GTAACGTCGT	CAGACCCCGA	420
	GTTTTGTTCT	GTCGTCCACG	AACGAGACGT	TCAACCATGT	GACGACGAG	GCGCGTTTGG	480
	CCTTCAACAC	CNNATTTGGG	CCTTCTGTCT	GGAACNCCAA	CCCCGGGAAT	TTCCCAACCT	540
55	NTGATTCCCN	AANTGCCCGG	CCNCCNTCCC	AAATTANAAT	CCCCAATTGN	GNTTGAAATN	600

EP 0 866 129 A2

GNCNAAATNA AACCCCNNTT TCCCCTNNTN CNNNNCCCNG GCCCNAANGA GCCGNTGGGG
GNTTAAANNC CCCNACCCCC AAANTTATAC CCTTTTTTTG NNCCCNCCCC CCNNCCCTNT
TTTTTINCCC NTCN

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720

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EP 0 866 129 A2

1233UP

5	GATCCAGCTT	CCATATAAGC	TCGTGTTTGC	GGTCGCGACC	TCTACAGAAG	TGGTGATATA	60
	TGATACTGTT	ACCACGAAAC	CCATTGCAGT	GGTGGGAAAT	TTGCATTACA	CCCCGCTAAC	120
	GGACCTCAGC	TGGTCTGACA	GCGGCCACCT	ACTCGTCGTG	TCATCAACAG	ACGGTTTCTG	180
	CTCCTATATC	TCAATGGAGG	ACAGCCTATT	TGGCGAGCCA	TACAGTTCCG	AGGCACAGCG	240
	GACGGATTCT	CTCATACCTT	CGACTCCAAA	AAGCAACATC	TTCAGGAACA	CCCTGCGGTC	300
	CAACCCGGTC	AACGTAAAGC	GGAAGCACTC	TGTAGGCGGC	CACAACGACT	CACCCATAAA	360
	GCGCGCTGCC	AAAAAATGTC	GCCGCTTTCC	CCTGTGGTCG	TCGATGAGGG	ATCTGCGCCG	420
	GCACACAACC	GCCTACTCCT	AGCAAAGATC	TCAAGCCTCC	GAAGGCGCAT	CCAACCCGTC	480
10	CTTGTTTAAT	GACAACAACG	GCGGCACCTA	GTATCCCCNC	ACGCCATCCT	ANAAGTTTNG	540
	ATTCCNNTAT	ACTNAAATAC	AAACCCGANA	ANCNNTTTTC	TTGTTNACAA	ACTTTTTTTT	600
	GACCTGCATC	ACACTATCCC	GGNGNGGTCA	TTCTTGCCGA	ATGCCCCCTC	CCCCTTANAA	660
	CNCCCNNTACN	TAAACCTTCC	CNCNTCCATA	TTTACTCATG	AATCNCNGCG	AANTCNCCTGC	720
	GGATCNCNCCA	NCTTTTGCCT	AGTNTTCCCC	TTTTTGTTCC	C		

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1235RP

50	GATCCTTGAG	AAGCCAGATA	ACGACGAGGA	CGAGGAGCCC	AGTGACGATG	AGGATGCCGA	60
	CGACTACGAC	TCGGATTCTC	CCCGGCCCGG	CGACAGCGGC	AGCGAACTCA	GAGACCCTCC	120
	TGCGCCGGCG	ACATTCTGCTA	CGGAAC TGCA	CGGATCCAGC	GTCTGGCCT	CCCCGTTGAC	180
	CTATTCCCTTG	CGCTCCGTCA	TCGTCCACTA	TGGCACACAC	AACTACGGAC	ACTACATTGC	240
	CTTCCGCAAG	TTCCGTGGTG	TGTGGTGCGG	CATCAGCGAC	GAAACAGCGT	ACATCGTCGA	300
	TGAAGCTGAG	GTCTTGTTCCA	CACCGGGCGT	TTTCATGTTG	TTCTACGATA	TGACTATGAC	360
	GAGGCGACCG	GGCAGTTGCG	TGACGACTTG	GGCTGCCCTAC	AGGAGCCCA	TCCGTGCTGT	420
	CAGATGGGGA	CGGAAGAATA	CGACTCATTG	ACCGGGTCCA	CCAAGACCTC	GATTCAACGA	480
55	NCCAGCTGTT	GCTCCCGCCA	ATAAACTTTG	TTTGGGGCTG	GCCGGCCATA	TNINCTCCAT	540

GCATGTTTCAT GCCCCCACCG GACATGTTTG ATCCANATAC TTTTGTGTTN GTTNCCCCCT
 TTCAGNGNTT CCCCCNAAGC AAGATTCTTA NNCTACTTGC CTNGTTGTTT CCNCCTGGTT
 TGGNACCCCA AATTCCCTNTT NNCCNTTINT GGCCCANCCC NNGGNAAACC CNCCCTTTTT
 TTTCAAACCA GGNTTNCCTT TTTNGCN

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1235UP

GATCACACCC GTGTTCTTTT CAAAGGTGAC CTGCAACTTC TTGTTATTCA AGATGATAGT
 CTCACGTGCC TTTGACACGC TAGCAGGGTA AAATACCGAC TCCTGCGCGT CAGCGTTTTT
 TGCAGCCATG TTATCCCAT TCAAGGTGCC TATTGGGACC AAACCTTTCCC CTCTGTGTT
 CAAGGCCTCC AAAAGCTCTCT CTATGAACCG ATCTGCTAGC TGCACGACCT TGTTAAGCAT
 TGGTATTGCT TCATATTTGT ATACCATTTT TATACATGTC CCGGGAAGGA CATCGTGGA
 CTGGCATAAC AAGATATCTT CCCATAGAGC GTTAATATCA TTAACAGGGT ACGTGACTT
 GTTAGGCGCT AGTAGCGAAA CCTTTGTGGC AATCCACTCC AAATCATGGA TCTTAACCTC
 AGATAGTCTC ATCAACCGTT TAACGTCTGC CTGTGTCGTA TACGTGCCTC CTATGGAAAT
 CAAAGTTACA ATCCGCCCCAT CCAAGTTGGC CAATGNGTTC CCANTGTCTG NCTTCNGCAT
 AATATCACCG TAAAAACCGT TTANGGAATC CCCNACCCCC NACCTTNGGG AANAACATTG
 CATTCCCGGT TAAAAATGAA CCGANACCCC CCATTGTGTC CACCNCCCCC TGTTTGAACC
 CCNCCCCCGN CNCCGNACCC NNAAAAANAA CCGTTGCCNA ANGTTTCATTN AAAGTTTTGT
 TCCCCCGGG TTTAAANCC NAATTTTNAN AAGCGTTCTT TTTCCCGGGG GGGTTG

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1236RP

GATCTCCCTC CGGTGCAAGT ACGTCGACTG TTTGAGACTC TGCAGGTCGT CTTTTGATAG
 CTTGATGCC TTAGCTCCCA TGTCTACTAT AACGCTGTCC CGGCCTCAG CTATGTGCGG
 GCTGCCTATC TTAGTGCCTA ACTCTTGGAA GCGTGAGAGG CCATAAGCCA CGATCGGCGA
 GCTGCTCAA TTATGTCTCT TGAAAGCGGT TGCTGGGTCC ACTTTCCCAG ACCCAAGGCT
 ATGCCGGTTA CCTGACCTCC GGTCCGGATG TGACGCTGGG AGGCGGTGCG ATGCCGGCCC
 TCATGGCTGT CGGTGCGGAA GGACTATCTA CCAGGGACTT GGCTGCCTGC GCAATTTGCA
 CTGCAGCTTG CAGTGGAGGT CTTGGCGAAG CTCACCGGCA GCGGCAGGCA GTTACAGCCA
 TGGCACAGGC CAAGCCCCGC GAGTTGACCG GAGTTGGTTG CCAGATATTG GGCCGTCCAA
 ATTCTGANTA GCCCTTTATA TNAGANCCCC NCCGTTGAAC CCAAGNTTT TTTATGCGGA
 TGTTTCGAAT TCNGCCCCCT GCGTTAACCC CCCCCGAACC CTNCCCCCG GCAAAANCA
 ATCTNCCCC NGTTCNAAAA ANCCGAACNC NNAAAATTTT AAAAGAGACA AATCANNNCA
 CCCGNGAAAA AGAGCCCTNT CTTTGTGAGAA TTCCCGGGG GGGNGTAA TTTNAACCTT
 GA

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1236UP

GATCTTCGTC CGCTTGCGGT CAGGAAATTC AAGCGGGATG AGCTCTTGTT TCAGTTTACC
 ATAAAAGAGC TGTTTTACAA GGTGGAATTG CTCGCCCTCT TCATCCAAGC TGAGCGGGAC
 GGACGCACTC TCAATTTGGT AGAGGACGTT CCCAATGCAT TCCGTACAT CTTGCTGTCT
 GCCAATCTCC AATGTGTTTT CTAGCTGGTC GGAACATAAT TTCGCAACAT AGGTGGAAGT
 TTCAGGGCCT TCGGCCTCTG GACTCCCGAC CATGGTGATA TCTTTACCTG AGTCATCATT
 CTCAACAGCC TGCCTATCCT CAAGCGGACC TGCGCTGGTG TTTTACCCN TTGGGNGGNN
 GAANTCCAAT ANNCCCCCTT TCTGGGGTTC TTGGAAAGNA TTNGGANAAT TTNNTGGCCC
 GGTTNTTACC NTTTTNGANA GAGACCCTTG GNNNTTCNAN ACCNAAATNN TCCCNNGGGG
 CNCCCGCNCG AATNTTTTTN TNTCCAAANT TTCCNAAANN CCNCTTTINT GCTTTTCCCC
 NTTTTNGNGG NAGCGCCCCA GGGGNGCCCC CGAANTATC NNGGGGNTGG AAAAAANAAA
 NAATTTCCCA NAGGGGTNTT TTTTTTCCN TCNGAGAAGG GNGGTTANAA AAACCCATT
 TTTCCCCCN NTAGANAACC CTTTTTNCNC CGGGGGNTCC NGCCGGGGGG ATTNNTGNGG
 GNGCNTGNN NACCTCCCTT CCCCNCTATA NAAATNCCCC CGGGGGGGG TTNNTTTTC
 CCCNNAAN

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1238RP

	GATCACGGCA	ATGAAAAACT	ACGCAAAACGT	TACAGACTTT	GAGTGGTACA	TCGCCCTGCT	60
	TTCGGATCTC	TGCATAGTCT	CCCAGGACCT	GCAAGACAAG	ACCCTCGCGC	AGAAACTGGG	120
5	TGAGCAAATT	AGAAACATCA	TGGTGAAGGT	TCCTGACCTG	CGGGATCGCA	CTTTGGCGCA	180
	GATTGTGCAG	CTGGTGAAGA	GCGAGGACAT	CACGGCCCGG	CTGCCCGGTG	TTCTGAAGGA	240
	GTGCATCTGG	TGCCTGGGCG	AGTATTCGTC	GTTGCTCGAC	AATAAGGATG	AGTATATTCT	300
	GCTATTGGCA	GAAAATTCTGA	AATTATATGA	GCCTGAACTA	CAGCAAACTT	TGATCCCTGC	360
	CATTTTGAAG	ATTTATAGCA	ATTGGTGTA	CGAGTCGGTG	GTCGACACGG	GTCCGTATTA	420
	AATGGGTTAC	CGAGCGGATA	ATCACCCAC	TAGAAGATCT	AATAATCTCG	AAGAACTTCG	480
10	AAGTCCAGGA	GCGGTCTTCC	GAGGCTCTCG	AATTCTACCC	TTNTTTCTGG	ACNCCCCCTC	540
	CNAAATNNTC	TGNATCCCTA	NCNGCTGGCA	NCTTACNAAT	TCCTNGCCCA	NTTCTNCAAC	600
	CCTTTGAATT	NACCNCTNNTN	CCNTCGGGCC	CCCAAAAANC	TCNNNNNAAA	CTNTTNTTCN	660
	ATGGGAACCC	CCTTTNCCCN	AAANGAAGCC	ANANNNNACC	GNAAAACNCN	CTTGAAGNGA	720
	TTTCCCGGAG	TTTTGANAAC	ATTTCNCCN	AATTTTCCGG	GACGGCCAAA	AAGGGTTTTN	780
	CAAAATTANTT	CGGGGGGGGA	AGGGGAANGG	GGGGGNGNNA			

1238UP

	GATCAGAAAC	GGCCGGCTGC	AAGAATGGAT	GGCGATGAGC	TTGAGCAGT	TGAGGCATCG	60
	CTTATGCAAA	AAAAGAAATT	CCTCAGATCA	CGTGACAAAG	TTTCGTGATC	TCTAAATGTC	120
20	GACGGTTGGG	CGAAATGTGC	CGTCCTCTGC	TATAAAATAT	AAACTAGTTT	CTCTACCACT	180
	AGACTGATTG	GGAATATCTA	AGCTTTCAC	TGATAGCAGC	AGGAGCACTT	CATAATCCAG	240
	TACCTTCTTT	GGCTTATCCA	CACTAGTCAT	CTCATCGAAA	ATGTCACAGC	CAGTGCAGAG	300
	AGCCGCCGCT	CAATCCTTGA	TATCCAAATA	TGTCAATAAG	GAAACGCTAA	AATACATGCT	360
	TACAACGCAC	TTCTGGGGCC	CCGTATCGAA	CTTTGGTATT	CCGATTGCTG	CGATTTATGA	420
	CTTGAAGAAG	GACCCCTGAGT	TGATTTCCGG	CCCCATGACG	TTGGCGCTCG	TGGTATACTC	480
25	AGGTATTTTC	ATGCGTTACT	CGATGGCCGT	CACTCCCAAG	AACTACCTCT	TGTTTGGGTG	540
	CCCACTTTAT	AAACGAGTCC	CGCGCAACTC	GGACAGCGTT	CCCCTGGCT	CAAGTTTCAA	600
	TTACTTCCGC	GAGAGCCCTG	CTGTCAAGGC	ACCCGAGAGA	CCCGCATAGG	TGCGTTTGCG	660
	TCCGCACACG	TTGCATTACA	GCGTCGACCA	CTACATAGAA	TATTATTAAG	CCGACTATCC	720
	TACACGTTTC	TAGAGCTAGT	CGAGATGCC	TTGGCTGATA	CTGCTGCGTT	GGGCCAGGCC	780
30	GTATCTTGCT	CCTCCTGGCT	TTGCTGCGTT	GCGCAGCTCC	CANTTGNCCG	TTNCGATNN	840
	TCCTGTGTCC	CGTATCCATT	GNCTAAATGT	CTCCC			

1240RP

	GATCTTAAAA	TAAGATAGAA	TGGTAATAAA	TATCATTCAG	GTACAATAGA	TGCTGGTGT	60
	ACTAAAGGAT	TACCTGGAAT	ATAATTATCA	GGATGTCCTA	AAGTATTAGG	TGAAAAGAAT	120
5	ACAAATAATG	AAAAGAAAAT	TATAAATACA	AATACTGTTA	CTAAATCTTT	AAAAATAAAA	180
	TAACCATGCA	TTGGTAATCT	ATCTAAATTA	CCTGTAATAC	CTAATGGATT	TGATGAACCA	240
	TGTACATGTA	ATAGCATTAA	ATGCATAATT	ACTATTGCTG	CAATAATAAA	TGGTACTAAA	300
	TAATGAAATA	GAAAGAATCT	TATAATAGTA	GGATTACTAA	CACTAAATGA	TCCTCATAAT	360
	CATAGTACAA	TATCATTTCC	AATAAATGGA	ATAGCACTAA	ATAAATTAGT	AATAACAGTA	420
	GCACCTCAAT	GTGACATTTG	TCCATATACT	AAACAATAAC	CTAAGAAAGC	TGCTGCTATA	480
10	GTTAAATAAA	AGATAATAAC	ACCAACTGTT	CCATACAATA	ACTCTAGGTG	ATTTATAAGA	540
	ACCATATAT	AAACCTTTAC	CAATATGAAT	ATACATACAA	ATAAAGAAGA	ATGAAGCACC	600
	ATTAAGAATG	CATATATCTA	ATTATCCACC	TATTGTACTC	TCTCANAATA	GTTCCCTACCT	660
	GATGANAAGC	TATCCATATT	ANAAGAATAT	GCATACCTTA	AAAATACCGT	TANAATTGAA	720
	TACTAACATA	ACCTATAANA	CCNAATTCAC	CATAATAATG	AGAGGGTGAG	GNGAACCATTA	780
	CNTACNATAC	TAATTTAATT	ATTGATTCT	TTCCCNTTTT	ATTATTAAAT	TTTAAT	
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1240UP

	GATCTAGAAT	TATTAAGTCA	ACTATTAACT	AATATCTATA	ATAATAATGG	TTTATCATT	60
	AAATCATTAA	AGATAATTAT	TAATAAATTA	CCATTTAATA	ATGATATATT	ATTATCAAAA	120
20	AATTATGTTA	ATAAAATAAA	TAAATATAAT	TTACTAATTA	ATAATAATTT	AAATAATAAT	180
	AAAAAAGATT	TAATTAATTT	ATATACTTTA	GATAATAAAT	TATTAGATTT	AAGTATTCTT	240
	AATAATATAT	TATTAGGTAA	ATATTTAGTA	GGTAGTAATA	TCCAATTAAA	GGGTAGACTA	300
	TTAAATAGAA	ATATTACTAG	ACTAATAAAA	ATAAATATTA	TGAAAGGTAC	ATTTAATAAT	360
	TATATATATC	AATGAAGTAA	ATTAAATAAT	TTATATAAAT	TAAATTATAT	ATCACTTAAT	420
	ATTAATAAAC	TTAATAATCT	ATTTATTAAT	AAAAATGGTA	TATTTAATAT	TAAAATTAAA	480
25	TTAAATACCT	TTTAATAAAT	ATCTATAAGT	AATTTCTTAT	TTATTTTATA	ACATTTTAAA	540
	ATGTTTTATG	TTTAAATAGA	TAATAACAAT	TAAATAATAA	AAATTAAGAT	GCCACAAATA	600
	TTCCCATTTT	CCTTTATGAA	TCAATTACTT	ATGGTTTCCT	ATTTATTTTA	CTATTTTATC	660
	CTTCTATCTT	ATGNTTTTAA	CCTAAGAATT	TAANAATATA	TACTCCTAAA	TATATATTCC	720
	NAAATTATAA	TAGTTATTAA	ATTTTAATTA	ATCCANTATG	ATCCNTATTT	ATAAATATAT	780
30	AAGAANATTT	TAATATATAT	ATATGAATNT	TATATCNCN	TGAACCATTG	NAATNNATTA	840
	TAGTTTACAC	CCCCATANATC					

1241RP

	GATCTAAATA	TATATAATTT	AATTTATAAA	GATTAATATA	AACTTTTTTA	TTATAATATT	60
35	TAAGTATTAA	ATTATTTTAA	CTATTATTAT	CATTATTTAA	TAAATTAATT	ATTTGATTAT	120
	TAATACTTAT	TATATAATTA	TTATATAAAT	TACTTAATTC	ATCATTATTA	ATATTTATAT	180
	AATTATAAAA	ATAATATTTA	ATATGAATAC	TATTTAGTCT	ATGTTCAAAT	TTTAAATTAG	240
	TTATTAAAAAT	ATTATTAGAT	ATTATTATTT	TCCTTAATAA	ATTATTAAAT	AGATTATCAA	300
	TAATTAATAT	ATTATTTTAT	AATTGTTTAT	TAAATAATA	TATTTTATTA	TTATAAAGAT	360
40							
	TTAATTTATT	TAAATATTGT	AAATTATTAT	TTTTATTATA	ATATCTATTT	TTATAAATAT	420
	TATGTTGATT	TATATTATTT	AATCTTTTTA	TAAGAATTAT	TATTTAAAT	AATTTTAACT	480
	TTAATTTCTT	ATTATTAATT	TTTATATTAT	TTAATAAAT	ATATTTCAAT	TTATTTATTT	540
	ATTTATTTAA	TTAAATTAAT	TATTTAATTA	ATATTTTATC	ATTATTTAAT	TAATTAATAA	600
45	AATATTATAA	AGAATGTAGT	TAAAAATACT	TATAAAAGGA	TCCGAACCTA	TATTATTGTT	660
	TATGAGACAA	ATGCTTTAGC	CCATAAGCTA	TATAGTTTGA	CTATCATTTG	AGANTTGGGT	720
	NCNCCCCCTA	TGCTNNCATC	CTGNTGTCCC	CNCTAAANGA	ATTNTNTTNT	TNANANATGA	780
	AAAANTTATT	TATCAAAGAA	TTATAATTTT	TTAANAAGGG	GNANAAGGAA	AGACCCG	
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1241UP

	GATCTGTATA	CTAGAGCTTA	TTTTACTTCA	GCTACTATAA	TTATTCTTAT	TCCTACTAGT	60
	ATTAAAGTAT	TTAGTTGATT	ACTAACTATT	TATGGTGGTT	CATTAAGATT	ACTAACACCA	120
5	ATATTATATC	TATTATCATT	TTTATTTTAA	TTTACTGTAG	GTGGTTTAAAC	TGGTGTAGTA	180
	TTAGCTAATC	TATCATTAGA	TGTAGCATTTC	CATGATACTT	ATTATGTAGT	ACTACATTTC	240
	CATTATGTAT	TAAGTTTAGG	TGCTGTATTTC	TCTATGTTTG	CTGGTTATTA	TTATTGAAGT	300
	CCTCTTGTTT	TAGGTTTAAA	TTATAATGAA	AAATTATCAC	AAATTCAATT	CTGATTAATT	360
	TTCTTAGGTC	TTAATATTAT	TTTCTTCCCT	ATGCATTTCT	TAGGTATTAA	TGGTATACCA	420
	AGAAGAATTC	CTGATTATCC	TGATCTATTTC	CTAGGTTGAA	ATTTAGTATC	TTTATTGGT	480
10	TCTATAATAA	CTATTATATC	ATTAATGTTA	TTCTTTTATA	TTATTTATGA	TCAATTAATA	540
	AATGGTTTAA	CTAATAAAGT	TAATAATAAA	TCTATTAAAT	ATATAAAACT	ACCCTGATTT	600
	TATTGAATCA	AATAATATTT	TCTTAATGAA	TACTACTAAA	TCACATCTAT	GATTTATATG	660
	AATCACCAC	CTTAATCNAT	CAATTAAACC	CTCTAATCCA	ACTTTAAATA	NNCTTAATTA	720
	TAAATTANNA	ATAAATTTAG	TGGAANAATT	AATNGTAANC	AATNTTTTNA	NGGANTTTAT	780
15	CTCNNTCCAA	CCGAAACTAC	TTTTATCCTT	AANNAAAACC	TTTAATNAAT	GGACCNCANA	840
	NTCNNAACNN	GTTTTTC					

1242RP

	GATCACGTGC	TAAATGTCCG	GGTACATTAG	TGCACCCGTA	CACCGCATTA	CGACATTACG	60
20	ACGCTTCTTG	ACTAACCAGG	TTATCACGTG	TATATAGTTA	CATACGAACG	TCTGGTACAA	120
	GGAAAGAGCCG	GCCGGAAAGT	CACCTCACCC	TTAAATTGCC	ACATTTTCATG	AGCATTTTACA	180
	ACAGAAGCAC	AGCTGTAAAC	GTTTCTCGAA	CTCGTGAAGT	TTCATATGTG	TCCTTAAGGG	240
	CCCTTGATGT	TGCAGTTCAA	GCTAGTTCTG	TTGGGAGACT	CGTCGGTCCG	TAAGTCGTCA	300
	ATTGTTTCATC	GCTTCGTGAA	GGATTCGTTC	GATGAGTTCC	GGGAAAGCAC	AATCGGCCGCC	360
25	GCATTTCTGT	CCCGTACCAT	CAAGCTGGCG	GACCACGACG	ACGCAATGAT	CAATTTGAGA	420
	TCTGGGACAC	CGCGGGACAG	GAGCGGTACA	AATCGCTGGC	TCCGATGTAT	TACAGGAATG	480
	CGAAGCGCCG	GTTCGGTGGT	TTATGACGTT	GACACAGGAG	GATTCCTCTAG	CAAAGGCACA	540
	GAGCTGGGTT	GAACGAATTA	AGAGCAGGTT	GGTGACGAGA	ATTCTGGTAT	CTTCCCTGTT	600
	GGGCATAATT	GATTNGGGGA	NGAGGANCGG	AACCNAGGTG	ATTGACNCGA	GAACNCAGGC	660
30	TCCCCAAACC	CNGGGTGANT	TCCCCNAGGT	TTNNNCCAAA	CCGGCCGGTT	NCCGGATTTN	720
	TTCCNGGGAT	TGGGGGAANN	CTAAAACNGG	GCNATTCENT	NGGGGCCCCC	CCGCNTCCCC	780
	ANTTTCCNTT	CAAGNCCCCC	CAAAGAACAC	CCTGGGGNTT	ACCCCCTCCC	N	

1242UP

35	GATCTTGTCG	ATTGTGAAGG	AGGAGACGAA	AAACGCTACC	ATCAGTGTTG	CCGTGAGAGAA	60
	CAAGCAGCTC	ATCCCAATTCA	TTTCGCTGGC	GGACGTGGAG	ATTTCCGAGG	ACGTGACTGT	120
	GAAGGCCCTT	CCTAACGGCT	CTGAGAAGAT	CGTTCTTATG	GGGCCACGCG	ATGAAGCGAA	180
	GGAAGCAAAG	GTGAATGTTT	AGAAATTACTT	GAACACTTTA	GCAAGCAAGG	TATCTGAGAA	240
	AAAGATTTTCG	ATTCCCTCGCA	AGTTCCAGCC	TCTGATCGAT	GCAGAGGATG	TCAGGGAGAA	300
40	ATACAAGGTC	TCCGTTATCT	TCCCAACCGC	CCTTGGTGAT	GATACTGTGT	CGTTCTACGG	360
	ACTGTCCGCT	AATCTTGATG	ACGCGATCGC	ATATGCTCGC	CAGTCGTCTA	AGCAGTACAT	420
	GGTAGAATCT	TTGGAGGTAT	CCAAGGCTCA	CGGAAAGAAT	GTCGCTCATG	CAAAGAATTT	480
	AATGTTCTAC	TTCGCCAGTT	ACGAACCTCT	CCAAGGATAT	TAAGGAATTC	GTTCCAAGGG	540
	ANTTGAANTT	TTGTNCTACC	CAC'TCCCGGA	GGGATTTGCC	CGNTTTAAAN	AAGNTTTTNA	600
	ATNCACANTT	TTTCCAAAGG	GNGAATTTTG	GGGNACAAAA	AAAANTGTNT	TCCCCGNCNA	660
45	TNCC'TTATTT	NTTAACNACC	CCCCCTCCCC	NGTTTCCNCC	GNTGAANACC	NAANTATNAC	720
	CCTTTCCCCC	AGNGATTTAC	CNGGGCCNTN	CAGGGGANTC	CNC'TTTTNTN	CTCCGGANTC	780
	AANAAAGGGA	AANACCNGNN	GCTTTTGGCA	GGNTGANAAA	AAATCCNCCC	CCCCCAGAGG	840
	TAAGANCCNN	GNAAGNGNG	CCCN'TTGGGA	GAA'TNCCC			

1243RP

50	GATCGCTAAT	CCCAGGTTT	GTTTTGAAGT	CTGTGATCAG	TTGGTTCTCC	ACATCTTTGA	60
	GAATTC'TAAT	AGCCTCCGAT	GGCAGTTCCCT	CCAA'TTCCAT	TCCGACCTGG	GCAGACTGTA	120
	TCTTTAGAGA	GTAATTTTCC	ACACACAAAG	AGTCAATCTT	GTC'TTGAACA	TCGTCAATTC	180
	TATACTTCAG	TACATCGTTC	ATGTTTGGTA	GATTTCACTGA	GCTTTTGAGT	GCGCCTTTTC	240
55	CTAGCGCCGA	AAGGTTCCCC	GCTTCATTCC	ATGAGAAGCC	TAGA'ACTGAC	ATCATGGCGT	300

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5 GGCAGCATGT CTTCCGCAAC TGTGACAACC AATAATTCAA GACTGCGGGG CCTAGATAAC 360
AGGGCCCTTG CCCGTCTGAG TCATAGCCTG AAGCCTCCAA GAAGGATTTC CATAGGTTAA 420
CATAATTATC ACGCTCTATC GGTGAGAATT GAAGTTGGAT TAAGTAATGA TGCTGCTTTG 480
GGATTTTAACT CTGATATTCG ACATCATTTCT TTGTATGACG GATACAAAGG TTGAAACGTG 540
GGATGATATC AAGAAGTTCT CTTGCGGTGA AAGTCACACC GTTGACACGT TGGAGCTTTG 600
CGAATTTGTT GCGGGATCTA GATGCATCCG ATTGTTGCCC AGTTCCCTGG TATTCTGGCA 660
GACTGTGTTC GATATACTTT GGAGATCCCT TGAAGGGATG CACTGCCATT AGAAATACAC 720
CTTGAATCCN CTAGTGAATG ATAGGTNTAC CCGAACCCCC ANTTTTGATA CCCNGCAGAG 780
TTTGTNCATC GGCCCCCTTCN NCTTCCTGCC CACATTGCCT CCCNATTTTA TCCTGAAATG 840
CTTA

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1243UP

	GATCTCGTCC	CACCACGGGC	GCAGGAACGT	GTACTGGCCT	TTTGAGATCA	ACTCTGTCAG	60
	GACGTCGATC	TTTTTCGTCT	AAAAAGGCGG	GAAGCCGCAC	AACACGGTGT	ATAGGACGCA	120
5	GCCGATCCCC	CACATGTCTGA	CCTTCATGGA	GTAGCGTTCTG	TCCTTCACCA	CCTCGGGGCGC	180
	GGTGTACCCG	ACAGTCCCGC	ACGGCGTCTGT	GGTGTGGTA	GCATAAATTT	GCTTCGAGAG	240
	TCCGAAGTCT	GCGAGCTTTA	TCACACCGAT	CCCGCCGCC	CCGATGCCAG	GTCGGAACAG	300
	GCCCTCGTCT	TGTTTTGTCT	TTGGGTCTGTC	CGACTGTCTC	AGCTGCTGGC	GCTTGCTGGG	360
	TATAAAATCA	ATTGGGGAGA	ACAGCAAGTT	TTCTGGCTTG	ATATCCCGGT	GGACAATGCC	420
	AAGCGAGTGC	ATGTGTTTTA	CCGCGAGTGC	CAGCTGCCTG	ATTACATGTC	TAGAAAGGTC	480
10	CTCCGAAAAA	TAAGTGAGTC	GCACGATTTT	TCCAAAAATC	TCCCCCCCCG	GCAAGCAGCT	540
	CCTGGACTAT	GAAGTAGTAT	GACTCGGTCT	CCCTGGAAGT	CGATAAACGT	CACAATGTTT	600
	TCGCCCCGAG	ACACCGCCTT	GTGGATGGTG	ATCTCCTTCA	GAACTGCTCT	CGCGATGTCG	660
	CCTGTTTTCG	CGGCTCCNCC	CNCTTNTNCC	GGGCCCCCC	NGCTGCCCCC	ATCGTTAANA	720
	GGNNCCTTTT	GCTGATCNCC	TTGACGGCNC	CGTTTNTTAC	NGNCNAAGTN	CCCTTTTCGGN	780
	CGNCCTTCAG	CGGNCCNCCG	ANNCCNCCGN	AAACCCCNCC	CNATTTNCCC	NAACTTNTCC	840
15	CNCAANCCAA	GNNCCGAANC	CCCCC				

1244RP

	GATCCTGCCT	TATCACGAGC	GCCATCCGAA	CTTCCCCCGG	GATGTCGTTG	AGAGGTAGCG	60
	AGCTCACCTC	CACAACTTCC	TCATCTGAAT	CGTCTTCGTA	TGTACTATCT	AGCTCTTCAG	120
20	CGTCGCGCGA	TGCAGATTCC	GCCCTGTCTT	TCACCTGTTT	CAGCACCGCC	TGTGCGTTAA	180
	GCTCAGAGAG	GCAGGCATGT	GTCGCACCCC	CGTATATCTG	GCCCAGGTAA	TACCCCGTGG	240
	CCAGCGAAGC	CATCGTAACG	CTCAGTATGA	ACGGTAAGTT	GATACCTGCC	ATCCTAGTTT	300
	CTGTTTGGTA	TTCTGCTATG	TGAGTGCACA	AGCCAAGTTG	GTTGAAAATT	CCTTCAAGCT	360
	GACAATCGCT	GGTCCCTGCG	GCAGTTC AAC	ACAGCAAAAC	TCAGAGAGAG	GTATAAACGC	420
25	CATATATAGG	AGGAGACTAC	TCTATTCACT	GCCTATCTTT	TCAGCCCACA	GTTCTCTGTC	480
	CTGCAGAATT	GTGTGTGTAT	TCCGCCAGCA	TTTTGTTCAT	CGTCTCGACA	TATTCGTCCG	540
	TTATGATTTC	GAATCCGTGG	AACATTCGCG	CGCCAGCCTG	TTAGATTAGG	CCACCCGCC	600
	TTGTGTAGAC	CATAGTCCGC	GAGTGCGATT	ACAGGTTATC	CNTCGAACAC	CATCCGTAGA	660
	ACCACTGGCT	ACNCTCCGGN	GTTAAACCCC	TACGCTNCCC	TTCCACTNTC	CGATAGTCCA	720
	TACGCGGAAT	TTGGGGGGCC	AAAAAAGTGC	CCNGCAGGAA	CNCAAAACGAA	GNNTC AACGC	780
30	CNTGTNTTGG	GCNGGTGCCN	TTTCCNCAAA	NCAGTGCGTA	NTTNTAANCC	NGCCNCTTAT	840
	TNTCCCCCAT	T					

1244UP

	GATCAATCTG	ACAGTTGGAT	TGATACCAGG	TGCTATCTCC	TTATCAGCCT	TTACAGTGAC	60
	GAAGGAGGGA	TTGGATTGGG	GAATGGAGAA	TAAAGATATT	TTTGATCCAT	CACCAGAAGG	120
	ATTTGATCCC	TCTTTCAGTG	AGCATGCCCA	ACTTTTACTC	TCGGAACGTA	TAATGGGAAA	180
	CTTTCTCGTT	CCAAAGTCTG	GCATCTGGAA	TTATGCAATTT	ATGGGTGCTG	GATTTAACAG	240
	AGAGCTACGT	TACGAGCTAT	CTCTCGACAT	ACCACTCGGA	TTTTATGATG	AACAGCACCG	300
40	TGCAACGCAT	TTTCTACAAT	TCAACGAAGT	GGCAGCTGAC	GATACTTTGG	AAGCAGAACA	360
	GGAAGATTTA	TTCTCCTAAG	TACATATTTA	GGATAGAGCC	AAACTTGCAA	CTAGCTTCAG	420
	TTGCGTATGA	ATCCCATATA	TGTATATATC	AATACACGGG	CCACTCATGG	CTGGTGACCC	480
	ATTTAAGCAA	ATACCATATT	TTTTAATGTT	GCGGTGATTT	TATAATCTCG	ATATCATGAT	540
	TTTATTTATA	GGAGATGACT	TTTCCCTCTA	CAACGCCACA	TTATAGAAGA	CCGTCAATGC	600
	AGCACCCAGG	CTGAAGCCAG	AACGGAAATG	TTGGAACCAG	AACAGGCAGG	TTTGAATAGC	660
45	TCGACATATG	AACCTCCCCA	GAACATGTTT	TTTTTGAACA	TCNAAATGANT	TTCTGCCAAA	720
	AACANGAAAA	TGGACNCCNN	GCATCATTTCA	AAAAAAAACCN	TCCTTGAACC	TGACAAAAAA	780
	TATGCACCCN	GATTTTTTTGA	TCACGGANNG	TTTTCTTTTAC	NCCAAATTAAA	TAGGNCCCCC	840
	NGAGATTTTTT	ACACCCNCC					

1245RP

	GATCAAAAAAC	AGAGTACCCT	CCGCACGAAC	TTCCCATATG	AGGCCCAGAG	AGAACAAACAT	60
	CGCCGATCAC	CTATATCAAC	AACGGAGACC	TTGGTCTGCC	GAGAACGTCA	CAGCTTATCT	120
	TATTATCGAT	CGAATGGATG	TTGGAAAGAA	GATACAAAAT	AACGCATAAT	TGCTGAATAT	180
55	ATTGCACGCT	TCTAACGCAA	ACGACGAGCC	TCACGCTCAG	ATTCCATCAA	GACCAAGATG	240

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	TCGTTCTCTC	TAACTGGGCC	CTTGACGTTT	CTGACAATGG	TTCTGGAAGT	GTCGTCCAAG	300
	AACTCAACGC	GGACCTGGGT	GACACCACCA	CGAGAACCGG	TTCTACCTAG	AACCTTGATA	360
	ACCTTAGCTA	GAGTGACTGG	GGTCTTGGAG	TCCATTTTGA	TCTATTGCTT	CTTGGATATA	420
5	AAATATCTAG	TAAAAAGTGC	TGAATAGGTG	AGAGGAAGAT	ATCATGAACA	GGCGGTTTTT	480
	TTTGATGCCC	CGAAAAATTT	TTCAGGTCTG	CGATGCCCAT	CGCAGGTGAA	ATGTGCTTGG	540
	GTTCTTGAAA	AATCACATCA	TACGATAACT	ATGCGTGAC	CCAAAGGCCT	TGGCAGCAGC	600
	GAAGTGCGCG	AAGGTIAGCC	AGCCCAGAAC	GAAACCTGAG	AACAGGTTAA	GCTCAGGTGA	660
	ATTGTTTGCT	TCTATTGCCT	TACAGTTCAT	CTTCCGGTAA	TTGCAGTATC	CGTTGATTCC	720
	CCNCAGCTGA	CCAGCCGTTN	ATTCCCCTTT	GAACTTTCAG	AGNTCNTGAA	ACCCTNGTNT	780
10	TTTCAACCCN	TGACACNTAT	ATCNCCCCCT	TATATGACTT	CCGTCNATNC	CCG	
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1245UP

	GATCCGGGTA	ATACAAACGCC	TCGGACCCCT	CGGCGGGCTAA	CGAGAAAATC	GCGCTAAGCT	60
	TCCAGCCTAA	TCATAATAAA	AGGGGCATTG	GTGGAAGCTT	TCTGGTACTT	ACGCGAGTAA	120
5	ACAAAAGGCG	CAAGGACGTT	TCAGAAGAAG	CCAGAAGCAG	CAATGAGCGA	GATCAACTCG	180
	ATCATTACAC	GAGTGAATGT	ACTGGTCTCA	AAACTGCCCA	AAGAGAAGGA	TGCAGGCCTG	240
	GAGAAAGAGT	GCGCGCTGAT	CAAGTTTCGGC	GGCATGGTAT	CTAACCAGCGA	ATCGGCGCTG	300
	TTGTTTGGAG	AACTGGCGCA	GCAGATGGAT	CGCACAGCGG	TGCTACGGCA	GCCATGGATT	360
	GTCGAGTTTG	TTGTGCGCTT	GGGCAACGAG	CTATGCCGGG	GTGGCGAGGT	GGGCGAGAGC	420
	TTCTGGGGCA	AGATATTGGT	TCCGTTGGAT	GGACAGACCC	CGTTATTGAC	AGTTACTAAC	480
10	AAGAATCCAG	GGTGCGAAGT	TTTCGCGTAA	TGTTGCGGTC	CATGGCCGGT	TGGTGGAGGC	540
	GCTGCTGGAC	GGCGCCTTGT	CGCGTACGGC	TCCCTGTGCG	TGGCAGAATA	TGGCGTTGTT	600
	GCTCCAGCTG	TCCTATNNAC	CNNCCGGATT	NTCCGGAAGT	TGNTGNCCCC	CCTTTACCCC	660
	CCCCCTNNCN	AGNATGGTTG	GNGACNNTTT	GNMCGNTTNC	CAACTTCCTT	NTNCCCCNCT	720
	TTTTTTGNAC	NTTGAANCNA	TTTTTCCCCC	TTNAANTCAA	CCNACCNGTT	NTNCAACCC	780
	CCCCCCCCTT	TGGGAAAANN	AGNAAAAAAN	ACCTTTTCCA	CCCNGGATNC	CCTTTGNGCA	840
15	NCTGGAACNG	NNNTNTTCNC	CCTC				

1246RP

	GATCAACAAT	GATTGTGGCG	ACGGGCGGGC	GGGCGTTCAA	ATTCTACGAC	GTGCTGCTGT	60
	CGGAATTTCC	GGGCGTGTCA	GATATCCTCC	GGCTGGACGA	GATGGACTGC	CTGACGAAGG	120
	GGTTGGACTT	CTTCATCCAC	AAGGTGCCCT	ACGAGGTGTT	CACATACAAC	GACCTGGACG	180
	GCGAAGGCAC	GGTGGATGCG	GTGGCGGATG	ATGAGATGTA	CCCGTACATG	CTAGTGAACA	240
	TAGGATCCGG	GGTCTCGATT	CTGAAGGTGG	AGTCGCCCCA	CGAGTGCATG	CGTGTGGGCG	300
	GCTCGTCATT	GGGCGGCGGC	ACGTTGTGGG	GACTACTGTC	GCTAATTACT	GGGGCGAAGA	360
	CGTACGACGA	GATGCTGGCC	TGGGCAAAAC	AGGGCAATAA	CGCGAACGTG	GACATGTTGG	420
25	TAGGCGACAT	ATACGGCACC	GACTATGCGA	AGATCGGCCT	GAAATCCAGT	AATATTGCAT	480
	CGTCGTTCGG	GAAGGTCTTC	CAACGGGAGA	GCGTCACCGC	GCCCCTCGGC	GGGCCTGACT	540
	TCGGCGTCTG	CGACCTCGAC	GTGTGAGATC	CGAGATTCCA	AATGAGAAAT	CCNNACGCC	600
	GAATNTTCCC	ATCCCTCMTG	TACCCATCTC	CAACAAATCG	GCCAAATGCT	TNCTGCAGCC	660
	AAATCCCCAA	CTCCAAAAAA	NNTCTTTGCG	GTCNTTATNT	CCCCGCCTTT	TACCCCTGTA	720
	CCCTTTACCC	CCCCCTAACT	CNGGTCNAAN	GNTTTTAACA	NCCNCCCCC	TNAGGNTTAA	780
30	GGTNNTGGCC	CCNNGGCCCT	TNTTGCCCCA	AAAATTTCCC	NNCGNTTCTN		

1246UP

	GATCGTAGAG	CGTGAGACGG	CACCGGCGGA	GGCGCCAGCG	CCGGACGGTG	TGCAGCCACG	60
	GGGGTTTCCT	GAGCTGTACC	GCCCCGCAGC	GATATCTAGC	TGGCGCCAAC	GGCTGCAGAA	120
	GAAGAATGGG	CAGCGCAGGC	CGCCCCGCGC	GGCCCTCGCC	GCAAGCGAGG	CGGAGAAGAT	180
	CCACAAGGAA	AACATGGCGT	ACATCGAGGG	GCTGTGCGAG	GAGCAGCGGA	CGGCAGAGCG	240
	CCGCGAGCTG	TTAGAGAGCC	TGGACCCCAA	GGTCGTGCAG	GCGTTGTACC	GTCGGTTGGA	300
	TGCACGTGCA	GCAGCGGACG	GAACGGCGCC	CTTAGTGCGC	GAAGTCGAGG	GAGCGGCAGG	360
	CACGTGGGTG	GGCGGCACCC	GCGAGGAGCC	GATGATGCCG	CGCCTGGATG	ACGCGACCGT	420
	CGACGCCGCG	CTAGGCGCGC	CACAGGCTTC	GATGCCAGAG	GCCGCGCCCA	CGTACGACCT	480
	GCCAGCGCCG	CTGGAGGATG	CGGACGACAT	CGCGCCCCCA	GAATACCAGT	TCATCAGCAG	540
	ATGGACCATA	TGAAGGACAG	GACTTGCTAC	GAGATATCCA	CTTCCTCCGC	AATGAGACTG	600
	TGGCGCCCG	ACTGGACATC	AACGACCCCA	ACTTTATGAG	CAGCTGCACG	AGAATACTTC	660
	CGGATNTTCC	GAAAGAAANA	AATAACTNGA	ATGGATGAAG	GCCACTGAAC	CCTGACACTC	720
	TTCTNCTAAC	TCNCCGATTT	TGCCGAATGC	CCTCCAACCT	AGGGCCCCATG	TCCCCCCCCC	780
45	CCGGAATTTN	NTCCCCNNAA	CNGCCTCNNC	CCTTCGAAAA	CCCCCTTTTN	CCGGCNTTCC	840
	TCCCATTTGC	ACNTTCCCCA	C				

1247RP

	GATCTGGCCG	CGCAGCTGCG	GCCTCGTATT	GCTCCCCGTC	GTTACTGTGG	CGCCGCCGGC	60
	GTGTCTTTAT	CGGCATCGCG	TACGCGTCAC	TAAGCCCCCT	CAGGACGGGC	ACAAAAAGCG	120
	CAGGGCGCTC	ATAGAGCACC	ACAGCGTCTG	GGTCGGGAAAG	CACGTGCATC	CGCGGCGTGT	180
	GCTTGCTCAC	CGCCTCGTGC	GCCTTGCCCC	GCTCTGCCAC	CGGCGCAGCC	GTTGCAGCCC	240
55	CGCGGGCCGC	GGGCGCCCTG	TGCACTGTAG	CGGCACGGCC	GCGGCGGACG	CTCCGCTTGC	300

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5	GGACCGCCTT	GATGACCCGC	TTTGCGCCCG	GCCCGCGCGC	GCTCGCCCGA	GCGAGCGCCA	360
	GCCCCCGCTG	CACACGCATC	AGCATCCCAT	CCACCGCTTT	CCTGTCGTCT	TCCACCACGC	420
	TGTGCGCTGA	AGCAGACTCT	GCGCTATCTC	CTCCGCTCTG	GACGAAAGGC	CTCGTCGCTG	480
	CTCGACTCGC	TCTGCCCGTA	CTTCCGTCGA	AGTACGCGCG	CAGTGCCGCC	GCGCGCTTCG	540
	CCTCCGCGGC	CGCCGGCGGC	GCGAAGGGCA	CGTTAGGGCG	CCGAGCCGCC	GTCAGACCCCT	600
	CCTCATCGAA	TCCGAACCGC	TCGCGCCGTC	GCGCCAAATCG	CCCACGGAAC	CANCCCCCG	660
	GGGGGTTNCG	NGGCCCGGCC	GGCCCCCTCC	TTTTNAAAAC	GACNACCNCT	TGNAAANCCG	720
	TTACCCCNEN	CNNTTCAAAC	NCCNGGAAAA	ATTTTCGNEN	ANNNNNNNNN	CCCCCCCCCT	780
	NTNCTNNGAA	ANAANGNCCN	GGCCCTNNGG				

1249RP

15	GATCATGCAA	CATTTCTTCT	TTTCCCGCTT	TCTGCCTGTG	CCGGACGGTG	TGTCCCCGCG	60
	CCGCACCTCT	GAGGAAGAGC	TTGCGGACTG	CAGCGAGCAT	GCCCACAGTA	CCTGGGGCGA	120
	CTGCTGCGGC	ATTCCGATAC	CCAGCGCGGT	GGCCGCCCTC	GAGGCCACTC	GCAAGCATTG	180
	TAAACCACTT	CCATTGCAAT	GAATCAAATT	ATATATACCA	TAAAGTAGAG	CTACCATGCG	240
	AACCTTAGCT	GGGACGCACT	AAAGATTGGC	GGTTTCCAGA	TCAGCTTCTC	GGGGTCGATC	300
	GATCGCCTTT	TCTTCGCTAT	CAGCTTCTCG	TACCTTAGCA	GCACGTCTCT	GTTTCAAGTAC	360
20	AAGATGTGCT	GGCCCTTGTA	ATATCGCAGT	ATGTTAAGAG	CCTTGGCTGT	GTGCAGTATG	420
	TCTGTAGTCG	TGAGCGATGT	CATGCTACTG	ATTTTCATCGA	TCGTGATCTC	GGTGGCGTTT	480
	TCGACTAGCA	GCTTGATCAG	GGTATCGGAC	CAATAGGCTC	TGTAGAGAGC	AGCCCAAGAT	540
	CAGAGAGCGG	CTTCTCCGGC	ACCCAACCTG	TTCTCCTTCT	TAGAGAGCTC	CATACGAAAC	600
	TCAATCAGCA	GCCTGCCGTA	CCCCATCCGC	TGGTACTGAG	GGAGCGTCCA	GAATACACGC	660
	CACATTGTAC	CCGTCCGCCA	NTCCTTTCCN	TTGGANAATN	CCCACCAAGT	NGGTGCCCCA	720
25	CTCACTCCCC	TGTGTCTTG	CANTAAAAAA	AAGGTCAANT	TCCTATNACT	CNTGTGNTCC	780
	AAAAAATTTT	GANAAAGNTN	GTGCGNACC	ACTTCCTNNT	NCCCCGTCAA	TTCAAAT	

1249UP

30	GACCTGCCGA	TGGACNGCCG	TTGGCAGGTG	ACTGCCCTAC	GGTCTTTAGT	CCCCGCAAAG	60
	CGGATGGCCT	TTGTCGGCAC	ACGCAAGAAC	TTGGCAATGA	TGTTGACCAC	GTCCATGGTG	120
	TCCTTATTCT	CCTTGATACAT	TGTGAAGTGC	ACGCAGTTCT	TGGAGGGGCC	GTACCCCCAG	180
	TTAATGACAC	CGTTCTCGTC	TCTTGTCTGC	TCCACATAGT	CCTCTTTGCT	GACTCTGGTT	240
	TTACGGTTGG	CCAGGGCAAT	CTGGAATGTG	TTGGACGCCG	AAGTGACCGA	TTCAAGCTCA	300
35	TTGTTGAACG	CCTTTCTGTG	CAGCTGGTGG	ATCTTCGTCC	GTGCAGCTTT	GTGCTCAAAG	360
	CTCCTGGTGG	TTTCCATTTT	CGTGACGTTT	CTGTACACGG	CCTCAATCTG	CTGCATGTCC	420
	TCCTCGCCCC	GTAGCTCTAC	CAGCTGGTTC	CGCAGCTCTG	CCTCCACCGC	GTGGTTGTGG	480
	CGCCGTTTCG	GCTCTTCAGC	CTGCTGTGCC	TTACCTGGT	CGGCAGAGGT	TTGGGTTTAG	540
	CAGGCATTTT	GAACCCATTG	TCCCCGCAAGT	ACACCACTGT	TCCATCCTTC	TGGATCTCAT	600
	TGACCATGAA	GTCGGAATAG	CGCTGCTTGA	TCTGCCCGCT	AAACCCTGGT	ACTCTGCTGA	660
40	GAGGTACTCT	GTGATCCAAC	GTCGATTCTT	TGAGTCCATC	GGTCTCCGNT	TTGGCCCCCT	720

45	NCCNCAAAAG	TTCTTGCTTG	CTCCNNANCC	GCTCTNTAAT	CCCCCGAAAN	TCTGTACNNT	780
	TCNCNATTTT	CNNTNTNNCC	TACCTNAACC	CTTGTNTAAC	CTTCCACCCN	ANAANTCATA	840
	AATATTCCCC	NCC					

1250RP

	ATCTTAATTT	AAAATTTTAA	TTAACTATTT	ATAATTTAGA	AATATATAAT	CTAGAGATAT	60
	ATAATCTTAA	AATCATAGGT	AAAAATACAT	AAGATAGTAA	GAATAAAATT	AGTAAAAATA	120
5	ATAGAAAACC	ATAAGTTAAT	TGATTCATAA	AGAAAAATGG	AATTATTTGT	GGCATCTTAA	180
	TTTTTATTAT	TTAATTGATT	ATTATCTATT	TAACATAAAA	CATTTTAAAA	TGTTATAAAA	240
	TAAATAAGAA	ATTACTTATA	GAATATTTAT	TAAATAGTAT	TTAATTTAAT	TTTAATATTA	300
	AATATACCAT	TTTTATTAAAT	AAATAGATTA	TTAAGTTTAT	TAATATTAAG	TGATATATAA	360
	TTTAATTTAT	ATAAAATTAT	TAATTTACTT	CATTGATATA	TATAATTATT	AAATGTACCT	420
	TTTATAATAT	TTATTTTTAT	TAGTCTAGTA	ATATTTCTAT	TTAATAGTCT	ACCCTTTAAT	480
10	TGGATATTAC	TACCTACTAA	ATATTTACCT	AATAATATAT	TATTAAGAAT	ACTTAAATCT	540
	AATAATTTAT	TATCTAAAAGT	ATATAAATTA	ATTAAATCCT	TTTTTATTAT	TATTTAATTA	600
	TTATTAATTA	GTAAATTATA	TTTATTATTT	TATTAACATA	ATTTTTTGAT	AATAATATAT	660
	CCATATTTAA	TGGTAATTTA	TTAATAATAT	CCTTTAATGA	TTTNATGATA	ACCNTATTTAT	720
	TATGANATTA	GTTAATAGTG	ACCTTAATAT	CCCNATCCNA	ATATATNTAT	TTATTTNTAA	780
	NAACANANAA	CTTCCTPATNN	CATATTTANT	TTNANTATTN	ACCNTTNCCN	NNNT	

1250UP

	GATCAAAATT	TCAACAATTT	CCATTTTCATT	TAGTACTACC	ATCACCATGA	CCAATTGTTA	60
	CATCATTTAG	TTTTATTAGGT	TTACTATTAA	CTTTAGCTTT	TACTATACAT	GGTATTATTG	120
20	GTAATATTTA	TCCTTTTATTA	TTATCTTTAT	TAGTAGTTTT	ATTACTAATA	ACTTTATGAT	180
	TTAGAGATAT	TGTAGCTGAA	CTTACTTATT	TAGGTGATCA	TACTTTAGCT	GTAAGAAAAG	240
	GTATTAACCT	AGGTTTCCCTA	TTATTTGTTG	TATCTGAAGT	ATTAATTTTT	GCTTCTTTAT	300
	TTTGAGCTTA	CTTCCATTCA	GCTATAAGTC	CTGATATTCT	ATTAGGTAAT	GTTTGACCAC	360
	CAGTAGGTAT	TGAAGCAGTT	CAACCAACAG	AATTACCATT	ATTAAATACT	ATTATTTTAT	420
	TAGCATCAGG	TCTAACTATT	ACATATAGTC	ATCATGGTTT	AATTGAAGGT	AATAGAAAAC	480
25	ATGCTTTATC	AGGTTTACTT	ATTACTTTCT	GATTAATTGT	TACATTTGTA	TTATGTCAAT	540
	ATATTGAATA	TAGTAATACA	TCATTTACAA	TTACAGATGG	TATTTATGGG	TCCAGTATTT	600
	TTGCTGGTAC	TGGTTACATT	CTTACNTATG	GTTAGTTTAC	TAATTAGGTA	GGTNC'TATTA	660
	NGAANAACAA	GAAATTNCCCT	TTAACNCCCN	CCCCCTCCGT	NGANATNNAA	CCNCACCTAT	720
	TATTACNNTT	TTTNAAAATA	CANNATTGTT	NTAANGAAAG	GNNTAACGTN	GNNTAACGTN	780
30	NACNCACCCN	TAGNNTTTNG	GTCCCCCCCC	NTGCTACCCC	ATTTTGNCCC	CCCCCACAAN	840
	AACCCCC						

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	GATCAGGAGG	GTTTTGCGGT	GCTGCGCGAC	GGCGGGTTAG	AGGTAATGCT	CCTGCGAGAG	60
35	GATGACAAGA	CTGTGCGTGT	GTACCGGGAA	GTGGCAGAAAT	AGTGTATACT	ACATAGTCAT	120
	AGTTATAATA	AACAAGCCGC	GGCGGGCTCT	AACGAAATGG	GGAGTTGCC	ATGCCACCGG	180
	GGCCGCCGGG	GCCGCCGGGG	CCGCCAAAGG	GCGCGTTCCA	GCGCGCACCG	GGGAGGAAAC	240
	CGGGCGGCCT	GCGCGGGTCC	GCGGGGTCCG	CGGGGTGCGA	CTGGCCGCCG	TAGGGCAGCG	300
	GGGCGGTGGG	CCGTTGTAGC	CGCGGATCGA	ATATCATGCC	GCCCTGCGGG	TTGGGCGCGG	360
40	GAAAGGGGTC	AAACGGGTTT	GGCCGCTTCT	GGCCGCTTGG	ATACAGGTCT	CTGTGCGCGT	420
	AGCCTGCAGG	GCTGCCAGGC	AGCGGCTGCG	CGGCGCCGGC	CGGGGGGGAG	AGAACCTCGT	480
	ACTCGTCCTC	GAAGCCAGGC	ATGTCGTGCTG	GCAGCCTGCG	TGCAGGAACC	TGCGCGCGGA	540
	TTGGCGGAGG	CGCGCCTCCG	CTGAGGGCGT	CNTAATCACC	GGGCTGTGCT	TTTGCGCNGG	600
	GCTTCTCNTC	CGCCCAACAG	GGNAATTTCC	CTNGNAAACT	TNCCGAACCT	CNCCCCCTTA	660
	AAACTGGCCN	CNCCCTTTTN	CCTNNCNGCT	NTCCTCCTGC	NNCCCCNTTT	CCCCCTCAAN	720
45	ACCCNCCTAC	CCNTNTCTNT	NGNTTCNNNC	CCTACANCCT	TTCNNCCTNC	TCCCCCNCC	780
	ATNTCCTCNT	TNTATCNNA	AATTTCTNTN	CTTTTACCC	CCCC		

1251UP

	GACTGTTTCG	TGTTGAGGAA	GATAATCAAT	ACCGGAATCC	TCTGAGCTTT	GCTTCGGCCT	60
50	CCATTGCGCT	ATTACGAAAT	TCGCGTGCTG	CTCCTAACGA	TGTTGTACCG	TTTATACAAC	120
	CGCTTGTTGA	TCGCTTTTTA	GCAGAAAGCCC	GTTTTTGAC	CGACAGAGAT	GACAACCTTT	180
	GCTACTTCTC	CGATCCAGTA	TTGTTTCAGTG	CTGTAGTCAT	CTTGCGATCG	TTGGTAAACA	240
	CATATACCCC	ATCGCAGTTG	GAGAAGATCG	ATACCACGTT	GCTTTCGCTC	TCATTTTACC	300
	CATTAATTTT	GCGCCTTTTA	TTGTAAAGGT	GCAGCACCAC	AGAAATACTT	GATAAAATCT	360

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	TAGGCAATGG	CCATATTGGG	AAGTTTATAT	TACTAGCAG	ATGGTTGCTC	ATCCCGGCCT	420
	TGTGCTGTTT	GTTCTAGGGG	GCGCTGTTAC	TACCTTTAGT	CCTGTGTTAC	TCACAGCTTG	480
	TTACCGGCCC	GGGCTTCTAT	GCAACTATTA	TATTTGCTTC	TAATATATAA	GTACTGACAT	540
	TTTCATACGC	GCCTAGCTAC	CGCTGCTTTG	TCTTCGGTGA	CTCTCTTCAG	AACAGCTTCT	600
5	TGGAATTATC	TTGTACTATC	AACCATGGAG	ACACTGTTAC	GCCACACCCC	GACCAAAAGG	660
	AGAACCGAAG	GACAATTTTG	ANCCCTCCCTT	TCCCCCGAAT	TANGGNTTNT	GAANATATNA	720
	ACCGGGACCG	GGTTCCCTNN	TCCCCCGGGT	ANTTNCCCNT	TAAATTTCGTN	TAAANTTANN	780
	AANGGTNTAT	GGGGNGAANG	AACCCCANCT	GACCCNAAAN	GTNGNTGGG	GTTTAACCTN	840
	CTNNINCGCC	GTNCCG					

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1252RP

	GATCTCCTAT	TAGTGGGTAG	CTAGCTAGTC	GGCCCGGCTG	GCCGGGGCCG	AACTGGTACC	60
	GGGTGCGAGG	CCGAGTGACT	AACACTCCGG	GTTCTTCTGT	CTCTTGCCAT	GCCGAACATA	120
5	ACCATGGCGA	CTTATATAAG	TTCGGGCGGC	GTGCAGTCGT	ATGAGCCCGT	ACGAGCAAGA	180
	CGTCCAGCAG	TTTGCAGCGC	GGTAGTCGGG	GCGTTGCAGT	TGTGTATATA	TTGCCACCCT	240
	TGCGAACTTG	GACAGCCGTA	TGCTGGAGGC	GGTCAGTAGT	AAGCAGGAGC	CGGTGACTCA	300
	AAGTAGAAGT	CGGATTGTAA	AGGACAACAG	ACCAGTGGCG	GTACGGACAG	CAGCGGGCCA	360
	ACGTAGTAAT	AAAATATGAC	GAGAGATATA	CAGAACCACC	TACTCTTCGA	GACGGCCACG	420
	GAGGTAGCGA	ACAAGGTCGG	GGGCATCTAC	TGCGTGCTGA	AGTCGAAGGC	ACCGGTGACC	480
10	TGCGCTCAGT	ACAAGGACCA	CTACCACTGT	ATTGGGCCCC	TGAATCCAGA	CTCGGTGCAG	540
	ATAGAAGTGG	AGGCGCTGGA	CTGGGAGGAT	GACAGCGTGT	TGGACCCGGG	AGATTGCTGC	600
	CCGGTAAAAC	GTCCCCTGCA	GCACATGCGG	AACCCCGCGT	TGAACTCCGT	ATATGCCGGT	660
	GGTTNGTGAA	GGTNCCCCCG	GTTATCTTGT	TCAACCTGTT	CCCGTACCCC	CCTCCTCCAC	720
	AATTGAAGCC	ACCTGTTGAA	CACTGCGGAT	CCCCCCCCCC	CAANAACCA	NAAACAAAC	780
15	CCATCCGTTA	GGTNCCCCNG	NCTGTCCCCG	AAATTAANGC	CGANCCNCNC	TCAN	

1252UP

	GATCTTTATC	GCAACNTTTT	GGTTCTGTTT	CGAGTTACGG	GCCTGGCGGA	CCACACCGAA	60
20	AGCGCCAGCT	CCGAGTGTTT	TGCCGAATAT	GTAGTCGGCT	TTGTTACAT	ACGAGGCTGG	120
	TTGACCTGTC	ACCTTGTTGA	AGAACTTCGT	CAACATGTTG	GCCTGAGACG	GAGGACGATC	180
	CTGGGGCTTC	GATGCGTCTT	CGTCGTGCTC	CCCTACACCC	TTACCGAGTT	TTCCGGTGGA	240
	ACTAGTGAAC	ACTGCCATAG	CCTCGCAGTT	AAAGTGATGT	GGCAATATTA	TATTGTAGTT	300
	TTGTTCTTTT	CTTGATTGTT	TTAGGCTGCC	GATAGCCAC	GAGGTGAAGT	TTTGTACACT	360
	TCACACATCC	CAGCACTGCC	ATCAGCAGAG	ATGTTGAAGA	TCAAATTTTCG	CAGCTACATG	420
25	CTGCATTGTG	GTGCTTGGGT	TAGCAGTAGC	GGCTAAGTTG	CAACTACATT	GTCCCCATTC	480
	ACTCAGAAGT	ACCTCGGTTA	AGCTCACTAT	GCGCTTATTG	CCGAGCGAAG	CCGAGCATTG	540
	TTACAGCAAT	GATGAGAAGA	GGCTATTGGT	ATGTTAACAT	AACGCCAGTA	GTGTTATATT	600
	TACCACTAAC	CATAGAAAAA	GTACAGAATA	TCCGTAGCCT	ACGAACTGAA	TGAATATNTT	660
	GCTTCCCCNC	CCCGNCCNTA	TACCAATGAA	TAATAAATTG	GATTTGCTAA	TATCTNCCCC	720
	ATATCCNGCC	GGGCCCCCGA	NNCCCTNCAA	CTTATTTGGTN	CACNCCNCCN	TGCCNCCN	780
30	TTTTNTTTTN	TCNNGGAACC	CCCCCCCCGT	CATCNTCGNN	TGNNTNAANA	TGANTACCCT	840
	CCCTTGNTCC	CCNCCCT					

1253RP

35	GATCCTAAC	AAGCTGATTG	ACTCCAACCT	TCCACTTGCC	ACATTTCGACA	AGCTGTTGCA	60
	GAGCTCGACG	GCCGTGGGGG	GTGGTGGCTC	CATATTGGGA	TCAGATGGTG	GGTGACAGA	120
	CACGGAGGCA	TTGGGACATG	ACCGAAAACG	CAAGAAGTTG	GAGCCCCGCT	TCCCGGCGCC	180
	TCCGCGGAGC	GTGGCACTCG	GCCCGCGCCA	TCGCCGATAT	AATTCTGAAT	TGGGCCCTCAA	240
	CTACTTGCGC	GAGAGCAACG	CGCAGCCCAG	CGTGATGCTC	CCGCAGGTGC	AGCAGCGCTG	300
40	GAACACAGCT	CCTCGACAAC	AACCCAGACA	ACAGCATAGA	CAACATGGGC	AGGCCGAGGA	360
	AACGGGTTCA	CCACCAATGG	CTCTTCGCTA	TCCCCCTCCA	ATGTTAATGA	ACAGCAATTA	420
	TACATTCCCT	GCCGGCCCCC	AGCAGCCGCT	CGGCCCGCAT	CCACAATCGC	GTGCCTCGAC	480
	GCAGCAATCT	GATGTCCCAG	CTACCCCTCC	CGGAATATCG	GCGTAGCACC	ATCGTCCCAA	540
	CTTCCCACAG	CCCCCACC GC	TGACTAGTCT	TTTGTCTAAA	CATCAGCCTC	ATCACTCGCA	600
	GCCTAATGAG	CTGCCTACCT	CCCATGCATA	TGTACAACAG	ATTTGCCTAC	TCCAATAGCC	660
45	CAGTTCTGAA	GTCTGCTTGC	TTACGTTGCG	CCCTCTCCCC	TTGGCCAATN	TATCCTTGTN	720
	NNNAAAACCN	AACCCNNGTT	CCCCTGTGCC	NGAATTTCTA	CTTTTACCGT	CCGTTATTCC	780
	NTAAATCATA	ACCCGGTTCA	ANAACCCTTT	CTTTGACNAT	ATCNCATTGN	GCNANCCNNT	840
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1253UP

50	GATCGACGAG	TTCGATGTTG	AGACGTTCAA	GAAGCTGTTT	GCGAACTGCA	TTCCGAAGGA	60
	TGTGGATGTG	CGCGAGGTTG	TCGCGGAGTA	CCGACTGATA	GTGCCGTGTG	AGGAGCCGGG	120
	TGGGGTGGCG	CGCGCGGCGG	CCGGTGACGC	GGCGGAGGCG	GAAACGGAAC	CGTTTTCCGA	180
55	GGAAGAGAGC	AAAGAGATTA	GGATCATTCT	GCCTCCAAAG	CCAATTGCGA	TTGAGTTTGT	240
	AAAGAATGTG	TGGGAGAACT	GCTGTGTGCT	GTACCGTTTC	TATCACCGCC	CGACTTTTCAT	300

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	CAGGAAGCTG	GACGACCTGT	ATGAGACAGA	CCCGCGTGAG	TACACGCACG	AGCAGCTACG	360
	CTTCTTGCCG	TTGTGCTACG	CTGTCAATGGC	AGTGGGTGCG	CTGTTCTCTA	GCTCCATGCT	420
	CCCTGGTCGG	GGAAGCGAAG	ATGCGGGCTC	TGCAGGCAGA	ATAACAGCGG	CTACATTGGC	480
	GGATACGGAC	ACACGGCACG	CTTATCTGCA	CGACGAGGGC	TACCGGTACT	ATGTGGCTGC	540
5	GAAAAAGCTA	GTGATCTCAC	GAACGCCCGT	GACACCGAGG	CGAATCAAAC	CTTGTTCCTG	600
	TTTGTGTTCT	CCCAAGTTCC	GCGCGGTCNC	CCCGGCATCC	GTTTTTCTGC	CCNGCTATNA	660
	ATTCCNCCCN	CCTNNAGANT	CCACCCACCC	CCCCCGANA	ANTAAAAAAA	TTTCCCCCCC	720
	CAACCGGAAN	TCCCNCCCCG	NTTTACCCCC	CTTANAAANG	AGGTTTTTTTA	AACAAANCGG	780
	GGNGCCCCNC	NCCCCCGGNN	CNNACATCC	CCCCCTAAA	TCGGAANATT	NNCCGAAACC	840
	GC						
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1254RP

	GATCGGCCAC	ATTGTCCCTG	AGGCCTATGA	AGGCGGCCCA	ATTGCGCTCG	TGCAAGACGG	60
5	TGACGACATT	GTCAATCGACG	CCGAGAACAA	TGCCATCAAC	CTCCTTGTGC	CAAAAGAAGA	120
	AATTGAGTCG	CGCCGCGCTC	GCTGGACCCA	GCCGGCTCCA	CGCTACAAGA	GGGGCACGCT	180
	CGCCACCTAT	TCTAAGTTAG	TCTCCAACGC	CTCCAAGGGT	TGTGTCTTGG	ACAGCGACGA	240
	CTAGCACCTC	GACGCAAGTC	ACTATTTTAT	AACAAGATTA	TGTATATAAG	CACCCCGCCA	300
	TGTCCATTGA	ATGGACCGCA	TATGTAACAA	AAATCGAGGA	TGCTTCCCTA	TCGTCTACAA	360
	ATCTCAGGAT	GTGAGTACC	TTTCAGGTGT	CTGACTGAAA	TAAATGTTGA	ACTTTGATAG	420
10	TACTTTTATG	TTTGAAAAAT	TTTAAATTTT	TATTGTATGG	CTGTCAACCAC	GAGTACTCAT	480
	CTTCAACCGA	CATTACGGGT	ACCTGAAGAG	CTTATCTATC	GATAACATGG	CGACTCAGGA	540
	GGCGGTATTT	ATCGGGCGCA	ATAGGCAGAC	GAAGGTTGCG	GACTTCTATT	TGCCGACCAA	600
	GACTGTCCAT	TCGACTGGAA	AGTGCAATCC	CTATGGAATC	CGTTGGACGA	ACNCATGCNG	660
	GNGTTTNGC	CATTGAAGGC	CNCAACCCGA	GNTACTCGGN	AATTTATGGG	GCNAAAAACT	720
	TTTGGTCACN	CTCINNCGAAG	CACAAATNCT	CGGCAAGNAA	NAAAAANGGA	ATTGNCCNAT	780
15	TTGGAGCCCN	AAACCTNTAC	NTNGCNTGGN	GNNGGGTANC	TCCNNTTCCN	ANGTCN	

1254UP

	GATCTCTGGT	ACCCAGCAG	CCCTGGCGGG	GACGTGGCAT	TGGTGACTTC	TCCCCAGGT	60
20	AACCGGGTGT	GCCTCAGCC	CCTTCCCCAC	ATTGAAGTTA	AGCTTGTTAG	CGGTACTCCG	120
	CTTCATTTTC	TGTGCCCGGT	CGACCGGTAG	CGTCATAGTC	CCGCCGTGTG	GCCGACCGCG	180
	GGCCGCCATC	ACAGGTATCT	ACAGTTCAAC	GGCCGCGTCG	CGATCCCAAG	CGCAGTCTGG	240
	AATCTCGAAC	GGTGCTACAA	AGAACGGATG	CGTGGCAGAT	CGAAGCTATC	GAGAAGGTGG	300
	TGGGGGAAAT	GAGTGAAAGT	ACACGAAGGC	AGGGTGTCAG	ATCTCGTACC	TCTCGCATAC	360
	AGTACGAGAA	GGAGTCGGCG	ACGGTGTTCA	GAAATCAGCG	CAGTGTCAG	TGCGGGGAAG	420
25	CGTGCAAACG	GAACTCGGAA	ACAATCCGAC	GGACCTACTG	CCAGGTCCAA	GCCCTTTCCA	480
	CGGTGTCACA	GCTAAGATGG	TGACTGGCCA	ATAATTTGTC	ATGCTGGTAT	TCGTGTGTCTG	540
	ACGATTATCT	ATTCCGGTTCA	GCCGTTCATA	TTTAGGTGCG	CTGCAAACGT	GGTGACATCA	600
	CGATTGCAC	GTATATATGA	TGGAGTAATT	CGCATACACT	GAAAATCMTA	ATAATCAATA	660
	ACCCATGCCN	CNACTCGNCA	ACTTCNCCNC	TTCNGCTCCN	GGTGAAATCC	CCTTCACTAN	720
	TTTTTTTTCAT	TGCCCATTTN	ACCGAACTTT	ACNAATNATG	CAATGANAAC	CNCCCCCTCC	780
30	AAACCTANAT	CCTTTTNTTN	NGGGTCCCN	ACNGTTNCCN	TTCCNGNCNA	NCCNCTTTN	840
	ATTCCAANAC						

1255RP

35	GATCGTGTG	TCAGGGTGCA	TTGCAGTGGG	CCTGAAGACG	GTGGGGACTG	ATCGGCGGCC	60
	GAAGAAGCTG	TCGCAGCTAC	AGGCGATTGC	GGCTGTGGGT	CAGGGCCGGC	TTATTGCGCG	120
	GTGGGACTCC	CTCTTCAGAC	CGTTCAACGA	GAAGATTGCG	CAGATTTTGT	TGACACGGAA	180
	CGACATAGTT	GACTGGTCGC	AGTATAAGAA	CGCGCAGAAT	ACGTTCACG	AACTGCTGGC	240
	GATGGGCGTG	ACGCCGATTG	TGAACGAGAA	CGACACGCTC	TCAATCAGCG	GAGTGAAGTT	300
40	TGGGGACAAC	GACACGCTGA	GTGCGATCAC	AGCGGGGCTG	ATCGGCGCAG	ACTACCTGTT	360
	CCTGATGACG	GACGTGGACT	GCCTATACAC	CGACAACCCG	CGGACGAACC	CGGATGCAAA	420
	GCCGATCTTG	GTGGTGCCGG	ATCTGTCAAC	GGGACTGCC	GGCGTGAACA	CCTCTAGTGG	480
	GTCCGGTTCA	GGTGTGGGCA	CCGGCGGCAT	GGCGACGAAG	ATCCTTGCTG	CAGACCTGGC	540
	AACGAACGCC	GGGTGCATAC	GATTATTATG	AAGAGTGAGC	GGCCGTGCGC	ATGGTGCGGA	600
	TCGTGGAGTT	CATGGAATGG	CGCAGCAGTG	CACTGCAGTT	TCTGCTGACG	CGAGACTTGC	660
45	AGACGGACGA	GCTGAATTTG	TTGCAGAGCA	CGGCGTCCCA	CTACACACGC	NCTTCNTGCA	720
	ACTTTGCACC	TCCTGAACNA	CNGATTCTNT	ATCCCNCGTC	TGTGACNCGG	NCGTATCTAA	780
	CAGGGGCTNA	GGCCCCCCCC	AACAACGTNT	CCCACGTNTT	CCGTGAC		

1256RP

50	GATCTAATGG	CATTCTCCCT	ACCAAATGGG	CCCAATTGTA	TATTGCCGAT	CTTCCTACAG	60
	GGNACTGGTT	TACGGATCCA	GCGAAGATCG	GGAGAGTTCA	GCTCTTGTTA	TTGCCGACAT	120
	TGTGTGCAAA	ACACCAGCTG	CAAACTTGAG	GCCATATGTC	ACTGTCTATCA	CAGGTCCACT	180
	TATCCGTGTT	GTTGGCGAAA	GGTCTAGCAG	TGATATTAAG	GCTGCTATCC	TATATGCCCT	240
	AAATGTTCTC	TTTTCGAAGG	TTCCACAATT	CCTGCGGCCA	TTCTATACCT	AATACAGAG	300
55	AACATTTGTT	AAATCTCTTT	CCGACTCAAC	CAATGAGACC	TTAAGATTGC	GGGCCGCGAA	360

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	GGCACTAGGT	ACTTTGATAC	AATATCAACC	AAGAATTGAC	CCTCTGGTGG	TGGAGCTAGT	420
	AACAGGCGCT	CAGCAGGCCA	CTGAAAGGGG	AGTAAGGACG	GCTATCTTGA	AGGCATTGTT	480
	GGAAAGTTGTC	TCCAAAGCTG	GCAGCAAGAT	AAGCGAAGCT	TCCAAAGCTA	ACATCATTAG	540
5	ACTTGTGGAG	CAAGAGATGG	CATCCACAGA	CAGCAAGTTT	GCAGTCGCTT	ACGCCAAGCT	600
	TCTAGGTGCA	CTTTCTGAAA	TCATGTCTCC	GGAGGAGGCG	CAGACCATAC	TTCACGAAAA	660
	GTGCTTGATC	CAATTTTGAA	GANGCACNGT	AAATTGCCGT	CNGACCCAC	TCTATCCTNC	720
	TACCCCTGTA	CNTTCTCCCG	CCATNCACCN	ATNTTGACTN	TTNGTGGTGC	ACGGATCNCN	780
	ATCCTTCCNN	CACACGTTTN	CCCNFNGNAT	TCCCCCNAA	NGAAAGTNAN	CCCCC	

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1256UP

	GATCAACTGG	TCGGGCGGGC	TGCACCACGC	CAAGAAGAGC	AATCCTTCGG	GGTCTGTGTA	60
	CGTGAACGAC	ATTGTTCTGG	CGATTCTGAA	TCTGCTGCGC	TACCACCCAC	GCGTTCTGTA	120
5	CATTGACATT	GATCTGCACC	ACGGAGACGG	TGTCCAAGAA	GCATTCTACA	CTACTGACCG	180
	CGTGTTCACG	GTCTCGTTCC	ACAAGTACAA	TGGTGAGTTT	TTTCCGGGAA	CGGGGGATTT	240
	GGATGAGATC	GGATGCTCGC	GCGGCAAGCA	CTTTTCGCTG	AATGTGCCGC	TCAATGACGG	300
	CATCGATGAT	GATTCTGTACA	TCAACTTATT	TAAGAGCATC	ATAGACCCGC	TAGTTACATC	360
	ATACAAGCCA	ACAGTAATTA	TTCAGCAATG	TGGAGCAGAC	TCTTTGGGGC	ATGACAGACT	420
	GGGGTGTTTC	AATCTAAATA	TCAGAGCCCA	CGGCGAGTGC	GTCAATTTGT	GAAGTCGTTT	480
10	GGGATACCTA	TGCTATGTGT	CGGTGGTGGA	GGTTACACCC	CCAGGAATGT	GTCGCGGCTA	540
	TGGACGTACG	AGACAGGCAT	CCTTAATGAT	GTGCTCTTAC	CTTCAGATAT	CCCAGAAGAT	600
	ATTCCGTTCC	GCGAATGGTT	CGGTCCAGAC	TATCTCTGCA	CCCAGTCTTT	GGATGANTTN	660
	TCCAAAATAA	ACNCCCAAAT	TACTGGANAA	NATACGTNCG	GNTTTAAAAA	NTAAATTNTG	720
	CNCGGGCCAT	TTTGNCTTGA	NNCGAATATC	CTCCAGATTT	CCGTTTAAACN	AAAAAAAAT	780
	GATCGGAANA	ACCAAAANAT	NCCTTGNTAA	CANTNAAGAA	NTTTGCCGNN	ACTTNTTANT	840
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1257RP

	GATCACTGGT	GTCACCAAGG	GCTACAAGTA	CAAGATGAGA	TATGTGTACG	CGCATTTTCC	60
	CATCAACGTC	AACGTTGTCG	AGAAGGACGG	CGAGAAGTTC	ATTGAGATCA	GAAACTACTT	120
20	GGGTGACAAG	AGAGTTAGAG	CTGTGCCTGT	CAGAGAGGGC	GTCAGCGTCG	AGTTCTCCAC	180
	CAACCAGAAG	GACGAGATTG	TTTTGTCCGG	TACCTCCATC	GAAAACGTTT	CTCAGAACGC	240
	TGCTGACATC	CAGCAAATCT	GCCGTGCCAG	AAACAAGGAT	ATCAGAAAAGT	TCTTGGACGG	300
	TATCTACGTT	TCTGAGAAGG	GTGTCATTGC	CGAGGAAGCC	TAAGTGCTTT	ACTGACCGTA	360
	TCTTGATAAA	TAATATGAGT	ATTATGTAAT	CAAAGAACTC	ACTGCTTTTT	ATTGGTGGTG	420
25	TTTTTCGTCAA	ACGCTCTTAT	TAGCGCCGGG	GTTAGAGTGT	GGGAATACTG	GCGTTATATG	480
	CTTTAGAAAT	TATGTTAAGT	AAATTTAATG	TCCTATCAGG	GCCACAGCCT	TAGCAACTAG	540
	GTGCAGGTAC	TCCTTTAGCT	TGCCACTGTT	CTGGAACAGA	AGATATATTT	TATCTGTCTC	600
	GTTGGCACCA	TCGTAGACAG	GTTCAACGCT	TCCTTGCAGG	AACGATGGAA	CGCCAGCTTT	660
	CCGCGGTGGA	AGTTATAGGA	ATTATGGATT	CCAATGACAG	TTGGTGTGTT	AACNANCTG	720
	ATTTGTCCAN	TTTCCCGTCT	CNGAAGCTNC	ANTGNTTCCN	TGACCNANCA	AACCCGGGAN	780
30	ACCCCTAGGG	CTGNNAGGCT	TGAATGCNTT	AAAANANTTT	CNTTGANAAA	NCATTGNTAA	840
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1257UP

	GATCGGGCCG	CTCACACACT	CAGGTACCTC	AAAGGAATAC	GAGTTTGTCTG	CACGCTTCCC	60
	GTGTCCAGAT	GCACAGAAAA	TCGATATGTA	CATCAAGGAG	CCGCAAAACA	AGTACCTCTT	120
	TTCCGGGAACA	GAGTACACTT	TCCAAATCAT	CTGCAGCCCT	GCAGACGGCC	TCACTCACGA	180
	TCCATACGAC	GCGCAAGCCG	CTGCGCCAAA	TGTGATAGTC	GTCCAGTCCC	CATCCGGCAA	240
	GATCTACCGT	CTGAAAAAGG	CGGAATCCGA	TGTCGAATTT	GGCGTATGCG	AAGCTAGGCT	300
40	AAAAGTGCAC	GAGCCAGGCG	TCTGGCTGGC	CCTAATTACC	TCTGAGGCAG	GTGCTGGTTG	360
	GTGCACTTTC	GCGAAGTGGA	TCTGTGTTTA	ACACCTAGAT	GCTACACAGT	CATCCACCCC	420
	ACGAAATTAA	TAGATAGTAC	GGGTACATAC	AAGCCCTATA	GTTTCTTAAT	ACACTTGCCC	480
	TATATTGAAT	ATGTCTACGA	AGTATATGGG	CGAGGCACCT	TCAAAATCGG	TGAAAAAANA	540
	TGCACCACTT	CGAAATCCAT	GTTTTATGAG	CTTAAACAAC	AGTGGTTGTT	GAAGAACCAAT	600
	ACCCTGCCAA	GGAAATGTCA	GGTACTCGAA	CCAGCTCTCA	ACAGATTCTT	AAAGATTGCC	660
45	AGTGTGTGTA	CCGAATCCAC	GTTTCGCTGAA	TGCTGGGACC	GACATCAGAC	CCTTGCAATTG	720
	GTACAAAATC	AGTCTATACG	GNGAGCGCCT	GTNTGCCCN	AAAANAAANA	CCACGGAAGG	780
	ACNCATTGTC	ACTTGAACNG	AGNCAATGTG	TNCNGTGACG	CGGNTNTTTC	GNTTCAAGCC	840
	CCAAGGACAA	NAACGC					

1258RP

	GATCCAACCT	TCTACTAGGG	TATTTTTCCC	TACCTCAGCC	TGCAATTCCA	TGCCATCGCT	60
	AACCAAGATA	ATATTCTCCT	CCAGTAGATC	CATATTCTCT	CCCGACTTCG	CACTAATCGG	120
	GATGCTGGC	ACGTTTCCAC	CCAGATCTTC	AGCATGTATT	TCTATGCTGTA	GCAAAATCATT	180
55	CATTATTTTG	TTGATCACAG	TTTCCTTTTC	TTTTGCCGAC	CGGAGTTTGT	CCACCTTGGT	240

TATGGCGACA	ATCAGCTCAT	TCCCTGATTT	TTTGACATGC	TTAATCGCTT	CAATGGTCTG	300
GGGTTTAAAT	GAGTCTTCGG	CAGATACTAC	CAAGACAACG	ATATCGGTAA	TATTCGCGCC	360
CCGTTCCCTC	ATCTTCAAAA	ATGCTTCGTG	CCCGGGCGTA	TCCAAAAACG	TGATCTTCCG	420
CTTCGAAACA	GGTGTGACAA	CCTGGAACGC	ACCAATGTGT	TGTGTAATGC	CACCAAACCTC	480
CTGCGAAACG	ATGCTCGACT	TCCGCAGATA	GTCCAATATG	GTGGTTTTTC	CGTGATCAAC	540
GTGACCCATA	ATCGTCACAA	CAGGTGGCCG	GTCCCTTCAGG	GCCTTCGGGT	CTGCAGGCTG	600
CTTCAATTCA	TCGTAAACGT	TCTCCGGAGT	GACAAATCCC	TGCCGGAGGG	CAGTTGGTAG	660
CTATCTCCTC	CCAATATAGC	TCGATGTAGT	CTCCTGGAAA	TATGTAGTCC	GCCTGGCTTT	720
TCAA						

pAG1258up

1 GATCCTGTTT ACAACTAAGT TCGCATCCCT ACCAGGGGAA AATATGAAAT
 51 ACCAAGTGTT GTATTCCGAA CGCTAGAATT CTTGTACAAA AACC GCGGCA
 101 TTCAGGAAGA AGGTATATTT AGGTTAAGCG GATCCAGTTC TCTCATAAAA
 151 TCTTTGCAGG AGCAATTTGA CAAAGAATAT GACGTGGATT TGTGCAATTA
 201 CAACGATAAA GTTCTGTCA CACCAGGAAA CGAAAATCAG GGCGGTCTCT
 251 ACGTCGATGT GAATACCGTT TCAGGTTTAT TAAAACTATA CCTAAGAAAG
 301 CTTCTCATA TGATCTTTGG GGATGCTGCA TATATGGATT TTAAGAGAAT
 351 CGTGGAAAGA AACGGAGATG ATAGCAAACCT AATAGCACTC GAGTTCAGGG
 401 CATTGGTTAA TTCCGGACGA ATTGCCAAAG AATATGTGCG CTTAATGTAT
 451 GCATTGTTTCG AGTTATTGGT GAAGATCACC GAGAACAGCA AATATAACAA
 501 GATGAATCTG CGGAATTTGT GTATCGTATT TTCGCCAACG TTGAACATAC
 551 CCGTGAATAT ACTACATCCG TTTATCACTG ACTTTGGCTG TATATTCCAA
 601 GATAAGGCGC CGATGGAGAA CGGACACGGT CAACATACAC ATCCCGCAAT
 651 TTAGTTCATA CTAAGTAAAA TACTATTAAC TTAGAATATG TGATAAGTGT
 701 TTTAATTACN TAACTTGGTA TTAGTCCNAT TGTNTAATAA TTGAATATGA
 751 ATGCNTTATT NTCTCTNANT CAATNTGTCA CGATTGGATT TACACCNGCG
 801 TCTGTAANGA CNTCTAGCTT GGTCATCCCA NTTCTCANTT NCTCCCGCTT
 851 NCA

1259RP

	GATCACACGA	ATATTGCGGG	AGTATTTCTC	CATCGTTCGC	CGCAACGCGG	CCTGCGCATC	60
5	GCGCGTGAGC	GATTTCGGCCT	CGTTGATGAT	CACACTCTTG	TACCTCCGCG	CTAGCCCCCTC	120
	CGATCCGCTC	TGGAAATCCA	CCTGCTCCAT	CTGCGCAATC	TCCTTCAACA	ACTCCTGAAT	180
	CACGATCCGG	TCATTGTGCC	CCATGTGCGT	CGGCGTGATC	TCGATGTGGT	ATGGGCTGCT	240
	GACGACGTTG	AGCTCGAGCT	TCTTGTTAGA	TGGCGTAACA	AATTGCCGCA	CATCAATCTT	300
	TAATTTGTAT	ACACCTGCTC	CAAAGATACT	TGCAAGGAGC	CCCATGCACC	GTGTCTTCTT	360
	CCCAC TTCCA	TTGGGCCCCGT	AAAGTAAAAA	ATGCGGCAGG	TCCTTCGCAG	AACCTGCTAA	420
10	AGCCTCGAGC	TGCTTGGTAA	GCGATGCCGT	ATGTGAAAGG	CTGGTCAACG	ACTTCGGTCT	480
	ATGCTTGTC	ACCCAAAGTG	ACATATTCTT	GTGTATCCTG	AGATGGGCTT	TTGTGTGTG	540
	TAGGGAAGGT	GAGCAATTCA	GTCGCAATTA	AATTCATTTA	GATTCGCGTT	TTAGCACAAA	600
	ACGATATGCC	CTCAGTAAGG	CCAGAATACA	TACACGTACT	TCGCCTACTA	CTTTTGACAG	660
	AAGTAAAGCT	CTCAGGAGAT	CGCTCGAGGA	GATGGCATGT	ATATAACCCN	CAATTACTCT	720
15	GATGCNAAAA	ATGTTGCACC	CNTGCCTTTT	TANTTCNGTC	GACAACTANN	AGAGCCTNTA	780
	TCNAGTCCAA	ATTTTNCCAA	ANCTGGGAAA	ACCTTNTNCC	GTGGTNTATN	AACACA	

1259UP

	GATCACCCCC	CAAATCAGCA	ATAACTCGAA	AACTGTGCCC	AGTACCTTTC	AACGCGCATG	60
20	AACCTAACGG	CGCGCAGCGG	TCATGGGTAC	TCGACTGCCT	TTGTATCCCT	CACACTGCGC	120
	CTCTTCGTGT	GCCGCACGTG	CTTGTTGATG	GTAGCGGCGC	GGCCCCGTGG	ATCTAAGCGC	180
	ACGTCTCTTT	GTACGTGGGT	CTCACGTGCA	CATCGTCATC	CATCCGCTTG	CGAATGAGTA	240
	GATCAGCACG	GAGACCATGC	TAGGCAGGGC	CGTTGGGCGA	GGTGGAAAGG	TTGCAGCAAT	300
	GAGGTGGAGC	AGCAAGATGA	CATCACAGGA	TAGTAGTCGG	AAGAAAGAGC	TATGTGCAGC	360
25	GTACAGCGTA	TGGGATGAGC	GGGTTCGCG	CAGCATGGAA	GAATGCGGAC	GTAGAAGGTC	420
	GGAGGTTCTA	TTGCTTGCCG	TTTCTAAACT	GAAACCTGCG	TCGGATGTGG	CGTACTGTGA	480
	CGAAGAAATG	GGGCTGCGGC	ACTTTGGAGA	GAACCTACGTG	CAGGAGCTGG	TGGGGAAGGC	540
	AGCAGAGCTG	CCGGGCGATA	TCCAGTGCCA	CTTTATCGGG	GCGCTGCAGA	GTAACAAGTG	600
	CAAGGACCTG	CGGAAGGTAG	TGAAC TGAT	CCGGTGGAGA	CCATCGACTC	GCTAAGAAGG	660
	CGCGGAAGCT	GAGGAGGCCG	TGCGAAGTTC	CAGCCGAGCC	CCCGCATCTG	TGTTACATTG	720
30	AGTGAACTCT	CTGGCAACNC	AAAGNNGTTN	CNCGATGAGC	NACNGTGAC	TGTGATTCTT	780
	CTNCCAAAAC	AAACCTTCCC	TGCCCAGCGA	TAAATGGTCC	TGGACCTTCC	CCGCGAAGGG	840
	AACCGATCCC	C					

1260RP

35	GATCCTCAGA	GGGCCCCGAA	GAAGCTTCGG	CCGAGACAGT	AACGATGTTT	GGCGAGGTTG	60
	TGCTGTATCA	CAGTTGAGCT	CTAGGTTGCA	CTTTTCGAAA	GAGCGCTACC	GTAGCTGCAT	120
	GAAAAAAAAG	TAAGGCTCAT	CAGTTTATGC	AGAGGCAAGA	ATAAGTTTGG	TAGAGCCTTA	180
	CTTCACAAGC	GTCGCTCTAG	CGAGCCATAT	TATTTCTATG	CCGGCAAGAG	AAGACCGAAG	240
	AAGGCCAGAG	CTCCATATCG	AAAGTACGTG	GCGGGTCAAG	GGTTTGTGCA	TACCTACGGG	300
40	GTTTCCAGTA	CTGAGAGTTC	AGCACACGAT	GAAAGCGGTT	TGTTCCCCGC	AGACAGTGGG	360
	GTGCAGGTAT	CTGACGATGA	TATTGCGAGA	CGACTTGTTG	ATATGACACT	TTCCGCAAGC	420
	GCAGCGTTTG	CCGGTGGAGC	GGCACCCATA	CCGTATCCCG	GACACTCAAT	GGTGCTTTCC	480
	TGGGAGCTGC	AGTTTTTGTT	TCTGTCCAAA	TGCAAAACTA	TTGAAACACA	CTTCATGCAA	540
	GTGTGCAGGC	GGTGGTATAT	CATGTGTCTG	CCATTGATCT	ACCGAGCACC	AAGGCTCTCC	600
	AGCAAGACTT	CTACAAGTTT	GTGGAGACAC	TGGTGGCAGC	CCGTAAACAG	AATTACCGGC	660
45	AATATTCTCT	GATCTCGACC	GTCCATGAAT	ACCNNANCGC	AAACCTTTTC	CAAGGTCTCT	720
	CCGTGTCTCC	CACCTTGAC	ATTCCGGCCC	CAAACACTCG	TATCCCCNTG	AATCTTACGG	780
	CNNCCCNNTT	GCAACCGATT	TGTCNTNTCC	CAACGTTANC	GAACNCNTTG	AG	

1260UP

50	GATCGACCGG	CCGCCCACGC	CGGTGCCGTC	GGTGAAGTCG	CCGCCCTGGA	TCATGAAGTT	60
	GCGGATGACG	CGGTGGAACG	TGGAGTTGAT	GTAGCCCGCG	GAGGCGTCCT	GGCTCTTTGC	120
	GAGCGTGACG	AAGTTGGCGA	CGGTGCGCGG	AGCGACGTCG	CCGAACAGCC	CGAGCACGAC	180
	ACGGCCAGT	GGCTCGTCGC	CGTGCTGCAG	ATCGAAGAAG	ACACGGTGTG	TGACGGTGGG	240
55	GTCTGCGAGC	GCGAACGCGC	AGAGCAGCGC	CTGTGCGAGA	ACGAAGAGGA	CCTGCATTGG	300
	GGGTGGCTGC	GGGAGGCGCG	GGACGCCGCG	GGAAAACGCC	CGCTTTTATA	CGCGAAAAAG	360

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	CTGCTTCGGC	TACGTAGCTA	GAGATACAGA	GCGGTGGACT	TGAGGCTCTG	CAGCATCAGG	420
	CGGTCCATCA	TCTCGGGCGT	CAGCACGTCC	GAGTAGCCCG	CGGTGCGGCC	GTCCAGCGCC	480
	GCGGTCAGCG	CTGGCGCAGT	GGCGCTAGAC	GCGGTGCTGC	CACTGGCCGG	CTGCACGGAG	540
	TTCTGCTCCA	CGGGCACGAA	GGCCGCGCCC	TGGCCAGGCT	GGAAGCGCGC	CAGACGCTGA	600
5	TGCGCGCCAG	CGCGGCCGAC	AGGTGGAAGC	CGGTGACAG	CAGGCCGTTT	TGCACCACGC	660
	TGTACGCCGT	GGCGCCTGTA	CCTTCCCCNA	ANANGTNTAT	CTTGACGCAT	CACCGTTCCG	720
	CCCCCGCTGC	TTCCGAACCA	AATCCGTCCC	NCTTAACCAC	CNTTTCANGC	CNTCACTTGC	780
	ACNCTGNCCA	CACNCTTCNC	GGTTACGTCC	CAATGCCGTC	TCCCCNNGGC	GCTTAGCNCG	840
	GCTCGT						
10							
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1261RP

	GATCATAAAC	GAAGAATTCC	TAATTAACAA	TTTGTCTCTGC	ATGTACTTCC	TCAGTGAGAA	60
	ATAGCGATAT	AATCATTAGA	AAGCTTCCCC	GAGCACTTTA	GCAGCACCGC	ATGCCAGCAT	120
5	AACCCCTGG	ACTCAGGGCA	GTATGCCGGC	TGGCACCTCG	GCACCTCATC	GCAGGCGAGA	180
	CAGTCCACCA	CTGCGAGCAC	CGTAGTATTT	ATACTTTTCC	AGGTTGAAAA	ATTTTCGACC	240
	GCCCCACGCC	GCAGAGGGCT	GGACGCGCAT	TAGGGCTCAC	AGCGGTCGAC	TGCCACTGCT	300
	GCCCCAACAG	CGCCGCGCAT	GTAACGTGAA	ATGATATATT	ATACCTTCTG	ACTACAATGT	360
	GAAATATACA	AAGGTGGCTC	ATAGGCGCAT	TGCATTTATT	CAGACGCAGT	AGCTCTGGTG	420
	TAGATAGCCT	GCTTGGAGTG	CTTGGAGATT	GGCTTGATGA	TGCCCTCGGT	CTCCAAGTGT	480
10	CTCAAAGCAA	CTCTGGCCAT	GGAACCGCCG	ATCTTCAATC	TGTCGACCAA	CACGGACACA	540
	GAGACGTATC	TGTAGGTTGG	GACCTCCTTT	AGGATTCTGT	CAAGCTTGTC	CTGGTCCAAG	600
	ATGACGGCGT	GCTGGGCCTT	GTCCTTGTGG	GACTTCTTGG	ACCACTTCTC	TTGGACTTCT	660
	TACCACCGGC	CATGGCGCGC	GCGCCTTCTG	GGCCTTAAAN	ATNTTGT TTT	TGGTGCATAT	720
	ACNGTGTGCC	CNTATACTGT	CCGCACCACT	GGCNTCTCTG	CGNAGGGTGG	TGAGCTTCCG	780
	TACTCCNCCC	CCTACCCNCC	CCCCCNNGNT	TGTCNNTTTC	NNCNNNCCTA	ANTCT	

1261UP

	GATCTGCAAC	AACACCATTTC	CATCGCGAAG	TCTTTCCAAT	TTCTGTTCTG	GAATATTATG	60
	AGGAAGTTTG	AGAACGATAT	TGGGAGCGAT	GATGAGGAAG	ATCCCTTCCA	GATCAACGAT	120
20	TTGGACGAGG	AGAAGACCTT	GCGCATGCTT	TCTAACCAAG	CCTGTTTCTT	CGGCTACCTG	180
	ATGGCCGAAG	GTCAGGTAAA	GTTAGATGTT	TTAAACATG	TATCCATTAT	GGGGTTGAAC	240
	TCTGACGGGA	GACTTTTCTT	AGAGAATCTT	CTATTTTCACT	TTCTGTTGGC	CTCAGCCAAA	300
	AAAGCAGAAA	CTAAAAAGAA	GGTGGGGAAT	ATCAAGGAAT	GGTCTTACAG	AGATGACTTG	360
	TTGCAGGGCG	CCCTGTCCGA	TGGGATCCAG	GCCGAAAATA	AAAAGATAAT	CTGCAAATCG	420
25	CTCAGGATGT	TTATGAGGAA	TTTTAGATAC	ACGAACTATA	TTCTGTTGTC	GCCTGGCTCG	480
	AAGGAGTATC	AACGTGACAT	GAGAAGGTTG	GACTGGGCCG	TTAAGCGTTT	TTTGGAACCT	540
	ATAGATGAAG	AACTGGATAG	TGCAGATTGT	GAAGAGCTTC	TTGTCACTAG	TCTGAATGCA	600
	TATTACGTGT	AACATTGAAC	ATACGTACTC	TATATTAAAG	TGGTGAAAGT	GATGAGAGTA	660
	TGACGTCCNT	GCTTTTATTG	CATACCACTT	NTGAATTACA	GTTATTTCGGT	GAATGACNAC	720
	AAACANGTTT	CATTACTTAC	TTGTTGACNT	CGCCNCGACC	ACCACCCGCG	CCACACCTTT	780
30	GTTTACCTTA	TAAAAATCTC	CACNTCCGNC	GTATANAGCC	TNAANAATTC	NTTCGCTCAT	840
	GCGGTTT TGA	CN					

1262RP

35	GATCTTTTGA	CACGCTGGTA	ATGTTTCCCA	CTAACTGGTA	TTTTTCCTTG	TCTAGATAGT	60
	CTGCCGTAAA	GACTCCCGAC	GTGATCGGCC	GGGCACGGAC	GCCCATCTGC	TCCAAGGCCG	120
	TCACAAGTTT	CAGGTTCTGT	TCCAGAAAGC	ACTCGCGAAC	TACTGTCATG	GTCACAGGAT	180
	CAGTTACGCG	AATTCTTCTT	ATATATGAAG	GCTCGATACC	CTGAGCCTCC	AATTTGTTAT	240
	TCACCTGCGG	ACCCGTGCCA	TGCAGCACAA	TCGGATAGAG	CCCCACATGG	TACAGGAACG	300
	CCAGGCATGA	AGCCAGTTCC	GGCAAGTTGT	CGCTGATGAT	GGCACCTCCA	ACTTTGATAA	360
40	CCGCGAATTG	CTGCTCCGAG	ACGGAAGTAA	AGTACTTCAG	GTA CTGTTCT	ACTTCACGCT	420
	TAGAGCCAAT	ACTGTTGAGA	AGCTGGATCA	CGGTGGACCG	TGCTGTCAGA	GACCCAACGC	480
	CCTCGTTGTT	CCCGGTTCTT	GCATAGTTCA	GCTTCTTTAT	AGCGGCAGTG	CTGAACAATT	540
	CGCGCTTGTA	TGCGGCACGG	ACAGCCCATG	GCGTCCGGTT	TTAGATCCTG	CTACCAGCGA	600
	AGCTCTACTA	AACAGTAGAG	AGTGCTCGCA	AGCATCTTGG	TACTCCGTTT	ATCCCAGTCG	660
	CGCGAGTTCT	AGCTCTCGAA	AGCAGTCCGT	GTGGCTTATA	GCCTAANTTC	TCTTCGGTTC	720
45	CATAACCACA	AACCGTCTCN	TTGNCNTTCC	TGANTTTCAA	GACCCCNANA	TTTTTACAAT	780
	TTNTGCATTT	NTCCNNGNGNA	AGGGTGCNAT	TTATTTNTTGC	ATNCNTTTAA	A	

1262UP

50	GATCACAAGC	TTGTTGAAGC	CAACTGCTGA	AAATGTCTCC	TACGAGAAGA	AACGATTCCCT	60
	TCCACTAGGA	GACGTGTGGC	AAATTTTAAA	AGGAGCCAGT	AAGACGCAGA	CTAGCCCCAG	120
	CAGAAGCGCC	AGTAGTTGTT	AGGAAGCATT	CCAGAGCGTA	TACGACACTT	TGAAGACGGA	180
	CAGCGTTTCA	AGAAGACAGA	GACAATCAAC	ACCAAACAAA	CATGGAGAAT	CCTCACGTAC	240
	ATGATAATTT	ACAACACATC	CAGGCGGTGT	TATCGAACTA	CGACACATCG	TTTCTCTCGG	300
55	ACGATGAAGA	GGACTACTGT	CCGCTCTGCA	TGGAGCCTTT	GGACATCACC	GATAAGAACT	360

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	TTAAGCCGTG	TCCGTGCGGG	TATCAAATCT	GTCAGTTCTG	CTACAACAAC	ATCAGACAGA	420
	ACCCGGAGCT	AAATGGGCGG	TGTCCTGCGT	GTCGGCGAAA	TATGATGATG	AGTCGGTGGA	480
	GTACATTGTT	TTGAGCCCCG	AGGAGCTGAA	ACTTGAGCGA	GCGAAGCAGG	CGCCGAAGGA	540
	GCGCGAGCGC	AAGCAGCGCG	AGAAGGAGCG	AAAGGAAAAC	GAATATGCCA	CCGCAACATC	600
5	TCGCCGGCAT	GCGCGTTATC	CAGAAGATTG	GTATACGTTA	TTGGCCTGAA	CCACCCGTAC	660
	CGTACGAGGA	GGTTGGTGCG	CTGTTGCGCT	CGGACAGTTA	CTTTGGCNGT	TNCGGGANAT	720
	TTACNNATCN	TCCGTGAACC	GCAAAAAGGCC	CCATGACCCC	NACGGTNTGG	ATNTNTTTCC	780
	TTCCCNAAAA	AAGAGCGGCC	CNNTTNCGGC	GTGGATGTNT	TTTNTGANGG	CGNGGTGAGG	840
	GGGTACGACC	NATNTGCCTN	TTTTG				

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1263RP

	GATCGCGCCA	TTCGCTTCTG	AATGGTTCCT	CACAGAAGGA	TTCGTCTACC	AATGGCATT	60
	GTTCAGCGAG	GTCCTCGCTA	CTAACAGAAT	CGTCTGTGG	AACTCTCTTT	AGGAAGGTGA	120
5	ACAGTTTCATC	TATCCTTTCA	AAATTGATAC	TCTGAAAGGG	TTCATTTGCG	GCGTTAAACA	180
	TACTAGATGC	AGTCATTAGG	GCGGCACTTT	CTTGGTTAAT	ATCGTCAGCT	ATCCTTTTTTA	240
	GTGCTTCTTC	CTCATTTTCA	TTGGGCTTGA	ATAAACCTCT	AGCTATCAAA	AACTCAATTA	300
	GTATCTTCCT	GACCTTAGTA	GTTGGTCCGT	CTGTGGGCTT	AGTCATACTC	ATTAAGTGAT	360
	GACGGAGCTT	TTGCACACCT	TTGCCAGAAA	ACACACAAAA	TATTTGACGT	TGGTTAACGG	420
	TAAATTCAC	AGGAGGAGGT	CTGCAAAATT	GTGTGATATC	TGGCCTGAGA	AAAGAAGTAC	480
10	CGCAGTCAAT	GACAAATGAG	AGAGCTTTGG	ACAAGCCATT	ACCAACTCAT	ATATTGGATA	540
	AATAGTCAAA	TTAGTACAAT	ATGATAGGTG	AACTCTTTCC	AATGTGTCTC	TCCTACCACG	600
	CAAAGCAATC	ATATTTAATA	ACCTCATCTG	TCATCTGAGA	ACATTCACCA	ACCTTATCTT	660
	TTTAGTTTGT	TAATTCCTCA	ATCATATAAG	TATGAATTGT	CCATTTTGTA	CACAACNATC	720
	CNCTTCTGAT	CNNGGANATC	CTGATTCAAC	CTTATCCCN	CCNGAATGA	ACNTGGCCAA	780
	NGANATTNTN	GTTTTTCCCN	CTTGAAANCT	CNAAATNCAT	ACCCCGCTTA	CC	
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1263UP

	GATCTTAAAA	GCTGGCCTCC	GCAGATAGAC	CTTCGCGCA	GAGGCTGGAA	ACCTCAACTA	60
	GCAAGTCGCC	ACCCGAATCA	GATAAGCACT	AGAGTCGTTT	CAGTAACAGA	GGAAGCGATC	120
20	AAGGAAGATA	GTAGAAGAGG	ACACTGCTGC	CAGGCTTGAT	CGGACAGAGG	GTTTAGCTTT	180
	CTGTTGAATT	TTAGAGTTTC	GGGGCTTTGT	TTACTTCGTT	TCATTCTTTC	GTGTAAGAA	240
	GCTGTTTGCA	GGCTGCCATC	ATTTGCCAGT	CGCCAGGTAG	GGTATTGCAG	GGCGACGGAG	300
	TCCGGTGAAC	AGAGACGAC	CGAGAACGCC	GATAGACAGG	CGTTTGTTTG	TAAGCGGTGA	360
	GAGCTGAAGC	AGGTCAAGAG	GCCGGCTTGG	GCAGGTTGTG	CGGCGGCGGC	AGAGCACAGC	420
	AGGGCATCCG	AAGAAGGCGG	AGCGTGCGGA	CAGGAGCGCA	GGCGCGCGAA	CAGGGGGGTG	480
25	TGATGACGAG	CGAGACGAAC	AACAACAACG	CGGCGAGCTC	GAACGGCGGG	CAGCTACCCG	540
	CATCGGGGCT	TCCGGCGAGC	TGGTTTACGA	CGCCATTCCCT	CGCGGCTCGA	CCACAGACAG	600
	ACAGCAGTAC	TCCCAGAAGT	TTCCGCGAGC	TGTTTTCGCG	TGACGCCAGC	GCGCCAGAAC	660
	TATTTTTC	CTTACCAACT	GGCCGNAATG	CCCCCCTT	TNTTGNCCAA	ANACCATTTT	720
	TCCNCCAGCN	CCCNCCCTNC	TAAAACCAAT	TCTTACNNGG	NCGAATGAAA	TGGGTTGNNT	780
	TTCCCGCCCC	NGAGAACACA	TTTTTCCNCA	CTGTGACCCG	ANTNNTTANT	CTCCCNAAACA	840
30	TTATTTTTTTC	C					

1264RP

	GATCTCGTTT	TTGTAATGCT	CTAGCTCATA	TTTGTTGAAG	GAGAAGGGTG	AAAACAGCTC	60
35	CGAGGCTGCA	ACTACTGCAA	AGAATAAAGA	GCAAAATATG	GCACATAAGA	TGCTTTCCCA	120
	ATTCATTTGG	TACAGCTCTA	ATACTGTGAA	CCCTTAATCT	CGGGTAGGCG	CAACAGTTAT	180
	GCGGCCAACC	ACGTTAACGT	GATAATGATG	TAGGTACCCC	GGTGAAAAAA	AGAGTATGTG	240
	GAACCGCCCA	GCTGAACCAA	GCGGATGAGA	CATGCCAACC	ATATCCAAGC	ATACTTGACC	300
	ATGATGACGC	AAAACATATC	AGCATAGTTA	GTCTTGACGC	TGAGACAGGC	TTCAATCGTA	360
	AACCTCCCA	CTTCACTATT	GTACAGTGAG	AGGCAACATA	ATTGATCTTG	TGACTACCAC	420
40	CCATACATT	TGCTACCACC	CATACATACT	AATTAATGGG	GAAAATAGCG	GCTGGTACAG	480
	ATTCTTGCA	CTCCCTGCCC	CAGAGGGCCG	CGGGCTCTC	GTTCCCCAGC	GCGCGCAGGC	540
	GGCCGCAGGC	CGACTGTCTT	ACTACGCTCT	CCCTGTTGGC	CCGTGGTTAC	CGCGCTCAA	600
	ATTACCAANC	CTCCAATTTT	TGANATTCCC	CGACAGTTNT	GTNCCNTNTT	TTTACCCCAA	660
	TTCCGGAATT	TCCCTATTAA	ANGGTAAGAC	CCNNNTTTAC	TTTTGTGGAN	TAACCTNNGG	720
	CGTNCCTNNG	GGNNTNCCCT	TNTTACNNG	CCCCNTTCNA	GGCCTTTTGG	TTCCCTAAAA	780
45	CCGGTNAAAA	AAAAAAGAT	T				

1264UP

	GATCTCATGT	ATCACAACCA	GACTATGATG	CGACTTGGGG	TGACTATGTC	TCCTTTGCCC	60
50	AGCGGTTTCA	AGAACGAGTG	AAAGACAAGG	ACCTTATTTT	GATCGACTCT	GGTGACAAAC	120
	GTACCGGTAA	TGCTCTCAGT	GATCTCACTA	GTCCGATGGG	TTTGAAGTCA	AGCGGTATCT	180
	TTAACCTTCA	GAACTTGAC	TTGTTAACTC	TCGGTAATCA	TGAACTGTAT	ACGGAAGATG	240
	TGGTTTCGCT	GGAATACTAT	GGAACAGCAA	TGGAGCCTGA	GCTAAGTGAT	AAATATGTCA	300
	CAAGCAATGT	GGAATTTATC	ACAGAAGATG	GGGACGTTGT	ATCCGTTTCG	CAATAAATAT	360
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	AGGTACTTTG	AAACGCCAAA	CCAGAATCTA	CGTGTATTGG	CGTTCGCATT	CATGTTTCGAT	420
	TTTCCCGTGG	GCTGCTAAAA	ATGTTAGGTT	AACCCCTCTG	GCCGAAGAGG	TTAAAAAGGA	480
	CTGGTTCACC	CAAACTGTGG	AAAAGTACCC	GCTGACAAGC	TTGATATTAT	AGTTGTCTTC	540
	CGTCATTTAC	CAGTCACCCG	TGGCGAAACG	AGAGCTTCTG	CAGTTACACC	AACGACTAAG	600
5	GGAACTTTAC	CCCGACACTA	TTATCCCGTA	CTTCCGAGTG	NNTACTCAGT	CNGAAANTCC	660
	CTNGTTTNG	ANAAAACGAN	TGCTTTACCA	ACGGCGAAAT	TCCTGAAACA	TGGAATCCNA	720
	TCAANANNNG	TTTCNCAAGA	AACCAAATTT	TCCATTTCNAT	ATGACTTACC	CAATTCCTTT	780
	TCCCTCCNG	NTTNANACTC	CAAATTCNT	CCAAGGAAGA	ANANTNACNC	CC	

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1265RP

	GATCTTGCTC	AGAAATAACT	TGCATTGTCT	CCACTATTTT	CTCAAGATTA	GCATTTATGC	60
	ATGTCAC TAG	GCATTGCGTT	TCAGGTAATG	CATTCCCAAC	AAGTGGCTTA	CGATCTGGAA	120
5	CAGATTGTGT	TCTTTGTGAT	TCTGGTGGAG	CCGTACCTCC	AAAAAGTTGAA	TCTTCGTTTT	180
	CCGCCGAGCA	GGAATTGCAT	GGACGAGACT	TCTTGTCAGA	CATAAACTCA	AGTGGCGCCG	240
	CTCTATCTGA	CATATCTTCC	TGACTCTCTT	CTGCATACGT	GCGGTTACCT	GGCTCTAGTT	300
	CGTCCCTCAGT	CCCTACGTCT	CTTCTTG CAT	GCATATCCCT	TGTCGTCAGA	TATGTTTCTC	360
	TCTTCGGGCT	AGAAGGGTCC	TCATTTGTAG	GATCTTGAAC	AAAAAGTAGT	TTGTTATTCT	420
	CCAGCTGCGC	AGTCTCTTCC	AGGTTTTACT	TCCGATGCTT	ATTAATACTG	GTTC'TTTAGA	480
10	TGGTTCCCTG	ACTTTGGCTA	TAGGCCATTG	GTTCCGGCGA	CTTGTAAGG	TATGCATTGA	540
	GAGTCCTCCT	GGTTAAACGT	GTNGTCCCCC	CGTTATTTTA	NCACGGCTTG	GCCGGAATGG	600
	TACACNGNTG	AGTTAATCNC	NGCGGGTTGC	NGTTCCATCC	TGTGGGGGGC	CCACCCAGAA	660
	CCCNAACTTN	GGCGCCACNA	TTTCCCNTCN	CCAAACNNTT	TGGCCNAAAA	AANAATTNTT	720
	CCCCCAAGGN	NGGANACGC	ATACCCCGAN	ATGNGTATN	TTGTGGGGGN	AACCCCNNA	780
15	ANCCCCNCCC	CCCNNGNGGAA					

1265UP

	GATCCGGTCTG	CCGCTGGTGA	AGGCAGCGAC	GTCGTTGTAC	CGGCAAGGCG	GCCTGCGCGC	60
	GTTCTACCTG	GGCAACGGGC	TCAACGTCAT	CAAGGTGTTT	CCGGAGTCGG	CGATGAAGTT	120
20	CGGCTCGTTT	GAGCTGGCGA	AGCGCGTGCT	GGCGGGCTTG	GAGGGCTGCG	GCGAGACGGG	180
	CGAGCTCTCG	CGCCTGTCTGA	CGTACGTTGC	GGGGGGGCTT	GGCGGCATCA	TGGCGCAGTT	240
	CTCGGTCTAC	CCAATCGACA	CCTTGAAGTT	TCGCATACAG	TGTGCGCCCC	TGGATACGCG	300
	CTGCCGGGGT	CTGCCGCTGC	TAATCAAGAC	GGCGAAGGAC	ATGTACCGCG	AGGGGGGTCT	360
	GCGACTCTTC	TACCGCGGCC	TTGGCGTTGG	CATTTTGGGC	GTGTTCCCCG	TACGCGGCGC	420
25	TCGACCTCGG	CACCTTCTCG	GCCCTCAAAC	GCTGGTACAT	TACCCGTGCG	GCAAATGCGC	480
	TGGGCATCTC	CCGAGAACGA	AGTGGTCATG	AGCATCTCCG	TGTGCTGCCG	AATGGCGCCT	540
	TCAGCCGTAC	TCCCGCGCCA	CGTGCTTACC	CTATCAACCT	TCTACNGANG	CGNTCCCAGC	600
	CCAGGAGT	TNTCNCNCCC	CCCTCCTACA	ANGNTTCAAN	TNTTTCGAA	AACACCNCNN	660
	AGGCCCCCCC	GCTTTTACAA	GGTTGGTTCC	NACATTGCCA	GGTNNCCCNC	ATCCCACTCT	720
	NTTTT'TTNC	NAAANTTAAA	NNCCANCCCC	CCNAATAAAG	GCCCCCTTNTC	CCCCCNACCC	780
30	CNGGAATAAN	GGTTCGGNCT	NNAAAACCAA	NACNCCCCC			

1266RP

	GATCTTATCT	GGAACACCCA	TTCAGAACGA	TTTATCTGAA	TATTTGCTCT	TACTAAATTT	60
35	TAGTAACCTT	GGGCTTCTCG	GTACGCGGGC	ACAATTTTAGG	AAAAATTTTCG	AAATACCCAT	120
	TCTACGGGGT	CGGGATGCTG	ATGCTACTGA	CAAGGAGATC	GCTGCTGGTG	AGGTGAAGTT	180
	ACATGAGTTA	TCCCAGATTG	TGTCGAAATT	CATTATCCGG	AGAACCAATG	ATATCCTATC	240
	GAAGTACTTA	CCTTGTAAGT	ACGAACATAT	TCTATTCTCT	AATCTCTCTC	CGATGCAAAA	300
	GGCAATTTAC	GAACACTTCG	TGAGGTCACG	AGAGGTTGCC	AAGTTAATGA	AAGGTACAGG	360
	GTCGCAGCCA	CTGAAGGCGA	TAGGTTTGCT	GAAAAAGTTA	TGTTACCACC	CTGACCTGCT	420
40	AGATCTCCCG	GATGAGATCG	CCGGTTCTAC	AAATTTAATT	CCAGATGACT	ACCAGAAGTG	480
	CTAGTGACAC	ACACTCCGCC	GCCGAAGAA	TTCCCCTTTT	GNATTCCAAC	GANACATTCC	540
	ATCNAAATTT	GCNATTCCTA	GAACGTTTTT	NGTTTTAGAA	TCCAGCCNTG	ATTCTNAATGA	600
	AAAAAATGTC	CCNGATTTCT	ACNNCCCCC	ACCTTGGAAT	TTNTCCAAAA	AATNTNNCCN	660
	CCNCCCCCN	GGTTTNTTCC	CANCTGAANG	NNCCCNNGAA	ATTAANNANC	TTTNAACCTT	720
	TTGAAAATTC	CAAAACCCCC	GGGAGAATTT	NTCNTTTTNT	TCCCCCNNGN	CNGGGNNGGG	780
45	NTCCCCCTTT	NGGCCCCCGG	NGAANTTTGA	CCCCAAAGN			

1266UP

	GATCTGTCAG	CATTCACAGA	AACCATCGCT	ACGAAAAGTT	TCCTACAAGT	AATCCCAGCC	60
50	AGCCGAAGGA	CTCCCCGTTG	GGTCTGTAG	CCGTCTTGGC	AGCGCACAGT	TCCAGGACT	120
	TGTCTTCTGT	TGGTCAGAGT	ACTAGGCAGG	ATGCGTTTGC	TATTCCAAT	CACAGTGTG	180
	TGGCTAATGA	TCGCCAGCCC	TCTTTACCGC	GAAACCCTGC	CCCAGACTCC	ACGTTCACTG	240
	CGGAGTTTAA	CCAGCTGCTA	TCTGAATCCA	GCAACTGCCT	TGAGCTTGAT	TCTATATCT	300
	CAGGCAACTC	AGTTCTCTGG	AATGGCGAGA	CCTTAACCTC	TGAAGCAAGA	GCTACCTCTG	360
55	AGGGCGATGT	GCCATCTGTC	TCGGAAGATG	CCCAGCACGA	CAGCCAGGCA	AATTCTGCAC	420

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5	AGAATGGCCT	GAAGTATTGA	GTCTAGCGGA	CACTGAGTAT	GCGGACCTGG	ATAGTTTGAT	480
	CACTAATTTG	TACTTCTACC	ATGCGAGGGT	TCGTCCCGCG	GGTCTGAACG	TTTGTTATA	540
	ATGATCGATT	TTAGAAAATA	TAAGAACCCC	CTTGAATATG	AATACNGNCN	NTTAACCCCC	600
	GGGGGTTGCT	GATACCCCCC	CTNTCCCCCN	CTNGGNTGAA	TTNTTACCCC	NCGGNGGGGN	660
	GANAAANAAT	TCCTGCCNNC	TTGGGTTCN	AANCCCCATT	CCCTTTTNAA	TNAAAANTGC	720
	TTCCNNGNCN	TNTTAAAAAA	AAAAACCGTG	TTGCCCCNAT	AACCAAATCC	CCNCGCANGN	780
	AATTCCTGG	GTTCAACANC	CGCTCAC				

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1267RP

	GATCCATTCC	ACCGGATTGC	AGCAGCTAGT	GCATTTGGCC	ATACGCCCGA	TTGCCCTTTC	60
	TTATAATGAA	TCCCGGCTTG	TAGAGCATCA	TCCGGCACTT	CACGTGGTAT	TGAATAGCTC	120
5	CTCATAACCG	CACCGGAAGA	TTTCAGGAAT	ATATCTGGTT	GTGTAGTGTA	GAGGTATCA	180
	CTGTGGATTTC	TGATATGGCT	GTTGCAGCTT	GAACATTCCA	CTAACCTCGG	TTCGAATCCG	240
	AGCACGAACA	ATTTTGTGNC	TNAANCCNA	NATTTTNNCC	CCTANAATAN	TGGNCTNNCC	300
	AAAATCNTCN	NNTTTNAATT	TTTCCAAAA	CTTTGTCCGT	GACCGGANTN	GAAATGNGGG	360
	NAAGTGGAAT	GTCCAAGNCG	GGNNCGCNA	ATTAGAATTC	CAGGGAAAAAT	TCCTACANTA	420
	NANAGGTGNC	ACCCNCGGNA	ACCCCGGGGN	GGNNNACTG	GNCCCTTTNA	ACCTGNGAAT	480
10	GCGGTTNTCC	AACCTTTTNC	CGGGNGGCTT	GGCCCCCN	TTAATNCNAT	TACCCNCCCC	540
	TNCTTTTCCC	NAAANNNGAT	CCCCCCNCG	GAAAGGTTCN	TTNNNNNANCN	TAGGAGGCC	600
	CTTNGGTCCG	GAATTNGNNN	CTTTTCNNC	TCCCCCCCCA	AATCCNGGAC	CCTGNAANNC	660
	CCTTNTNCCC	CCNTTTTAC	NNTTTTCNN	GNAANTNCTT	CCCTTGGCCC	ATCCCCGGAC	720
	NNNAATTGGG	GNTTTAANGG	CCCCCGGNC	CCCNCTGN	AAAAAGNTNN	GGNNCCCCC	780
	CCCCCCTTN	GN					

1267UP

	GATCCGCATC	GTTTTGTTGA	GTCATACTAC	CTGGACGCCA	TGTTCCGCCG	GCTGGCGCCG	60
	CCGGCGAGTC	TCGGGTCAC	GGTCGGCTTG	TGCAACGCGG	ACTGTGCCCC	CTCCTACTGG	120
20	TTGGAGCTAC	CCAAGGACCG	TATCCTGTTC	CTATGTGCGA	TTGCGAACCT	CGTAATCAGC	180
	CACCTCGTGA	ATGTAGACCC	AGCAGCAAGG	GACATGCACG	CCTTCTGGGA	GAAGGTGAAT	240
	GCGCTCTTCT	TGGAGAACCG	CTCAGGGCGG	ATGCTGCAGA	AGGAGGCTTT	GGTGCCGCAA	300
	CCGAAGAGCT	GCGAGAACGA	TGGCGGCGAG	GCGAACGTTT	CTGCGTCCCC	GATTTCCCGT	360
	TCGCAGACAC	AATACACATC	GGACCAGGGC	AGCAATTACA	TGAACCCGCA	CGCATTCCGC	420
	ACGGCGGCC	ATGCGGCCGG	CACAGGCGCC	TCGTCTGTTG	CGCCTAACAG	CGACACCCTC	480
25	TCTGTGCGAC	TGGCTTCACA	CAACGCCTGC	GCCCCAGAAG	CGTCGCGCAG	ATTCCATACC	540
	AGACTTGCTG	ACGCAGCGTC	GAGGACGCCA	TCAGACAGGG	AGCTTGCTGC	TTTGACCAGA	600
	AGGGCTTGAG	CAGGATTCCC	AGGACGACAC	GACCGCNCCTG	TAATGCAACT	GTTGTCTTTC	660
	CNATTTGCGC	CCTATCCCCC	AATGGAACGC	CACCTCCCCNG	AAAAAAAAAA	AATTTTCCGN	720
	TGGATATTTG	ATGAATTGAA	TTAGAAAAAT	TACNTTTC	NNATTCCTGC	GGTGCCACAA	780
30	CAATTGCGAN	TNCTAGACCC	GCGNCCTGGC	NTTNGGTTTT	AAAT		

1268RP

	GATCCTGAGA	ACACTTTTTTC	TGTGGAGGCT	TATCAATGCT	CTTTCTATCC	GCAGCTTCTT	60
	CCAGGCAGAT	GAATACTGGC	AGTCGCTGGA	GCCTGCGCAT	GTTAAGGCGT	TTGGATATGG	120
35	TGGGCTGACT	TGGGAGTGGC	AGCATGGGCT	GCGCAGCTAT	GCATTCCCGA	TGCTCTTTGA	180
	AATGTGCTAC	TATGTGGCGT	GGATACTGGG	TGTGGCCACC	CGGATGGCGC	TGCAGGGGTT	240
	GGCACATGCC	ATGCGCTGT	GTGGGGCGGT	GGTGCCGAGC	GGCGCGGCGG	GCGTGGCCGC	300
	GATGAAGGCC	GTCTGGGAGC	TGCCGGAGGC	AGTCGAGGAA	CTGGTGGAGT	ACTACGGGGT	360
	TATTGTACGG	GCCGCGAAGT	GGTGATGGCG	GCGGTAGCAG	CGTTCGGGGA	GTTCTACAGC	420
	GTGCTGCTGG	TTGCGCAAGC	TGTATCTGCG	AGTCGCGGAT	AAGGGGGACA	CCAGAAGGGC	480
40	GACGCGCGCC	GTCAGCCGTT	GCGCTGATGC	TGACCATGAC	AACTTCTTCA	ACTGTTTCTT	540
	CGCGACGCGA	ACGTTTCATCA	CTCCTTCGAG	ATGACGCTCA	CGCGTCGCGC	TCTACCATTG	600
	ATTGAACGGG	CCTCACTTGG	TTCTCTNGCT	TCNCCCAACT	TGCGGTGGCT	CTTTTGCCTG	660
	CCTCACGCCA	NTACTTTTTTA	TCTGGCNCCC	TGCTNTTCTT	GGTGNGANCC	TGTTCCCCCN	720
	ANNGTGNCN	CCTTTTAACC	CGNCCCAAGT	TGCCCCGAGC	CCCTGCGGTN	TTTCAATCCA	780
45	ANNANNC						

1268UP

	GATCCAGGTA	TACCCGCCTC	CGTCGCGCAG	CGAGCTGCGC	AGCCGCTTCA	TCGCTGCAAC	60
	TGAGAATGCC	CTCGACCTGA	TGTGCGGTAT	GCTGACGATG	GACCCGCACA	AACGGTGGGA	120
50	CACGACTCGT	TGCCTGCTCA	GTCAGTATTT	TGTAGAGCTT	CCGGAGGCGA	CACCTCCTAC	180
	GGAACTTCCA	AAACTAAATA	AGTAATGACT	ATGATAACCT	AGATGGTATA	CTCGGACGTT	240
	TTGTGTTTGT	GCTTTGAGGC	GATGACATTG	GCTTTTATGG	TATCGCAGAC	GTTGCCTGAA	300
	AAAGATTCAA	CGTCTCGGTA	ACAGATTTGC	GCAGACTACT	TGTTGAAAGA	ACAAAGACCA	360
55	GAGCGCTGGG	ATGCTCACCC	CAATGACGAA	CCCCTCCGC	CTTATTGGCG	CTGGCTGCAG	420

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	GTTCCCTTAGC	ACCAACAATA	GGCCGCCACT	GCACAAGATC	TTTCCCTCCC	AAGAAGCTGG	480
	TGAACAGGAT	GCTGTTCGAC	CTTGATAGCC	GACTGACCTT	CCCGGAAATT	ACTGCCTGTA	540
	TACGAGCAGT	TGTACACCCC	AATTAGACAG	TAGTACGGCG	ATTTGTAGTA	CCCCGCGCGT	600
	TGAGGGCGCC	ACGACGTTTA	TGATTCATGA	AAAGGTGCTG	AGAAGACTCG	CCCCCCAGAA	660
5	CGAGAGCTCC	CATCGCCNTC	TACTTGCNCC	GGANAACAAC	TGCTTTACTT	GCTGCCCANT	720
	GGANACNAAA	ATGCACGNGC	NCTNCCCTTG	ANCCCGTGCA	CCGNTTCGCC	NAAGGNNCGA	780
	AATGAATTTG	CAATTTAGNT	CNGATTTTAC	NCTCTGGNTC	CCCCCCCCCA	CTGANNGANC	840
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1269RP

	GATCCCACTC	TTGGCAAGCT	ATACGGTGAC	ACTATCATAG	CTCGCGGTGG	CCTCTACGAG	60
	ATGGAAGACA	ACCTGGGCGA	GTTCTTGGAC	AGAGAACCCA	ATAACGAGGC	GTACCTCAGA	120
5	GATCAGGGCC	TAGCCTAAAT	GCTCCTTCTT	TTTCGCGGCT	TCCTGCCCTC	CTATGTATAT	180
	TCCAGCTAGA	GAATCGCAAG	CAAGCCATAC	TTAGAAATAG	GATATTGTTC	CGGGAACACT	240
	GATTTACTGT	GCGTTACTGC	TCCGGAAACT	CACCTGTTCG	GTATCGAATA	ATTAGCGTTC	300
	GACTACCGCC	AGTGTGATGC	TTTCTTTATA	CCGGCATACT	AAAACAGGGT	CCTCAGTCGA	360
	ATCGTGTGTC	ACTGAATATG	AGCCCCCTCA	TGAGTTCCCA	TCGCGTAGAG	CGTCTATGT	420
	GCAGACCATA	TCAACACCCT	CTGTACACGC	GTGGAGTTCA	ATATACGCGT	ACGACGCACA	480
10	TACAATAGTA	CGTGTGCGCA	ACCGTTATAC	GAAGAGCTGC	GTTCTGATTG	CAGCATTTCC	540
	CAAGCCCCGG	AAATACAAAA	CCGCATTTTT	AGCCCAGTGC	GATAGATGTC	CTGAACCCANG	600
	GAATTACANC	GAAGGNCGAT	TGCTACTACN	ANCATCANCC	AGGGCTCGNG	TATTTCTCAT	660
	CCATCCCCCT	CNAACNAAAA	ATCCGGANTT	TTTAAATTTT	CATGCAAACC	ATNCANATCC	720
	CCNTTTNGAT	ATTNCCCCAC	TGGCCCCCCC	NCCCCCANNT	ANCNGTCGGG	ATCCNGNATT	780
	CCCCGGT						

1269UP

	GATCGAACTC	CATGAAGGAG	CGTAATGGCC	TGCTGGAGCT	GCACCGCACT	GGGTGCGTAC	60
	ATAGCGGGAT	GTAGGAATGC	GGGGATAACG	ATTCGGAAAA	GCTGACTGGG	CTGCGCCTCT	120
20	AGCTTCAGCT	CAAGCTGGCG	CAGCAGCGTT	GCTATAGGCT	GTTGTGGCGA	CAAGGTCGAC	180
	ACTTCAGTTG	CAGTAGGAGC	AGGTAGCATA	CGACTAGTTA	TATCGAACTG	GTGCCGGTAA	240
	TGAGGATGAG	GGTCAATTTT	TGGCTCCGAG	CGCTGGCTAG	CACCACAATT	ATCACCAGT	300
	CCATACCTCC	GAGATCTTGG	GAGATCTTGG	CTACGTGCGA	CCGGTTTTTG	ACCCCCCTCG	360
	GCTAAGTTTT	GCACCGTGAC	CTTCGATTCC	TCCTGGGAAA	TGCGAGATTT	CTTTACCTCT	420
	TTACGTGTGC	CCTGGAATAT	CCCCGGCAGC	TCCTTCGCAT	ACTGAGTGTT	GAGCGTGTAT	480
25	ACCACCACAT	GCGTTATCCC	CCCCCCCCTGN	GGGCCCCCNAN	TTTCCCCCCC	GGTTATTTCT	540
	GTCCCTGCGC	CTGCAANAAC	TTCCANTTAC	GANGCAATCT	GGTCCCCCTG	TTCTTCCCCC	600
	AAAACATCTG	GCCCATTGGA	NCCCATATGC	CCTAGAACCN	ATCCAATCTG	CANCCCCGNGA	660
	NTTTTTTGAA	ANNAATTACC	GGNAAGGANC	AACCCGGAAG	NAAAGCCCGC	CCCCCCTGTG	720
	GAGCCNACTT	CCCCCCCCC	NAAAACCNGA	ANTTNTTTTT	TNNTTTGGCC	CNANCGNCCN	780
	TTTTTCNGCCC	NGCCGGGGANG	GCCTTAAAAAN	TTCTNTCCCCC			

1270RP

	GATCATATGG	TGAACCTGGC	ACATACAGTT	GAATCATCCC	AATAGCAAAG	AGAACGTAAG	60
	ATTTACCTAG	CGCGGCATCA	CCTGGAATAT	CTAGCATTTC	CAGCGCAGGT	GAAAAGAATT	120
35	TCTCATGAAT	TGATTGGAAA	TGTGGTTCCG	TGTGTTCCAT	TGCTAAGCCC	GCTAGTACAC	180
	GATAATCATC	ATTAGACTCA	CAGGTTAGAT	GGGCCCTTAC	TGTTGCCTTA	TACCAGTCTA	240
	ATAGAACCCTG	CCTGTAACGA	GCATATTGAT	CCTGAAGAAT	AACCACCGAT	GCGTCAACCA	300
	TCGAATTGAG	CAACAATGTC	GCGTCATTCA	CGGTTTGAGT	GATGTGACTT	CCGGTGAAAT	360
	TCTCAAAGGA	ATTTAATTTT	GGTATCAACC	CCTTCAACAA	GGAAGCTGTG	AAGATATCAT	420
	CAACATGCGA	TTTGTAAGCT	AAACCTTCCC	GCATCCATAG	GAAATCAAAA	GTGGCTGGGA	480
40	AAGCATAGTT	TGCGCTATTG	GCTTTGACTA	ACTGCGAAGT	TAGAATACTA	CTTGTGGGCG	540
	CCAGTTTGAA	TAGCAGAGTT	AGACATTCAA	CGGATTCTNA	GAATATAATC	CTNGCGAATT	600
	TATCCATCCN	CCTANAAAAT	TNTTTCCNCC	TTGATCCANA	ACNANAAAAAT	TCCGTTGACC	660
	NCTGAAGACC	TATTCCTNCC	TTTNAAAGAC	CTGCNCATTC	TTCNATTTCC	CNAANGNNTC	720
	CCGTTCTACC	NAGAAANTTC	TTGCATGCCN	NCATGGTTTN	AACCNAAACN	TCCTTTGANG	780
	NTANTNACTT	CCCCCINNCC	AATTTA				

1270UP

	GATCCGATTG	TCAAATTTTC	TGAATGGTAT	GGTAAGAAGT	TTGGGGCTGG	AAAGGCTAAC	60
	AGTGGTGTTA	TATCTTTGCG	TGATATTTTA	GCTTGGGTGCG	AGTTCATTAA	TAGTACCTAT	120
50	AAGGCATTGG	CTTGCCCTTA	TGCTTCATTA	ATCCATGGGG	CGGCAATGGT	ATTCAATTGAC	180
	GCCCTTGGAA	CCAACAACAC	AGCGTACCTT	GCCGAGAGTG	AGGAACGATT	AGAACACCAG	240
	AAGCAAGAAT	GTCTCAAATA	TCTGTCTGAA	CTAGCAGGAA	AGGATTTAAA	CAAATACATG	300
	TCTGGTCCAT	TCGATGTTAA	GATTGACGAT	GAAACTCTCC	AATCCGGGCT	TTTTAGCCTA	360
	CCCAGAGTTT	CTTCCTCATC	TGTCCAACCG	GTTTTCAATC	TTGGCGCACT	ACTACAGCCT	420

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	ACAATCTCAT	GAAAGTTGTC	AGAGCAATGC	AAGTACAAA	GCCATCTTAC	TGGAAGGATC	480
	ACCTGGTGTT	GGTAAAACCA	CATTAAATTC	CGCATTGGCT	GACTGTACCG	TTACGAATTA	540
	CCCNTTTTAA	TTATCCGAAC	CAACTGATTT	GAATGAATTA	TTTGGATCCG	AAGCNCCCCG	600
	AAAAAAAAAAN	GGNAATTTNT	TTTGN GTTGA	TGCCCCCNTT	TTTNAAACTA	TGCCAAAGTG	660
5	GATGGTTTTN	TTTAAATAAA	ANNANATTGC	NCCCCANCCN	TTTTTAAGGN	CNNACCCTGT	720
	TTGTNNCCNT	GGNGAACCCA	NTCCCAAATT	TAANAAAATT	TNTCGCCCCC	ATCCGCTTTT	780
	TTGNTNCCCA	AACCCANACA	GGGGNGGTGA	AAAGGGNTGC	CAANCTTCCC	TC	

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1271RP

	GATCATTATA	TTATAAAATA	TAATAAAGAA	TATATTTAAA	TAATAATAAT	AATATGAAAT	60
5	ATTATATTAA	TTCTCCATTG	GAGCAATTTG	AGATTAGAGA	TTTATTAGGT	TTAACATCAC	120
	CAATAATAGA	TTTTAGTTTT	ATTAATATTA	CTAATTTTGG	TTTATATCTT	ATAATTCCTT	180
	TATTAGTAAT	TTTACTAATG	AATTTAATAA	CTAATAATTA	TAATAAATTA	GTAGGTTCTA	240
	ATTGATATTT	AAGTCAAGAA	ATAATTTATG	ATACTATTAT	AAATATAGTT	AAGACACAGA	300
	TTGGTGGTAA	AGTTATGAGG	TTATTTATTT	CCATTAGTTT	ATACATTTTT	TATTCTTATT	360
	TTTACTATAA	ATTTAATTAG	TATAATCCTT	ATTCAATTGC	TATAACTTCA	CATGTAGTAT	420
10	TTGTAGTATC	AATAAGTATA	ATTATTTGAT	TAGGTCCTAC	TATTATTGGT	TTTTATACTC	480
	ATGTTTAAAT	CTTTGTTTAT	TTTACCACTA	GGTACACCAT	TAATTTAGTA	CCATTATTAG	540
	TATCCATTGA	ATTATATCCT	ATTTGCTTNA	ACTTATTCCA	TAGGTTTTTA	AAATACACTA	600
	ATATATACCG	GTCCATTTAT	AATGGTTATT	TAGNNGGTTT	AATATTNAAT	TNAAAACCAN	660
	AATATTTACA	TTTTATGGTN	NCCNCCCAAN	AAGGCATTGG	TTTGGTTNTT	TAAAAAGGCN	720
	ACCTATATCN	CCTANTTGAT	NTTTTTTTATN	CCCCCTTTTA	AANANCNATT	TTNNCCTTAT	780
15	TAAANTAAAT	C					

1271UP

	GATCAATCTT	TCGATCATTG	TCCAATATTC	CCCCTGCTG	TATCATATAG	ATATTGATTA	60
20	TAATTTCTAA	ATCAACGTGA	TTGTTCTAAC	TTTAATTAAC	AATTATGAAT	TTTTGGCTAG	120
	TTATTAATTT	TTAATTAACT	AATACCTAAA	TCATTATAAG	CTTGACTTAA	AACAAATAAT	180
	TATTACATTA	TTCTTTATTT	ATTATTTAAT	ATTTAGTTAA	ATTTTAAAGT	CATTATTCTT	240
	AATTTTACT	CACGAGTACA	CCACTTATTA	ATACTATTAA	TTAATAATAT	TAACGTTTGA	300
	TTGCGATGTG	TAATGTCCTT	AGTTAGCGCT	TAATCTGAAC	CAACATCATG	TTCTCATTAT	360
	TATTAATAT	TTTTAATAAT	TTTAAATAAT	TATTTAATAC	GAAAGTTATA	GGATTTCGAAC	420
25	CTATGAAATC	ATAAAGATTT	ATAATAGCTC	AAATATTACA	CTTTAAACCA	CTCAGTCAAA	480
	CTTTCTTAAT	ATATATACCT	TATATATGGT	TTGATAATTT	ACTTATAATA	TATAGTATAT	540
	AATTTAATGA	TAACCTTTAT	CATTTAGGTG	CGTAGGGTTC	ACCCCCCTAT	TGCTAGTCAG	600
	CATATGAGGT	ACCTCCCCCC	AATGATAAAA	GTTATAATAT	ATAATATTAT	ATTAAGTATT	660
	TAAAGAANAT	AATATAATTA	TTTAATAATA	TTTTTATTTA	GGNNAATAAA	AAAAANTTTC	720
	ANNTTTGAAA	NANGGTGCNG	AGAATTANAA	AAAGCNAATA	ATATGTTCAA	TTTGACCCAT	780
30	TAANAATGTA	GTNCNCTGAC	ATCNCCTATT	TCCTATANAA	ANTTTTANAAN	AANA	

1272RP

	GATCAAATCT	AGGTTCTCCG	ACGGCAACGG	TGACGAGTTC	GTGAACGCGC	TCAAGCTCTG	60
35	TGGCTTTTTT	CATAAACACA	CAGACAACAG	CAATAAAATG	TTACACGAAGT	TTGAGTTCTT	120
	CAAGCCTCCA	AAGGAGATCC	TAGAAGAACG	CAAAGCCAAG	CTCGAGCGTA	AGCAGAAGTT	180
	CATCGAAGTG	GAAACAGAGA	AGGAAGCTCT	AGAGTCTAAG	CGGTCGGAAA	ATCCAGAAGG	240
	AAACTGGCTA	CTAAAGCCAT	GTATATATAA	ACGGAGGTGA	TTGCCTAGTC	TCTTCTCAGC	300
	ATGCGATCAT	ACCTTATTCT	TGTAATCTTA	TCAAACTATA	TATAGGGCGA	CCGACAGCTT	360
	CAACCGTTCC	TAAAAAAGGT	TTGGAAGGTG	AACAGCCGCT	GGATGTTCTC	CACATTTCGT	420
40	AATGTAGGCA	TTTGTGGCCA	TATGCTGCTT	GTCTCCGAGC	TTTTCTTTGT	GGGCTCCCAT	480
	CTGTCGCCAG	GAGCGGAATC	CCGTACGCAT	TGTACCTGTT	ACCCTGCTGC	GAACAGCACC	540
	AGAAGAGGCT	GATAATTGTA	GTCNCAGCAC	ACCATAGACG	CCGAACAATG	CCCCAAGCGC	600
	AGTGCTGCGT	TAGTTTGAAA	TCCCAAAACA	CTTCGAATCA	TCGGTTCCCC	GGAGGCCCAA	660
	TTATCCGAAN	TTGGCTTTTA	AANTCCNAAT	ACAANGANTG	CGCCCCNTGT	CCCCTGTACA	720
	TTGTGCCCCN	CCTAGGNNGC	CCACTCCCN	CNCGAANTTT	TTATTCAATTT	AATTCTNCNG	780
45	NCCCCNCTTT	GTGANAATNG	AATTCANTTT	TTN			

1272UP

	GATCGACCCC	GCGCGCATCG	GGCCCTCCGG	CCTGCTGCGC	CCCTCGCGCC	TCGGCTGGCA	60
50	GCTCGTCTAC	ATCCTCACCG	TCGCCATCTT	CACCAACGAC	TTCTTCATGT	CCGGCTTCTG	120
	GCTGCGCACC	TTGCGCGCGC	GCTCCAACCG	CGACCTGCTG	CTCGGCTGCT	CGCTGGCCGC	180
	CGTGCTGCTC	GCCGTCGTGC	TGCTGCTCGT	CGGCGTCACC	GGCCTGCTCG	CCGTGTGGGC	240
	CGGCTACGCG	CCGCTCGCAG	ACCTCGACAG	CGCCAGTTTC	TTCTGCTGCT	TCGCGCGGCT	300
	GCCCGCCTGG	GCCAACGGCG	TCGTGCTCGC	CCTCGTCTGC	GTGCTATCCA	CCTGCACGCT	360
55	CGACTCCTTC	CAGAGCGCAC	TCGTCTCCAC	CATTTCCAAC	GACCTCTTCC	CGCAACCGCC	420

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	TGCCCCCGCT	CTACGCGCGC	GCCGCGGTCG	CCGTCGTCAT	GGTCCCCGTC	GTCGTCGTCG	480
	GCCTGCTGGC	CACCCGACAT	CCTGGCCATC	TACCTCATCG	TCGACCTGCT	GTCCGCGCGC	540
	GTCGTCCCCG	TCATGCTGCT	GGCTTCTGGC	CGCGCGCCCC	CGCGCCCTGT	TCTGCCCTGG	600
	AGCTGATCGG	CGGCGGCTCC	GGNGGGCTGT	CTGCGTTCTC	NTCTTTCCGG	CCATCTATAA	660
5	CGCTNTNCCN	CNANGGGGNC	GCNTGCTATT	TATTGNAANG	NCCCTACTTN	AATAANGGGG	720
	NNCTTNNNGN	GCCTNGTCNT	TCCCCCCTN	GGGAACTGTT	TTTCCCGGNA	NAANTTCNGC	780
	CTGGGNNCCC	GTGGGNCCCN	CCCGGANANT	CANGNTAACC	NCAGGGGAAN	TCCAAANCTT	840
	CTNC						
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1273RP

	GATCCCAATA	CAAGCAATAT	TGTCGCTACC	AGAATGCCCC	ATTTGCGACC	CATATAATCA	60
	CAAGCGAATC	CCATCCCCAC	CTGCCCTATG	ATAGTCCCTA	TGAGTGATGC	ATTTGAAACC	120
5	CTTGTAAGATA	CATCTGCACT	ATATTCTATC	TCACCGTACT	GATTTCTGAA	TACACGGTTT	180
	AACATCGACA	TGACATTATT	TTGGTAACCA	TCTGAAATAA	GCGCAAATCC	TGCCGCCAGG	240
	ATACTGAATA	GATGTAGCCA	TTTGCCCTTC	TTCCCCACAG	CAAAACGTGC	TTTGCGAGCC	300
	TCCGCGTCAT	ACTTTAGTAA	CCCTGTCGTG	GACATCGTAT	TTCTGCAAGC	CCCGGCTATC	360
	CGAATAATAT	CTAGCGGGTC	AAGCGTTAGG	TTGCTGCATT	CTATATTATA	TATTTCCCTCT	420
	CTCTACCACG	TGCAAATTTA	CCTGTATGAT	TATGCTGCAA	TCTCCGCGTT	CTACTTCCTT	480
10	TCTTTGGAGAC	CGCTACCGAC	TGCTTTATGA	TTATCGGTGC	ACCATATGGC	GTCAAGCAGC	540
	ACTAGCTTTT	ACCTGTGATA	CCTTCCTTTA	CTAACTGNAT	TCCGAACCTAN	TTTGNNCCCA	600
	TACTATATCC	TTCCCTTAGA	GTGAAATAAC	CCTCCATTTA	GGTTNNTCCC	ATTCCTCNGAA	660
	ACAGCTTTT	AANAAANACA	ACCTTTATCC	TTNAACCCCA	AACGCCCCAA	AAANAAAAAT	720
	TCCCCATTTN	CTAGGTTTTT	TGNGCCNGGA	GGGAAGAAAC	CCCCCCTAAC	CCCCTAAANA	780
	ATTCTCTTNC	CC					

1273UP

	GATCGGCGTA	TAAAACTGAA	AGTTCATGTA	TGCTGTCTTG	AATGCAGAGA	CGCGGCGCAC	60
	TTTACACATC	GGCAAGCCTT	GTGTTGCGAA	TGAAACATTA	AGCTTATGTC	AAATACCATG	120
20	AACTGTATGC	CAAATTTAGT	AAAACTCGTA	CGTGCTGGCA	GCATAGATAG	AGCTGTTACC	180
	GATATCTCCC	TTGAGGCTAA	AGCCGAGCAT	TGGGTATTAA	CTTGCTTGA	CTATTCCGAA	240
	TCAGAGCTTT	CAGATTCGTC	TTTATCATGG	TCAGTCATCA	AAGTCGTGCA	TGTAGGATGT	300
	TCTATTTTCC	CACCGCAATA	AAGTGCAGTA	TTTATGCAAT	ATTCAATAAG	CTTACCTCTC	360
	ACCTCGATAT	CTAGCACATC	AGCTGGAGCG	GAACCTAACC	AGACACGAAG	TTTAGTGGCC	420
	AGCTCTTCGA	ATAGCGGAAT	TATTTCTTGG	TCCGGCAATG	ATCCTCATGC	GCCATTATAT	480
25	GGCGTAACGT	TAGGTACATA	CCTGTGACAC	CCAACAAAGT	ACAGTTGCTA	ACGTCCCAAT	540
	ATCTTAAAGG	ANCCGTTTTA	ACCNCATATT	AAGGTGAAGT	TTATGAACCT	TTGANAGTAA	600
	CTGNNTCNTT	ATAGCGGAAT	ACCANANNAA	TAACGNCTTT	GTTANGGNAT	CTATCGAAGG	660
	NTTACTTCCN	NTTCGANCAT	TTTATAGTTC	NTNCTATTAC	CCCCGANAAA	TTTGAACAAC	720
	CNTGAGAAAA	GTNTNNTCCN	CNGGGAAANG	AAAANTNTNC	TTNTGANTCC	CCCCGTTTAC	780
	CTTGAAGNTT	CTCCATTTCN	GAGATTCAAA	TTTTTNTAAN	AAGGANTTTN	TAA	

1274RP

	GATCAGAACC	AAAAAGCAGT	TCGAGTATAT	CAGTAAGCAC	TGGGAAGTTT	GGGAAATAGC	60
	AGTGTCTAGA	GTTACGGGAC	AGATTGGCAA	AGACACATTT	GCGATGGAAT	TTAATTCGCC	120
35	GCAGCCAGAG	CACGCACAAT	TACACATTCA	CCCTAAAGGT	GCAGCCCGGC	TGCTGGGAAA	180
	ACTGCACGCG	GAGGGTCGCG	TGATGCACCA	CGAAGATAAC	CAAGAAAACC	GGGGCCGGGA	240
	AGGACCGCTG	ATTCCGTCAC	CGCCGCTGTC	ACCACGAATC	GGGCCGGGAG	AGAACCGGGG	300
	CGCCGTNGGA	ACGGAATCCC	CGAACCTTTT	TTNTTACCCC	AAC'TTGGNTC	CCNGCCTTAN	360
	TTTCAAACCG	NTTNCAAACC	CCNNCCCTGG	GTTTNTTNGC	CCNNTNCCCA	NTANTTGGGG	420
	TNCGGGGGGG	GGGGCCNGN	CCAAAAAATA	ANGGGGTNTN	CCNGGGNGGC	CCCCNGTTTT	480
40	ANCAAAAAT	TTNCCCCCGG	GGTTCNCCCC	CNNAAAAGGT	TTTTTCCCCC	CCCGGGGTTT	540
	ACCAAAAANC	CNGCCCCCCC	PTTGGANGGT	TTCCCNNTCC	CCATGGGGGG	TTTTTCNCGG	600
	GCTCCCCCN	GGGGAACCCC	AAAAAAGGGC	CCCCCCTTTT	NTGGGGCCCC	NAAANNCCCC	660
	CNTNNTTTT	CAGANGGGTT	NCCNCCCCCC	TTTTTTTTTCC	CCATTANNCG	GGAANTCCCN	720
	NTNTTCCCC	CTTTNNCCCC	CCCCCAGAAA	ANNAATTTTT	TNNATTAAAA	GAGGGCCCCN	780
	NGAAAAANAA	NACCCNNCCC	CAC				

1274UP

	GATCAATTGC	GGATACACGA	GGCACAGGGC	GATAGGCCAA	GCTTCCAAGA	ATGGGAAGAG	60
	TACCTAGTCA	GGGTGCTCCT	GGTAAGACTG	AACCGCTGCA	AGCAGCTCTA	TACACAAAAT	120
50	GTAGAGATT	TATTCGATAT	ATATCCGCAG	ATAGACCGCC	CATAAACACT	AATGATACGC	180
	TAATTTCATC	ACCTACAGCG	TGTACATCAA	ACACACACAC	AAGTTTGATG	CACACGCTTT	240
	ATTTGTTTCT	TGCACACACT	TGATTTAGAG	GGTCAACACC	CTCAAGGTGT	TAGAGTGGCC	300
	AACACCAGAC	GCGAAACCTT	GAATAGTGAC	AATAGTGTCA	CCCTCGCTCA	GGATACCAAG	360
	CTCTTGGAC	TTCTCCACAC	CGAAGTTCAA	TCTGGCCTCG	ACGTATCTCG	TCCACTCATC	420

AGCTGCCTCC	TGTTCTGTAGA	CGAATGGGAA	GACACCTCTG	TGCAAGTGGC	AGTATCTGGC	480
CGCTCCTTGG	TTTCTGGTCA	CCATAACGAT	TGGAACGTTT	GGCTTGTA	TGGAGACCAT	540
CTGTGGTGT	CACCCGAGGT	TGATACACGA	ANATGCCTTG	GCTTCTGCTC	GAANTNCCGC	600
GAAAGCAGCA	CACAAGNCCC	CGAGGTTGAA	TTGGCTTGNT	CATTTCTCTGA	GTCACCGTAT	660
TTGAACGTTT	GGAAGGCCTG	CNCCACNATC	AAAATCTCGC	CAGNCNTAAA	CGTNAATGGT	720
TGANACCCCTG	GGGNTCCCCN	AAAAATAANA	TCNCCC GCCN	GAAAAGTTCC	ACTTCGAACN	780
CCCCNGTNGT	CTGGTTTGTN	TGGTANCCCA	ACCG			

1275RP

TGACTCGGCT	TCGTGAGGAA	CTGACGCTTT	TACTACATGT	AGATTGAAAC	CCGTTTTCCT	60
GGATCGCCTC	GTCTCGTTGC	TTGGTATCTT	TGCCAATCCT	CCTGAGTGGG	CGCTGCCTGT	120
AGAGGATCTT	CGCGATGGGC	CAAACACGCC	CCACCAGCCC	AAAGACGTTG	GAGAGAGGGC	180
TGAAGAAGGT	TCATTGACCT	CCTTTATGGC	TTCAAATGCT	GACGGAAGTG	ACAAATCGTT	240
CCCAAGACGC	ATGTCCGACA	ATTCTCTGAC	GGTGGACTCC	AAGACCTGGA	TGCGCTCTGC	300
CCTGGTCTTT	GATATTCTAT	GGATAGTGGC	AATGTCCTTT	GAGAGTGTCA	TGTTCTCGTT	360
TGTGAGGTTT	AGGTTATCAA	GTTGGGCAAT	AGCGAGCTGC	TCTGCAAGTT	GGTGGTTTTC	420
TCCACCAGCT	GTGCCCTCTGT	GTGTTTCAGG	TCTGTCTATCA	GTTTCTTTAA	GCCTCTCCTT	480
ATCGGCCGAT	CGTCCACCTG	GACTGNTATN	TTTTTNCCAC	NCCCATTNNN	CCATAATTGT	540
NTNAAGNAGG	TNCCCNCNCG	GAATTTNGNT	CCCGTTTCCA	NAGNTCGGNC	CGGGGATAAT	600
TTAAACNTTT	AAAAATTANC	CCCGGCCCTA	NTTCTTTTIN	CCNAATNNNN	GNNCCCCCN	660
GNAANNTTTT	NCAANNCTTN	TGNNCCNTAN	CCTTTTINNC	CCCACGGTTT	TTNNTCCCCC	720
CCCNTCCCCN	ATTNNGGANT	TCCCCNTTN	CCCC			

1275UP

GATCGCCAC	ATTATGTCTC	AGGGTACTTT	GTACGTTAAG	AAGACCTGCC	GCTCGATGCT	60
GCCTCAGAGC	ATCGTCGAGC	ACTACAACCT	GGACGTCTCT	ATTGTGATG	CCGACAAGAA	120
CGAGGAGTTC	GAGAAGAAGT	TCCCATTGAA	GCGCGCTCCA	GCGTTTTCCT	GTGCGGCTGG	180
AAATCTAACT	GAGACCATGG	CCATCACCTA	TTACTGTAAG	TTGCCACCGA	CTACACACCG	240
AAGCATGGAG	CCCTAGTGTG	ATGAGAAAAA	CTTTCGAAAA	AACAGTTATC	CCTGTCTGAA	300
TGGGCATAAT	ATCTGGTTGC	ACATGTGTCTG	AGAGACCATA	CTCTGATTTA	GAGCTACATG	360
CGAGGTTCCG	AGGAACACGT	ACTAACCAGAA	CAACAGTGGT	CAACCTAATC	CAGGACGAGA	420
AGGCCAAGGC	TGCTCTGCTT	GGCTCCACGC	TAGAGGAGCA	GGCACAGGTG	TTGCGCTGGG	480
AGTCTTTGAC	CAACACCAAC	TTTCTTGACG	ACGTTGGCTC	TGCCTCCTAT	ACCTAGAGAG	540
GGTGTGGTCC	CNTTNCACCA	ANNCNACATG	GAAAAACGN	TTCCCNGNGG	CGAAACNTTN	600
CCCNAGNGTT	TTNNAAAAAA	GAAATAACCN	CTTCCCTCCC	TTACCCCCCG	AAANTTTTNT	660
TTNCCGGGAN	NCCNTGNCNN	TNGGGGGGTT	GAACNNANTT	CCCCACANTT	NGGGGNGNNN	720
NTGGGNCNG	CCCCCCCCC	CCCNNNNANG	GTTACCCCTT	GGGTANCCCC	NNNTNAAAAA	780
CNNCCNCCCC	CCCTTNGGTC	GGACCNAAG	GGGGGNGCCC	CAAANGAAAA	AAAAA	840
AA						

1277RP

	GATCCGTCAC	GGACAGACTG	AATGGTCAAA	ATCAGGTCAA	TACACAGGCT	TGACAGACCT	60
	TCCGCTGACC	GAATATGGTG	TCGGCCAGAT	GCGGCGCACT	GGTGCTGCGA	TATTTAGCGC	120
5	AAAATACATT	GATCCTGCGC	ACATAACATA	CGTATTTACT	TCTCCACGCC	AACGCGCGCG	180
	GAAGACTGTG	GACCTGGTTT	TGGAAAGCCT	CAGTGAAGAT	GAACGTGCAC	GCATCCAGGT	240
	GGTGGTGCAC	GAGGACCTAC	GGGAGTGGGA	GTACGGTGAC	TACGAAGGTC	TGCTGACAAG	300
	CCAGATTATC	GAATTGCGTC	GTAGCCGTGG	CTTGGACTGC	AAGCGCCCAT	GGAATATATG	360
	GCGCGACGGC	TGCGAGAACG	GCGAGAGCAC	CCAGCAGGTG	GGCCTGAGGC	TATCACCAGT	420
	GATTGCCCGG	ATCCAGGCAT	TACACCGGCA	GCACCAAGCT	GAGGGACGGC	CGAGCGATAT	480
10	TCTGGTGTTC	GCGCATGGCC	ATGCTCTCCG	TTATTTTCT	GCGCTCTGGA	TGAAGATGGG	540
	CGTCGAAGCG	CCGACGCCAG	ACTGCGCCAT	CCCCTCGAGT	AACCGGAATG	ACGATCCGTG	600
	CCCTTGGTGC	GGCTGGAGCA	ATCCGTACCT	GCAGGACACC	CCACTTCTTG	CTAGACGCAG	660
	GTGGCATCGG	TGTGTTGTCC	TACCCCNCCN	ATTTGAGACC	ANTCTACTCN	CCTGGCCNTT	720
	CNTTGGCCCC	CCGAGATCCC	CCCACGGTNA	GTCCACCGA	AAATTTTAT	ATCTACAAGN	780
	GNGTCCCCC	ATGAATATAC	CNTATCTTCT	TAATCGTCCN	CN		

1277UP

	GCCGTCTCTC	TGCGGCCAGC	GCGAGTCCAG	GTGCCGCAGC	ACGCCCCACG	AGCGCGACCT	60
	GCGCAGGCGA	TAGTACCGGT	ATGCGACCAG	GCCCCCGGCC	AGCACGTTGC	TTGCGCCGAA	120
20	GAACCAGAGG	AACCGCGAGC	GGCTAACCAG	CTGCACCAGC	TGTCCGTAAT	CGTGCCGCAG	180
	CGCGTCCCCG	GACGCCAGCC	CCATGCGTGT	GCCCCACAGT	CCCAGCATCA	CGCCGCCCCC	240
	GCAGATCAGC	ACCGTCCCCA	CGCACGTAAG	CATACAAAAC	GGCTCTGCGA	GCAGCCAACA	300
	CGAAAACCA	CTGTTGAACA	GCACTCCGCA	CGCCTGCAGC	GGGGCCAGCA	TCACCAAGTG	360
	TAGCGTGGCA	ATCTGCATCG	TGCTTCCGAA	CACGTTGCGT	AGAATGAATA	GCGTCAGACC	420
25	CATCTGCCAT	AGGCGGCTAC	GGTACACCAC	CTGCACAGTT	CCCCGTGCCA	CTTGCAGCGC	480
	AGCCTTGCGC	TGAAAGTACC	AGGCCCAAAA	GACTGCATAC	GCTTGAAACT	ACCGCCACCA	540
	CGACCCATAA	TAACCAAGTT	ATCGACCATT	CGCTTGATA	CCCTGCACCC	TTGCTGTCAG	600
	AGTACTCTAC	TGTGGGCGCC	TTTGGGCTCT	AGGTCTCTAC	GCTATGCCAA	ACATACTGGC	660
	TCCGGTGCGT	CATGTTTCGAT	GCTGTATGTC	ACGTGACCGA	TGACAGGGTA	CCTGTGCGTT	720
	CTCTTCCGGT	TCCAGGGNAT	GATACCGAAA	NCCGAAATTA	NCCGGATGAA	TTTCCCAGCC	780
30	CTGCGANTAC	GACNCCAACN	GGAGACGCNG	TTTTNTGT			

1278RP

	GATCTTCAAC	CTGCTTCCGC	CTATGAACAT	TCTGTTGTGA	TTGAGAGGCG	ATACCGCCTC	60
	CACCTTTCTT	CGAGCCTGCC	CGGTTTGGT	AATCCATACG	TTCTTCCCCA	TTCTTTTGGT	120
35	ATTGGTATAA	GCGATGCAAA	TGAAAACAGC	CTCTTGAATA	CAAATCGACT	TGCCTACGTA	180
	TAAAATTATA	TTTTTATCAG	AAACTTGGCG	AGCATCAAGC	TCGGCTTCAT	TGATTATAT	240
	ACTAAACAGA	ATACACTACA	TGCTACCGTC	CGAAAACGAA	TAATCTATTT	CCAATATATA	300
	TATATATATA	TATATATATA	TTATAGTTGT	ACTTTATAAA	TCTGAACTAG	GTCATACAAC	360
	TCTCAAATCA	AACGATATTT	ATTCTACATA	TAGCACGGGC	GACGCACCAA	TTGAAGACTC	420
40	TAGGGCGCCT	GAACCTGGCG	CTGCCCTGTA	TCTTTAGCCT	GTTCTTTTAC	AGGGTCATAA	480
	ACATAGTACA	TACCGCGCTC	TAGTTGCTCA	TACTGGATGT	TCCTCTGTTT	CAGCTGCGGC	540
	CAATTTTCGT	GAGGGATATC	CCACCCACAT	TTCTGAGCTA	TGAAAGCTGC	AACGTGCTCG	600
	CACAGCCCCA	GTAACCTTAGG	TCAATTCGCG	TGCTTAACGG	GTCTCCTATG	ATAGTACTTG	660
	TGGTACGTGA	GCTGGACCNT	GTTTACATCN	CGGAACTGC	GCNCCTTCAN	CTNTTCNATC	720
	ANCNCAATCG	CATNCANNTT	CTGGCNANTT	TTTTTGANTC	CATGACCCCC	CCNAAANTNT	780
45	TTCCGGTNG	ACCCACACCC	CCTTGAAATN	NCTGATNTGN	AGANGCNC		

1278UP

	GATCTTGGAT	GTACTGGGGG	CTCATACTTC	GGCTTCTGTT	TCTTGTCTTT	TTTGCCCTTC	60
	TGGCCCTTGC	CATACGTCGA	TGCTCCTTGG	CCCATCTTAG	AGATATCTGC	TGTGCGGCTA	120
50	TGGAGTAACG	CTTCTGCTTG	CGAACTCTAA	GTAAGTGTAT	CAACTTGTGT	GTATCATTTT	180
	TGCCACCTGG	AATCCATCAA	TTTCACCTAG	CCCAACCCAA	GCTGCGACCT	ATCAAAAAAC	240
	AGGAGCAGGA	AGCTGCCTGA	AGAAGCGCTC	CAGGGGTCTA	CCGACGGGAA	AAACTACGAG	300
	GACTGGTGCT	ATGACATCCT	TCCCGGGATC	CATCCCGAGT	TCAGTGCTTT	CGAGCTGTAC	360
55	AATTGCGTCC	GAGCGGTTCG	AGCGCAAGCG	TCGTGACAAC	ATCAACGACC	GTATCCAGGA	420

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	GCTGCTCAAC	GTGATTCCAG	AGGAGTTCTT	CCAGGACTAC	TACCAGAAGA	AGAAGGACCA	480
	GGAGTCCGAG	AGCGGGACGC	CGGGCGCTCT	GCCCAAAAAC	AAGGGAACTG	GGACGCGCGA	540
	CGGCAAGCCC	AACAAAGGCA	GATTCTCACG	CAGGCCGTCG	AATATGTGAC	CTATCTGCAA	600
	ACCAAGTGGAT	CTGCGCACCG	CGAAGAGGTG	GAGCTGATCC	TGAAGGTCAG	GAGCTGTGTC	660
5	GGCAGACGGG	CAGCATCGTG	AACGACGTGA	ACTAGAAACA	CCATTGCCGA	CTCGCGCTGG	720
	GAAATCGCGT	TGGGCNCTGC	AGCGTGCTCC	GGAATTNTGC	GGCCNCAGGG	CAGCACACCC	780
	NGGCAGCACA	CCGCCCCAGA	CCACACACTC	ATTTGGGTCC	CATTCCGACG	CNTAGATTTT	840
	CNCCTGGNCT	GTTTT					

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1279RP

	GATCCTTCTG	GATGCTGGTA	GCTCCGATGA	GGAAGTCGTA	CTTTTGGTAA	TGTCAGTCTG	60
	GCTTAAGCAT	CTACTTTCAA	AGCGTGATAT	ACAGAGAGCG	TTTGCTAAAA	GTGGTGGATA	120
5	TACGTTACTG	TTCTCCATAT	TAAAAGATAT	CCAATCCGGG	CTTACAGGAA	AAGTCACGAA	180
	TCTATTGTGC	ACCTATGCAT	TTGGAAATCA	TATTGTCCCA	ACACACAGCG	AAAGCACGTC	240
	CCTTCTTATT	AGACCGCAAG	GCGATGGGCT	ACAAAGGATA	GTTTTCGAAC	TTCATTATTT	300
	GGCAATTGCA	TTGTTAGAGA	TAGCGGTGAT	AAAAGCCCCA	AAGGAGGATC	AACAAGAGTT	360
	GAGTAAAAAC	ATTATTACGT	ATATCAACGA	GTTGGCGTTA	CTTCATAGTA	CTCACTCTCG	420
	AATATCGCTT	TTTGATCCAA	GCGTATGCCA	ACTTCATGAG	AGATTGTTAA	CTTTGTTATT	480
10	AACTTTGACA	GATCCCAAAT	ATCAGGGTTT	CTATATACAG	GCTATTCTGG	ACATTGAACT	540
	TCTATTGAGT	AACAACATAT	CTTTCACCTA	AAGAATGATG	ATCCACCACC	TTTTCGAACT	600
	ACTTGCAAAA	TATTTTGGTA	ATGAAAGGGA	CATCCGATTA	GTCCTAGCAG	ATTACAGTTA	660
	GTAACAAAGG	TCCAATTATA	TTGAGACCAC	TATATTNTAA	AATTGTCCCC	NTGTTATTGA	720
	AAACTTNTGC	CCNGGGTACA	CTTATTGCTN	TTCNACACCG	TCCTGNAAAA	ANTGTGNTTT	780
	GTTACGATTA	ACTCGTTTCC	TTGATTGAGC	AACTTTTGNT	TTTTATCATA	G	
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1279UP

	GATCAAGAGT	ACAGTTGATG	AAAAGGAGTT	CCATGATGAA	ATATGTAAGA	TGGACTTGCT	60
	TAAGAAATTG	ATAATATAAA	AGGCTACGAG	CTTCAATATT	ATAATACGCA	TTGCATAATT	120
20	TATTACATTA	AATTGATATA	GGTATATTTT	TCTTCGAAGA	ATTAATTCTA	ATCATTTTCCA	180
	TGTGAAGATA	TCGCCCTCTG	TGTTACCTGC	GGATATTTTCG	ACTCTTAGTA	TATCTACATA	240
	TTTTGGCGAG	CCATTATTTA	AACTCGCCAG	CTTGACTCTG	GACCCAAGAG	CCGTAATGGC	300
	AGCAGCTCTT	CCTGAGCGCA	ATTTCTTCAA	GCAATTGAGG	CACCATGTGC	CGTTCCTTAA	360
	TTCAAGCACA	TATAAACAGA	CCGTCCCGTC	AATAAACCTT	AGCACAATTA	TATCCTTTTC	420
	TTTCCAATAC	ATGTGCCGAT	ACCTGGACAT	TTCTTGAGAT	GCAAAGTTAA	CAAAGCTTAT	480
25	AGCAGTGATA	TCTTGCGTTA	GAGACATGCT	TGCAAATTTT	GAACCGTTGA	GGTCATAAAC	540
	ATGAACGTTA	TTTGAGAATA	TCAACCACCC	ATTAAATGAA	CTGTACCTGT	TTGAAACCGC	600
	AATGCACTGG	NNTNNTNGA	AATATTCNCC	AACCCNCCCT	TAAAAGNGTC	CCCCTTTATT	660
	NNGNCCTNCG	TATTCCCAAA	AACNTACCCG	NTTCTNTGTG	NCNCCAAGGN	NTTTTNNCNT	720
	TNTTGGCAGC	CTTTTAGAGN	TTTAAANATN	TTCCAANCCC	CAAATCCANT	TTTTAAAGGN	780
	CTCCCTTNA	AANNTCNTGA	ATGANCAGGN	GAATTCTGTT	GCCNTTTAAC	TTCCCAGTNA	840
30	G						

1280RP

	GATCATCAGA	CCTGTCCGGAG	GGTTCGGTAG	TGGAACCTCT	TCGTAGGGGG	GAGCCGCTGT	60
	TGTGAGCCTT	GAGCCGCTCT	GGAGACGGCG	GCCTCGAGTG	AAACGGAGCT	CGTATCGGGG	120
	ATCGCGAGAT	GTACTGGGGC	GACCTTAATG	CAATTTTCTT	CTCGAAGGAC	TTTGTGGGGA	180
	CGGAGGAAAG	TCTTTCAAAT	ATTGACGCAG	AGCGGCCCTT	TGAGATTGTG	CTCTGGAAAG	240
	ACGGTCTTTT	CAAGGCCGCG	GGCAGCTTTT	CTCCCGTGCT	TGCAGCGCTT	GCCGCAGGTG	300
	CAAGCACGGC	CGCCTTCGCA	AGAACGGGAC	TCTGCTTCAG	TAGGCTTGTC	TTGGTCATCA	360
	TCGGCTGCAC	CACCAGCGGA	TCCTTGTTTCG	GCAGCGGCAC	AAACATGTTG	GACCGCCGGA	420
40	GGGTGCGGTC	ACGGCTCGGC	GGAAATCACGG	CTGCCGTCCG	AAACGTGAAC	GTGTTCTCGG	480
	GGCTCTTCGA	CATCGAAACC	TTCTGTCTCGT	TGATGCGACT	TCTCCGAGTC	CACCTCCTGT	540
	ACCGTCGTCT	GCTCCCGCTC	CTGCGTGCGC	TCCGGCTCCN	GNCCNCCNGT	TCCTGCCTCC	600
	CTGACTNNTT	CCCCCCTTTT	AGGGGAACAC	GGGAAGAAAA	NAANTNCCCT	TTCTNNCCCG	660
	GCCCCCTGTG	TCGCCCCCN	NNNNCCCCCN	CCCTNNNNNN	NNNNNNNNNN	NNCCNNCCNN	720
	NNNNNAAAAT	NTAGGGGNGG	GAAAAATGNG	GTTAGNGTCC	CCCACNGAA	CCCCAAAAAA	780
45	AACCNCCCAT	GTNTCCAGGG	NCTTNATGAN	CANCTTCNCN	NTGGGA		

1280UP

	GATCATAATG	CGACTATCGC	CCATAAGCAG	GGCAATACGC	CTATCCACAT	CAAAGTCCCT	60
	GACCGTTCCA	TTCTCCGCGA	CCGTGACGTG	CCTGTGTACA	AAGGCTCAGC	GCTCCAGGCG	120
	CGCGATGTCA	TCCCGTATCA	CGAACTATCA	AACTCGAACT	ATTTCACTGT	GAATCTGGT	180
	GAAACACTAA	CATTTCTGT	GTATGAACCG	GAGTTAAACA	TCCAAGGCAA	CATTGTGAG	240
	GGGCGGCAGA	TTACCAATTT	AACTCAGGGT	GTACCAGGCG	ATGTCCCGAT	TTCTATTCTA	300
	GACGGGAACA	ACTATACCCA	CTGGCAGCCG	TTGACAAGT	CTGAGAGGGC	ACTCTTGTTG	360
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	ATTGATTTGG	GTTCCGAAGA	GGAGTACGAG	ATCACAACGG	GTTAAAATTT	TGTGGGGCGC	420
	TCGTCCCGCG	AAGAACTTCT	CCATCTCTAT	TCTCCCCAAC	TCAAAGCACA	TCACAGAGAT	480
	ATTGACAAAA	CTGACGGCCA	TGATGGACGG	COGGAATACG	GACTTGTCTC	CTGCTCAAAG	540
	TGCCACGCCG	TCTCTTCCTC	GCAGCATCTG	CTCGGCGGGC	TGGCGAATGT	CACCGATTCC	600
5	AGGGAACTCG	CGGCCATTGA	TGAAAACGTG	GANNIGTTTT	TAAAAAATTT	CNGTTGGACT	660
	TTCANCTCCN	NCNNTTCACN	TTTCCCNAGG	CGCCAATNCN	GANCTCCTNA	GGCCCTGNAA	720
	CACCATTNAN	CNTCGACCTA	CTCAAAAGTN	TTCTATCCCC	CAATNTCNTT	TCCAACACAA	780
	CGATCTGCTA	ATTGNGCGNC	CAACCATCAC	TTNNTGCATC	ATTTTGCCAC	AACAATGNGA	840
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1281RP

	GATCCGACGT	TCAGTGGACT	CTTCCCATTT	AAGGTTTTC	ACAAATTCCA	AACTCATGTG	60
	TTTAATGCCT	TGTACCATAC	CGATGAAAAT	GTATTTATTG	GAGCTTGTA	GGGCTCGGGT	120
5	AAAACGCAA	TGGCAGAATT	AGCTTTATTG	AGTCACTGGA	GAGATGGTAA	GGGACGTGCC	180
	GTCTATATAT	GTCCATCTCA	GGAGAAAATT	GATTTTCTGG	TGAAGGATTG	GCGAAACAGA	240
	TTTTTAAATG	TGGCAGGTGG	AAAGGTTATT	AATAAACTCA	CATTGGAATT	AACTAACAAAT	300
	CTTCGAACGC	TAGCCCAGTC	GCATTTAATC	TTAGCGACTC	CAGAGCAGTT	TGACCTGCTT	360
	TCTCGTGGCT	GGAAAAGAAG	AAAAAACATT	CAGACATTAG	AGCTGTTGAT	TCTAGATGAT	420
	CTTCATATGA	TCAGTAGTGA	CTTGCCCTGGC	GCAAGGTATG	AAAATATAAT	ATCCAGAATG	480
10	CTGTTTCATT	GGGGTCAACT	TGAAACGGCC	TTGCGTATAG	TCCGTTTATC	TACCTCCCTC	540
	GCTAATGGTG	GCGACTTTGG	AGAGTTGGCT	CCGAGCTAAA	AAGCTACATT	TTTATTTCTC	600
	CTTTCACGAA	GGGTTATGCC	CTTACAGATC	CNCTTACATC	CGTTCCCTAGA	NGCATGAAAN	660
	TCTTTAATTG	AACTATGGCC	AATCGCTTCC	TGACGNACAA	CTCTGTGATA	CTGCCANTNT	720
	TANCTTTTGT	TCCATTAGAA	ATGTTTCAAT	TCTGTCTNCTG	CACGCCGCGC	GGANGAAATC	780
	CTGGTCNCCN	ATTAGTTGGA	ACCATTCTAG	GNNAAGAC	TCTTATCCTA	ACN	

1281UP

	GATCTGAACG	TATGAGAGCG	GGTTTTTACT	AATTATAGAA	CCATATGAGA	TAGAAAATGC	60
	GGCAGTTCCA	AATCCAATAA	TGCGATTAC	GTGCCCTGAT	GCCTCCATG	CAATCAAACC	120
20	AGTGTTTGAG	AAGTTTTCGT	CAGTTATTAT	TACATCGGGG	ACCATTCTCT	CGCTTGACAT	180
	GTACCCTCGA	ATGCTGAATT	TTGAGACAGT	TCTTCAAAA	TCTTACTCCA	TGACGCTGGC	240
	GCAGAAGTCC	TTCTTCCCAA	TGATTATAAC	CAAGGGGTCA	GACCAGGTAG	CCATCTCTTC	300
	TCGGTTTGAG	ATCAGGAATG	ATCCCTCAAT	TGTCAGGAAT	TATGGTTCCA	TATTGGTTGA	360
	ATTTGCCAAG	ATTACTCCTG	ATGGTATGGT	AGTGTCTCTC	CCCTCATATT	TATATATGGA	420
	ATCCATTATT	TCAACTTGGC	AGACAATGGG	GATCTAGACC	AGGTTTGGAA	ATACAAGCTC	480
25	ATCCCTCGTG	GAAACACCAG	ACGCCACAGG	AAACCTCCTC	TACCTTTAAA	AACTNACCNA	540
	AGGCCNGCCC	NNAATGGGNC	GGGCCANTTA	ATTTCTNGTG	CCGNGGGAAA	ATTCTNAGGA	600
	ATGGATTING	ACNCCCTCGG	NGGGAGTGTT	TGAAAATGGA	TCCCTCCCTT	NACCGANAAC	660
	GTTTNTTTAG	GGAGGGTTNT	NTCCNTNANA	AAANATCCAA	ACCGGGAATA	CTTTTCTCTT	720
	NNAGCATGAA	NCCCCCCCCT	TTTGGGAAAA	TTCAGGGGTG	AGGAANATAT	GGTTAATGTN	780
	CCCCCCANCN	GNNNCCNNAA	AAAAANCACT	CCCAATGTCC	CAGGNCCTTN	NGNACCACCT	840
30	CTNNNNATTG	GAT					

1282RP

	GATCCGGAAT	TATAGAATCG	ATGAGCATT	CATTTAGCAA	CCTTCTTCCA	ATTCGTAATG	60
	GTTTCATAT	AAACTCCCTA	GCTTCCTCTT	GATAAATCCT	TTCAAGAACA	GCACCGTCGC	120
35	AGTCTGGGTT	TATCTTTATA	TTATTTCTTG	TTATGCAACT	CGCATGGTCT	ATGAGGTCCC	180
	TACATACATT	TAGGTCGCCC	ATCAGTACCA	CCCTCTTCCC	CAGATTCTCT	ATGTTCTCTA	240
	CACGTTTGAA	TAGAGTTTTC	AGGAAACGCA	GCCTAAAAAC	TTCACCCTCC	TCAGTGTTCA	300
	TAGAATTAGC	AGGGCAGTAT	ACGGAAATGA	CCACCACCTT	ACAGGCCAAT	TCGACTAGAA	360
	GGCATCTCCC	CTCACTGTCT	AGTTCTGTGT	CATTAGCATC	ACTCCCATAG	GGCAAGCCAT	420
40	CATAACCACC	AATACCAATG	GTCGGGTCTT	CGCAATATGC	TACCAAGGCG	CCATCTTTT	480
	TTAATTTTTT	AGTCTGCCTG	TAATACCTCC	TCCCGCCTTC	AATACTTGTA	ATGATTATCG	540
	CAACGATCGG	CTGCTTCAGG	GATTCGTGTT	CACNCCCACN	CCNATACCCT	TCTCCTGN	

1282UP

	GATCTGCGCA	AACACCCCCA	CTCTGTGTAC	CTCCTCGATG	CTGTCAATCG	AGTCTTTGTC	60
	CATGCTTCTA	TCCTTCAGCA	GGAACGCGCC	TAGGTACGGG	ATGTTCCGCC	GCAGCAGCCC	120
	GCAGATAGCT	TCGATGACCG	CGGGGTCGTA	CACGGTCACC	GACTTGTAGT	ACCCGGGGAA	180
	GAGCGGCCGG	TTGCTCATCG	GTAGCACCAT	CAGCTCCTCG	TACTTGCGCG	GCACCTCGCC	240
	CTCGCTCGGC	GGGTTTCGAC	GGCCCGCGCC	GCCCGCCGAA	GACGCCGAAC	CGCCGCTGCC	300
50	CCGCGAAGAA	CTAGCCTCCG	ACGACCGATT	CGCCTGCTCT	TCCCGTGGCT	GCCGCTCCGC	360
	CTCCTCGTCG	CGCACCCTTT	CCTCGTCGCG	CCCCTCCTCC	GCGCGCGGCG	GCACCTTTTT	420
	GTCGTGCGTC	TGGTCCGGCT	CCCCGGTCTT	GCTTCAGTAT	GCAACTGCCC	GCCGCGTGTA	480
	TCCCCGACTG	CTGCCGCAAG	GCCACTCTTT	TTGGGGGGGG	GGGGGGNNNG	NNNNCCCCNC	540
	CCCCCGCCGG	GCGGCGTTGN	CCGCCCCGCG	CCGTTTGTGC	TNTTCAGGCC	GCGGCTTTGG	600

CCATCCCCCC CTNNTTTTTC CT

1283RP

	GATCAGGAAA	TCGACGGGAC	TGGCTGATTG	TCTTTATAGT	CAAGCATATT	AAACACACGT	60
	GACTTAAACT	AGATTTACAC	GTGACATGCA	ATTGTGTCGT	TTCTTTTTTA	TTTGAAAAAC	120
5	CTGCATCGAG	CTATTAGATG	CTCATCGACA	CTAGTGACAA	AACCAGTCAA	GGCTTAAAAG	180
	CTCTGCAGCA	TGGACCAAGT	GAATAAGGAG	CATCGTCCTA	AAAAGGAGAA	GGCGACAGCT	240
	AAAAAGAAGC	TGCACTCCCA	GGGCCACAAT	GCGAAGGCAT	TCGCGGTGGC	CGCTCCGGGA	300
	AAGATGGCCA	AGCAGATGCA	GCGCAGCAGC	GATAAGCGGG	AGCGCGCGCT	GCACGTTCCG	360
	ATGGTGGACC	GGACGCCGGA	CGACGACCCG	CCGCCACTCA	TTGTTGCCGT	TGTAGGTCCC	420
	CCGGGGACGG	GTAAGACAAC	NCTGATCAAT	CGCTGGTGCG	GCGGTTGACC	AAGACGACCC	480
10	TCGGCGAGAT	TAACGGTCCG	ATCACGGTCG	TCTCCGGCAA	GCGCCGCCGT	CTGACGTTCA	540
	TTGAGACGCC	CGCGGACGAT	CTGAACCTCG	ATGTGGACAT	TGCGAAGGTT	GCAGATTGCG	600
	TGCTGCTGCT	GATGGACGGT	ACTTTGGTTC	GAGATGAGAC	ATGAGTTCCC	TGACCTGGCN	660
	CACNCCACGG	ATNCCCTTTT	NCTGGATTAC	AANNCNCAT	TTTTCATTNC	NAGGCCNCTC	720
	CNGCTCNAAA	ACTTTTNACC	TCGTTCTGAC	NATTTTNCCN	GGGGNNCUNT	CCCCTTCTGN	780
	TTTTTTATGN	NGNNCCNT					

1283UP

	GATCCGCTGG	CCCATCGCCG	AGAGCTATGT	GCATCGCCTC	ATAGTGGCCT	TGATACGTGT	60
	CTCAACCAAG	ATTGTGGAAG	ACACCGTGCA	CTCCACGAG	TATTTTCAGCA	AGGTCTGCGG	120
20	CATATCGAAG	AAGCTCTTGA	TGCGCCTCGA	GCTAGCCCTC	ATACTCGTCC	TCCGCGGCGA	180
	GGGTTTGATG	GTCACGGCTG	CAGCTCTAAA	CGCTGCCTCA	AACGCACGTG	CTCGGCTTCG	240
	CGAGCAGTCT	GCGCTGCCAG	CCGCTGCTGC	TCAGTGATAA	TCGCCACTTC	TAGGCCACCA	300
	ATTTCGGTTAT	TTAATAAGCA	ATAAATACTC	CAACACTAAT	AGTATACACC	GTTTTCGAGA	360
	GTAAGCACGC	AGCAGGAGGT	GGCAGCTTTT	CTGGTACCAC	CTCAAGCCCC	TTGCCATTGC	420
25	TGCCTATCTG	GTTTAGGCAT	GAGCAACCTT	AGTCAGTTTC	GAACCCGTGA	TATATGTTTC	480
	GAACACGTTA	CCTTTTCGGT	GAAAAGAAAA	AGCCTAAAGG	CGAAATGTTT	TCCATGTTAA	540
	CACAGCAGAT	TAGAGGTACC	TTGTACTGGA	TATTCTGTAG	GATCACGGGC	TACGAGCATT	600
	CATCCAGAAG	CTTTGAACCT	ANGGTGTTTC	NGGATGGCAG	TTNGGGACTT	ATNCCGTGNN	660
	TNTAAANAAA	TACTTCGTCC	TAGTCTTTGG	AACAAACNTG	CATTTGTTGT	TCTTNGTTTG	720
	GANNATCGGN	AAGACANCCT	TTGCCCTGCT	AANAAGACNG	TTGGGAACNG	NNGCCNNTGN	780
30	CCCNCCTCGA	GNCNNGAACN	GGCCCCNTTN	CNNTTCNNCN	GGGGNNNNC		

1284RP

	GATCGATCTG	GTCAGGTCTA	TTTGTGGCAC	CGATGACAAA	AACATTTTTC	TTTGCAATTCA	60
	TACCATCCAT	TTCAGTTAAC	AATTGGTTAA	CGACTCTATC	AGAGGCGCCA	CCAGCATCAC	120
35	CCATTGAGCC	ACCTCTAGCC	TTTGCAATGG	AATCTAGTTC	ATCCAAAAAG	ACAACGGTTG	180
	GCGCTGCGGC	TCTAGCTTTA	TCAAAAATAT	CACGAATGTT	GGACTCAGAC	TCACCATACC	240
	ACATGCTTAG	CAACTCTGGA	CCCTTCACAG	AAATGAAATT	AGCAGATACT	TCAGTTGCGA	300
	CTGCCTTTGC	CAACAACGTC	TTACCAGTAC	CTGGAGGACC	GTAAAACAAC	ACACCTTTTC	360
	ATGGCGATAG	ACCAAACCTA	ATGTATTGGT	CAGGATGCAA	GACGGGATAC	TCAACGGTTT	420
40	CCTTCAACTC	CCGCTTTATG	TCATCCAACC	CACCAACATC	GTCCCAAGTA	ACGTTAACCG	480
	ATTCAACCAC	GGTTTTCAGT	AGCGCGGATG	GATTGGAGTT	CCCAAGTGCG	AATCTAAAGT	540
	TATCCATTGT	AACCTCCTAAG	GAATCCAAGC	ACTTCAGCGT	CGATTTTCATC	CCTCGTCCCA	600
	ATCAATTAGA	CTCATCTTCT	CTCTAATCTG	TTGCATTGCA	GCCTCTGAAC	ACAAAGAGGC	660
	ATATCAGCAC	CCACATACCA	TGGTTTCAGC	AGCTAGCACT	TCCAATCACG	TCATCAGCCA	720
	TCTCANTTCT	TGNTGTGGAT	GTTTAAATTC	CCACCCTCCA	GTGCTCTGGA	NACCANTTTA	780
45	TTNNNGTCAA	TTTACCAACT	TTTAGNCGGN	TNNATGG			

1284UP

	GATCAAGCTG	ATATGTATTTC	TCGGGCTACT	GGTCGTATCC	GTGGTAATCT	TCTTCGGCGG	60
	CGCTCCCAAC	CACGACCGTA	CTGGCTTCCG	CTACTGGAAG	AACCCGGGGC	CCTTTGCGAT	120
50	GAGCCTCGCG	CCAGGAAGCA	CGGGCCGTTT	CTTGGACGTG	TGGCGCGCCG	TGATCAAGTC	180
	GGCCTTCGCC	TTTATCCTAT	CACCAGAACT	TATAGGCATT	GCATGCGTCG	AGGCGCAGGA	240
	CACCCGGCGG	AACACTGAGA	AGGCATCGAG	ACGTTTTCATA	TACCGTATTA	TCTTTTTTCTA	300
	TGTGAGCTGC	GCGCTCATGA	TCGGCGTCAT	CTTATCAAGA	ACTGATCCGA	AACTCATAGA	360
55	GGCGCTGGAG	ACAGGCGCGC	CAGGCGCTGC	CTCTTCTCCG	TTCGTGCAGG	GGATTGCCAA	420

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	CGCAGGGATT	CCCGTGCTCG	ACCACGTCAT	CAACGTCGCG	ATCTTGTCCTT	CTGCGTGGTC	480
	GGCAGGCAAC	TCCTTCATGT	ATGCATCCAC	GCGCATGGTG	CTAGCGCTTG	CGCGCGAGGG	540
	AAATGCGCCA	AAGTTCTCTCA	CCAAGATCAA	CAGATATGTG	TGCCCTACAA	CGCGGTCATC	600
	GTCTGCACGC	TCGTGCGCTG	TCTTGCCTAC	CTGAACGTCA	AGACGACTCC	GCAATGTGTT	660
5	CCAGTGGCTG	TCGAACATAT	GCACCATCTC	CGCTTCATCC	GCTTGTTTCGC	CATGGCTCCC	720
	TTATATCCGT	TCCCNCGCGT	TCTTTTCACA	CTCCNANCCN	TNCCCTNCCA	GTTCCCTGCA	780
	CCNTTTCNCC	ACTATTCCTT	TNTAATGTNT	CTTTTTNGAC	AATGTTCCCT	C	

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1285RP

	GATCCGGGTC	CGCCACAAGC	TGCTGGTCCA	CATCGTGCTG	CTGCGCGGCC	CCCCGACGC	60
	GCCCCGAAAG	AAAACCGAAA	TCAAGGCCAG	CATTCCGGTT	ATGCTCTACA	TATCGCCGCT	120
5	CGTACCTGTG	CAGGGCCGCA	CCGTCTGGT	TGATAACGCT	GGCCGCTTCC	ACATCCGTCC	180
	CGGCGTGCTG	ACAGACCTAT	TCCGGACGCG	GAGCGCGGAC	TCACTTCCGA	GCTGGGACGC	240
	GCCGCCGTCC	TACGAGTCGC	GCGTGCACGA	TCCGCTGTAC	GATGGCGACG	TAGGCTCGCT	300
	TGCTTCCGGC	AGGGGGGGCC	CGCCCCGATT	GGCGGCGCCC	CGCCCCCGC	CCCGAGATTC	360
	GCCACTGGGT	CTCCTTCCGC	CCCTTCACGC	CTTGTCGTTG	GATGATCTAA	GCAGGGTCCC	420
	CACGTACCAA	CAGCAGCACG	ATGGACACTC	CCTGCCATTG	CATCACCTCT	CCCCGGCGTA	480
10	TGCCGCCACC	GCGCCACCNG	CCGGGGGGCA	ACAGCGCACN	TGACAATCAC	TTNTGCGGTC	540
	CGTCGCGGCC	CCCCGGACCC	CCTTGCGCCC	TTATTCTGCC	CCCCCAAAC	CNACNTGCN	600
	CCCAATAGGG	TCAAACCGCG	GNGTGGNAA	TTTNCCTGNT	CNGNNNCNG	NNCNGGTTTT	660
	GGGCCCCCCC	GGTTNCCCCC	CNNANTTNGC	CCAANCAGAA	NCCGGGGAGG	GTTNNNGTGN	720
	NNCNGTAAAA	ACTTNTACCC	CCCCNCTTTG	GGTNCNNGG	CGGNGGGTTT	TTTTTTTCCC	780
	CGGGGNGCCC	CCCCCNNGGG	ACCNTTNGGG	NACNATT			

1285UP

	GATCTTCTTC	ATGACGCTAC	TGTAGACAGT	TTCACAACCG	ATAGCCTGAA	GACACAGTAC	60
	AACCAGAGCA	AAAGATATCA	ACTGTTTCGG	ATTCCGTATT	CGGAGCATT	CAGCTTTAAG	120
20	GACCTAAGTA	TTTTCGCAAC	CACGATCCAG	ATGAACGCCA	TTCGATCTAC	AGTGAACCTG	180
	GCCTCTTTGG	AGATGCATCG	CATGTGGTTC	GACACTTGGT	CTCGTATTAG	AAACGAAAAA	240
	TACCTGCGTA	AATTATGATT	ACATGTTATA	TATAGTAAAA	GATAACACGC	CACTCAGTGT	300
	TAAATGGTCC	ATCATGCCTC	TAGGACTCGT	TGTCGTTGCT	CGACAGAACT	GCAGTCCCCA	360
	TTTGCTGGT	AGGTTTTTGT	GAGGCTTTTT	TCTAATTGTC	TAATTTAAAG	TCCTGAATAT	420
	TATCCTCCAA	TTGTGGAATG	AAAGACACAT	GTACCACTAG	AGGTTTCAGC	CGATGGCTGC	480
25	AAAACGGCAT	ATTTGTATC	CAAATCATGC	CGCTGGTCCA	ACAGTTTAAT	AATGTCTCTG	540
	GAACTTCGAC	TACGTCCGGA	ACTCGTCTAT	CATCTGGAAT	ACCNCCTCCT	GTTATGCNTT	600
	ACCATANTCC	CCTCCCTTGG	TGGCCNAATT	CTTAANCAAT	TTTGNNTTAA	ATNCCCCCNT	660
	GCTTNNTAA	GGTNAATTCC	NNTTGGCCCC	CCCCTTCGGG	TTTNTCCGTT	CTTTGGAATG	720
	GAGGAAGCCC	AGGCTTGNCC	CCCAATACNC	GCCCTCCGGG	AAGNGTCCTC	CTTINGCCTT	780
30	CCCANTGGGN	TNCTTGGGTT	NGNNGCAAAN	CNACNNCNGG	CCCTCCTNCN	C	

1286RP

	GATCGCACCT	ATAATGAAGA	CCGGTTTTTT	TTTATGAGAA	ATAGCAGCCC	TCCAGGGGTT	60
	ACTTATTAAA	TAGCTACAGT	AAGATTAGGT	TATTCGTTTG	CAAATTCATT	GGTAGATCAA	120
35	CTTGTAACACT	TCAAATAATG	CTTCGCTGGC	ACCGTCATAA	AACATGTTAT	GCCCCGTGTT	180
	GACAACACT	CTGAAGCTAT	AGTCAGGGTA	GTGCGTGGCA	TTAGCTGGAC	ACACCTTATC	240
	TTCACTGCCG	ACCAAGACAT	GCCCTGTGCA	CCCCGTGTGC	AGCAAAGGTG	GGCCGTTAAT	300
	TAGGTCTTGC	CAGCCTAGAA	GATACTCAGT	GATGGATTTC	GTCGAAACTG	CTACACCGTC	360
	GTAGAAGTGA	TTTAGCTTCC	TGTACTTGTT	CCCCATGTTG	GAGAAAAAGA	ACTTAATTCC	420
	GGAGCTGTTT	AACCCCTTCAT	CTGGTTCGAA	TTGGTCCCTA	TGAATTTGAG	AAGCATGATC	480
40	AAGAAGGGCT	TGAAGAATGT	TAGTGAAGG	TTTAGATATG	GCTCGACGAT	ATCCAACCTT	540
	GATTTGAGAG	TTCTAGGTGG	CGGCGGCGCC	AATAGAATGA	TCTTTCTGCG	TTCAATTGTT	600
	GACGCCGTAT	CCTGAAGGCT	AATGCCAAGC	CAAAATGCACC	CCATCNATTG	CCCAAACTC	660
	CCACNGACAT	TATTATGGTT	GGCNCGTAGA	CCATGAATCT	AAACCCCTTA	TCACNCACCC	720
	CCCCACANG	GTTACCATCG	CCCATGTCCC	TTCCCCANCC	TGAGNTCNAC	CCCATTNTCC	780
45	CCCTATTTNC	CACATATCNT	CC				

1286UP

	GATCTTTCGCA	GCCAGCGCGT	AGTCCACCGG	CGTCAGTCCC	TCCGAGAACG	CCCCGCCGTG	60
	CACGTACAGC	ACCACCGGGT	CGTCTGGGTG	CCGCTTGTGC	GGCCGCGACA	CATACACCGC	120
50	GCGCGCAGTC	CGCTCCGCGG	CCGCAGCCGC	CGGCCCCCGG	AGCTCGAACA	GGTCGCTATC	180
	CTGCACAACG	TACGTCTCCT	CCAGCACCTC	GCCGCGCGCG	TCCGAACGACC	GCCGCGCGTG	240
	CCACCACGGC	ACGCACGTCC	CGACCGACGC	CCGCAGCGCG	GCCGCGCGCG	CCGGGTCCGC	300
	GTGCCGCGCG	GCCTCTACGC	CCAGCAGTCC	CAGCAGCGTG	CGCCGCCCGG	CGCGCGCAC	360
55	CACCGAGTAT	ACCAGGCGCG	CCAGCGCTGC	CGGCACGCCC	AACCCATAGA	ACTTCAGCAG	420

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	AAACGCGAGT	ACGCTCCACG	TTTGTGTTGG	AGATCCCATG	ATGCCGGCCC	GAGGGACGTC	480
	GACGCCCCGCC	ACCTGACGGG	GCGGCTACTT	ATACACCACA	AGATTCTATA	GAAAAGGAAT	540
	GCGACCAACG	ACGAACGGTG	TATCGTTTGG	GAAAAAAAGG	AGTCCCCCAA	CTAAAGCTTG	600
5	CTTGCTGGCT	ACGAGTTTGT	GTTTCAGGTT	TCTTCATAGC	ATCCCAGTTG	TTTTGTTTGT	660
	TTGGCAAATC	GCAATATGAAC	CATAAANAT	CAAANNTTGT	ACAATTGCTG	CCGACCGTTG	720
	CCCCATCCNC	CGGCGAAANA	TCCAGAAATC	GAGANAATTT	CAGACGCCGG	GTTTGCCAAA	780
	NTCCCGAAAC	CCCAAANTCC	CAACATTCT	GNCACATTG	ATTCTGNNNC	NNNCA	
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1287RP

	GATCCCACTG	GTATTAGGTG	TCTGAACACG	GCCAAATAAA	ATACGCAAAA	TGAAGGGCAT	60
	TAATAATCTT	TCATCAGTGT	TGACAATAAC	CCTTGACTCA	TTCTGAGCAA	ATAACTTTGT	120
5	TACTTCGTCG	TTGAATAACG	TGTCATCTAA	TAAGTTCTTC	AGATTGTCCC	TATATTTTAC	180
	AGCTACTGGA	TCCTTGTATG	CTAACAACGC	ATCTAGGGCC	AGTTTCTGCA	CTTCCAGCGT	240
	TCGACTACCC	AATAATTCCA	TCAACCTTTG	GCGGACATCT	TCGGATTGTG	AAATAGCTTT	300
	GATATTCTTG	AACTTGCCCA	ATAATTTCAA	AATTAGATTG	CTATCCGTCT	CAGACCATGT	360
	ATCCGCAGAG	TGCACTGCTA	ACTCACCCAG	ATGGTCTTCA	TCTTGGTTGG	CATCGAATTG	420
	ATCATTGCGT	TTTAAGACAA	AAGGTACAAT	GAATCTGCTA	TTTTGCTCCC	GCGAGCTGTN	480
10	GCAGCGCGAT	TAATATCTTC	AATGCTTGTT	TCTAATCATA	CCGGATATCC	GAGTGAACCG	540
	CGANCCCCCT	TAAGGTTTTT	CAACCAAGGA	TTTTTCGAAA	NCAACATNCN	TTTNGAACNT	600
	TCCNAANNCA	AATAATTNAT	CCTAAAAAAT	TTNTGCCCN	NTCCAAAAAN	TCCCNAGGG	660
	GTNNAAAGAG	TGGCCCCAAA	TTCNAAATNA	GNNTTTTTTN	GGGNTTTNCC	NAAAAAAAAT	720
	CCCNCCCNAC	CNCGNNTTTA	ANAATTTTTG	GGAANCCCAT	TCCCCCCCCA	AGGGGAAAAA	780
15	AGNGTGNCC	CNATTTTTNA					

1287UP

	GATCAGGTGG	TGTTGGCCGA	TACCGTGACG	GAAATGGATG	TCCTGGCCAT	GCCCGAGATA	60
	GATTTCTCTG	ACACAACGTC	CTCCTCGAAG	GGCCTGATGC	GGCGAGAGCG	CTCAATGGAG	120
20	AGGCACGTAC	AGGGCGCGAA	CACGGTCACA	GACCCATGGG	ACATGCTCTT	GGAAGTGGGG	180
	AGAAGATACG	CCCCTGACGA	CGACCTGGAG	CAACAGACGT	CGCTACTGGA	CCTCAACTTT	240
	GAACTCAGTG	ACATGCAGAA	CTCCAAATCT	TGGGGTGAAG	GGACGCACAA	TTCCGAAGAG	300
	ATCAGTGCCA	ATGTGCTTGC	AGAGTCGCAA	CGCCAGGAGC	TGCCCCGGAA	CGAGGGCATT	360
	GAGCGTGAAG	AGGATCTTGA	TTGGAATCTG	GGATTACCGG	AACCAGCAAT	TGTAGTCCCT	420
25	TCAAGCGATT	TTGAACACGA	TAACAGCATA	GAAGTGGGCC	GGAGAGCAGT	CCCCGAATGC	480
	GGACCTTCAG	GAAACTGTGG	ATTTGGGATT	CGACTTGGAT	ATTGCCAGGG	TTGACATTGA	540
	GGCTACAGCC	GGCGAGCAGA	TGCTGGCAGT	TTGCATCTGA	GCTTTCCGGA	AGTATAGTAC	600
	GTCTTCTTGG	AACACTGTNC	ACANCCAAAA	CAAGAAAGGC	ACCTGGTTAT	CAATTCTACA	660
	TTCACCCCCA	CCGATTACT	GAAAGGTGNT	CNAAAACCCC	CCCNACANTG	CTCCNTGANT	720
	ACCCATCCCN	NCCCCATTN	NCCCNAAAAC	GGNTNTCGAC	CCTTTNAAAT	GATCCTNCAA	780
30	TTTTGCNTGA	CATCCTGCTC	NTTCCAACG	AGNCCCA			

1289RP

	GATCGGGATT	GACCGTAATA	TTTCAGCTTT	TTGATGTGAA	TTGCCAAGAG	GACCAGCGAT	60
35	TTGAATCTCG	CTGACTCTGT	TGTGAGTAAT	TAGTACAAGA	ACCTGTGGCC	TGTCACAATT	120
	AAGCCCTGGG	AATAGGACTT	CAACTTCAGA	AGCCACGAT	CGTCAAGCGA	TGATACAAGT	180
	GCCTACCAAC	ATTGACTTAA	CATGAAAATT	GATAGCATT	TTATAACAAT	GGAAGCAAA	240
	GACTAAGTCC	TTCACGTGGT	CGCCAAATGA	GCCTGTTAGC	AGGTTTCCGC	ATATTCTCTG	300
	AAGATGTCAA	CCTTCCAAAA	ATATTCTCTA	GAGCATTAA	TATCATTACA	CAAGCCCTTG	360
	GTGTGAGACA	GAATCTTGAG	AGGTGCTGCG	ATAAACTCA	AAATCGCAGT	GCTTGGATTA	420
40	TAGGGCTTAT	ATACTGATTT	AAGTGGTGGT	GGTTATCTAT	TCAGGGTTGT	ATAAATTAAA	480
	ATATCACAGT	CGGTATACTC	TTACACACTA	ATTATAATCA	CGTGATATTT	GACTATTTAT	540
	TACACCAGGA	CACCTCGCTA	TGAAAATAGC	AACAGGCTGA	TGGTATTAA	ATCTGAAGAT	600
	ATCGCCAACA	TTAGAACACA	CTACTGACAC	AACGGCCAGC	CATTGAGAC	TATGGCTCGT	660
	ACTACTGCAN	TACTGTGATG	CTTATCTGAC	NCTGACCNC	TGATTGTTGC	GGAAATCCNT	720
	TTGATCNGCA	AAATCATNTC	GNTGACCNCA	ANTTCTACTN	TATTAACCCC	CCCACCGCCA	780
45	ACCTTTG						

1289UP

	GATCCAGGC	TGCCCCAGGA	TGACGGAAAG	TTGCATGTTT	TTTTCGGCGC	TACAGGCTCG	60
50	CTTTCCGTAC	TGAAGATTAA	ATCGATGATC	AAAAAACTCG	AAGAGATTTA	TGGTTGGGAC	120
	CATATATCCA	TTCAAGTCAT	ATTAACCTAA	GCCGCTGCGC	AATCTTTTGC	TAATAAAAA	180
	CCCAAGAGA	AGAACCCTTA	CGTGTCTAGC	GAAACAACT	CATTCTCAAA	CTCCGTGGCT	240
	CACCAGGGGA	AACCTGCAAC	AGAACAACCT	AGACGCATCC	TACACTGCGG	TAAATAGCGT	300
	CTCCAATACC	CCTGCACTTG	GGGGGCGCAC	ACCAACGCCA	GCGATCTTTC	TCCAGGGCGC	360
	AGCGCCGCAA	GGCGCGGGCT	CCGGTCTAAG	CCAGGGCGCA	GCTGCGGCGA	AGATTGAGCT	420
55							

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5	CCCTCCACAC	ATACAAGTCT	GGACGGATCA	AGACGAGTGG	GACGTGTGGA	AGCAAAGAAC	480
	AGATCCGTAC	TGCATATTGA	ATTACGCAGG	TGGGCGATAT	CCTTGTCTGC	GCGCCACTTA	540
	CGCGAATACA	CTTCCAAATT	GCCCTGGGCC	TTGTTAAAAC	CCGCGAACAT	GTTCTNCGGG	600
	NNTGNAACCA	NTTTTCCAAT	TCNTNCNCCA	NCCGNGTTTN	GNGNTNTTNA	ACCCCCCCCC	660
	TACCCCCCNA	AAAANAANAA	NAAAAACCCC	GTNTNCNGTG	TTTCACCNCC	CANAAAAANAG	720
	GGTNCNCCCGG	GAAAACGAAC	TGGGGGGAGA	GAGAGGNANN	AAATTNCNAN	AATCCTTTTA	780
	NCCNCGGG						
10	1291UP						
	GATCGTGCAC	GGCAAGACGT	CGGAGCTGCG	TCACGACGGG	CGCGGGCTCT	TCCAGGGGGT	60
	ACCCCAGGCC	GTGGCAGTGA	CACGGTACCA	CTCGCTGGCT	GGACTGGCGT	CAACGTTGCC	120
	GGCGGAGCTG	GAGGTGACGG	CGCGCACGGA	GACAGGCGTG	GTTATGGGCG	TGCGGCACCG	180
15	CAAGTACACC	GTGGAGGGTG	TGCAGTTCCA	CCCAGGATCG	ATTCTGACGG	ACCACGGGCA	240
	GCTAATGGTG	CGCAACATGC	TAGCGTTGGA	AGGCGGTACG	TGGGCTGAGA	ACGACAAGCT	300
	CCAGCTGCGG	GCAGGCGCGG	GCTCTGTGCT	GAGCGAGATA	TACGCTCAAC	GACAGGAGGA	360
	CATGGCAGCG	CAGATGGCTA	TGCCGGGAAC	TGGTATGGCG	GACCTGGAGG	CGAGCTTTCG	420
	ATTGGGGGTT	CTGCCGGGCG	TGGTGGACTT	CCATGAGCGG	CTGGCGCGGG	ACGCCCGCGG	480
	CTGGCTGTGG	TAGCCGAGAT	AAAAGTGCCT	CTCCGTGCGG	TGGCAATATT	AGCGAGGCGC	540
20	TTGGCNCCAN	AANANGCGCT	TNCNINTTGC	CGAAGGCGGA	ATTTTCCGCC	ATCTCCGGTG	600
	CTTTACCGAA	CCCACTGTTT	TAAAGGGACC	CGCNAGANCN	NAATTATTNC	CCGACCCNCC	660
	CTTTGANAAA	AACNANACTG	CCCAANACCC	GCCGCGTTTG	CTNCTTTANG	ANATCTTTAT	720
	TNTCCNTTCC	AATNTTTTGA	GCCCGNTTNC	GGCCNACAAT	TTCCCTTATT	TTNAAATTTT	780
	NAACCACCCC	CCCCCAGACC	NTTTTNTTN	CCC			
25	1292RP						
	GATCCGTGTA	TTTTTTATTT	ACATTATTTA	ATTAAAAATA	ATGATTTAAA	TAAATATTTT	60
	TTATAAAAAA	TAATTAGTGC	ATTGTTACAT	GTTTATTAAA	GAATGATTAT	TATCAAAACC	120
	ATCAACTAAT	TGTTATATAT	TTATTAAATA	TTAATTTTAC	TTAATTAAGA	ATTAGGAACT	180
30	TTATCTATTA	GTCTGGGCTG	TTTCCCTTTT	GATTATTAAC	CTTATCGCTA	ATAATCTGAA	240
	ATATTTAATT	TTAGATTAAT	AATATATTCT	GAGATTTAAT	ATTTTTAATA	AAATAAATAA	300
	TTATTCCCTA	AATAATATTA	ATAACTATAC	CATATATATC	TAATATTTAA	ATAATCATAC	360
	TAACATATGT	TTCGTAGAAA	ACCAGCTATT	TGCAAAATCAG	ATTTGACTTT	CTCTACTTAC	420
	CATTATTTCAT	CAGATAATAT	TGCTACATTA	ACCTGTTCAA	TCGTTTTTAT	ATTTTATTAT	480
	ATTTTAAATA	TAATAAATAT	ATATTTTAAT	CATTTGATAA	TAGTAAATC	ATCTGCTTTC	540
35	GGTTTAATTA	ATATTAACCTA	AATTTAATTT	ATTTTAATTA	ATTTTACATN	GTAAANATT	600
	TAAATTAATT	TTAAACCAN	TTTTATTTTN	AAATTTTGNC	AAATTAATAC	TGGGGGNCCC	660
40	CTTTCCAAGG	GGCCTNNNTN	NATTTTTTNA	AAAAAATAAA	AAAGGGCNNN	ANAAACCTTT	720
	TAAAANTTCC	CCNCGGCCCC	NNAANANTNA	AANATTNAC	CCNAAAGGTC	CCN	
45							
50							
55							

1292UP

	GATCCAGTTA	CTTAGTAGAA	TGATAAAATT	AATAAATATT	ATTTATTAAT	ATTTGGTTAA	60
	CAATAAAATT	CAATAATTTA	TTTAAATAAT	GATTAAATAA	TCTCAATATA	AAATTATTAA	120
5	TATAATGAGA	TATATATTTT	TAAAAAGAAT	ATATAATTAA	ATAATCCCAA	CCAAAAATTG	180
	TGCCAGCAGC	TGCGGTAAGA	CAAAGGGGGT	TAGCGTTAAT	CGTAATGGCT	TAAAGGGTTC	240
	GTAGAATGAT	TATTTAAAAAT	AATAATTAGA	ATTAATAAAA	ATAATTTAAG	AATTATTCAA	300
	GTAAAGATGA	AATAATAATT	ATATGAATAA	GACTTATAAA	GTGAAAATTT	AAATTATATA	360
	TTAATTGACA	TTGAGGAACG	AAGGCTAAAG	TAGCAAATCG	GATTCGATAC	CCGAGTAGTT	420
	TTAGCAGTAA	ACAATGAATA	CCTATTATTT	TTTTATTAAAT	TAAAGAATAA	ATTAAATGAA	480
10	AATTAAAGTA	TTCCGCCTGA	TGACTACGTT	TGCAATAATA	AAAATCAAAA	CAATAGACGG	540
	TTCCGACTTA	AGCAGTGGAA	CATGTTTTTT	AATTCGATAA	CCNCCANAA	ACCTTACCAN	600
	TTTTNGAATA	TTTAATTATA	ATAATTTINTA	ATTATTACGG	NGTGCAATTT	NTCTTCCCTC	660
	CGGCCGGCNA	GTTTTTNAAT	TATCNTNAAC	GAACAAACNC	CCATTTTTTT	TTTNANAAAA	720
	ATTATTTATT	TTTTGAATAT	TNAAAAAATA	TAAANATCCT	TTNTCCTTTT	TAATGGNNGA	780
	GTNTTTTTTT	TTNTTCNN					

1293RP

	GATCACCGAG	CAGCTGGTTG	GCCTCGGCAT	AAGCGCGCTT	GGTCTCTGCC	CACTGTTCTC	60
	CAAGACCAAG	CTGCTGTGCC	TGGAACAACA	GGTTTGTGAG	CTGACCACCA	GGAATTTTCAT	120
20	GTTTGTACAC	CTCTGGGTCC	GGGCCCTTGA	GGTCCGCTTC	GAAGCATGAG	TACAACAGTC	180
	TCATCTCCGC	CCAGTATGCG	TCTAGTTCGA	TGCGATGATC	GGGGTCTACA	CCCGTCGCGA	240
	TATCGCCACC	CAATGAGGCC	TGCAAAGCCG	TAATGGAGGG	CTGGGACGTT	AAGCCAGACA	300
	TCGAGTTGGT	GGCGACGTCC	ACAACATCGG	CGCCAGAGAT	GGCGCATTGG	ACCATTGATG	360
	CGACACCTGT	GCCTGCGAGAA	TCATGTGTAT	GCACATGAAT	TGGGAGGTCT	GGATACTTTG	420
25	CCCTGATCGA	GCCAATCAGT	AGCTTTGCTG	CACCGGGCTT	CATGGTGCCG	GCCATATCTT	480
	TAATACCCAA	GATATGTGTG	CCCCATGGCA	ACAATCTPTT	CAGTCAATCC	AGTAGTAATC	540
	AAGGTTGTAC	TTCTTGCCCTG	CTGTAGCATA	TCACCTGAGT	TACAGATAGT	GCTCAACCAC	600
	CCTCCCGCTT	TCTTCACGGG	TNNAACCCA	CTTCACTGTT	CTAGTCNTCA	CCCNTCNAAN	660
	CTCTGAAATN	TCANNCATCC	CCTTGCTGTT	TGACAAATGT	CATCCCNPTT	CCGCNAAAGA	720
	ATTAACACCC	GTGGCCCCAA	CNCCCTGAAN	GATTTTGGCC	NG		

1293UP

	GATCTTACAT	CTGACAACAA	TACGCTGGCG	GCAGATGAGC	TGCATTGATG	GAAATTTTAA	60
	CACAGCTCGG	GCAACCAGCT	ACACGGGATA	TATAAACTCA	ATGCACGCCG	CTCTTTACTG	120
35	ACACAGTCCA	TCAGCATCAG	CACCACCCCC	AAAAATGAAG	ACTACACACA	TCCTATCCCT	180
	AGCAACACTT	GCCGCTTCGG	CACCTGTTCA	GCCCCGACCT	GTTCAGCCCA	CGGACCTCGC	240
	CGCAGCGGCA	AACGTCCCCG	AGAAAGCTGT	TCTCGGCTTC	TTCCAATGTT	ACAATGTGGG	300
	CGATGTGGAG	CTGCTCCCG	TGGACGACGG	CGCACACTCC	GGGATCCTTT	TCGTGAACCG	360
	CACACTAGCG	GACGTGGACT	ACTCCTCCGA	GCATGTGGTT	CAAAAATGGT	TCCGTCTGTC	420
	TCTCCACCAT	GGGCAAAGTA	TGTAAGGCCG	GACCAGAGAC	AGTTTGCCTT	GAGATATGTA	480
40	AGTTTACTTG	GTGTCTTACA	CCATGCATTA	TGACACGGGC	TTACGTACCT	GCTTCTATAA	540
	GCTAGTTTAA	ATGTTTTCTA	TGCGTATTAT	ATGGTTTACC	CGCGCCGATA	GTTCGCAGAG	600
	GCTGCTGTNT	TAAGGCCNAA	CTTTATTCCCT	AANANGGTGG	ATTACCCGGT	NGAAANAATG	660
	AATCTGAATT	GGCGAAATTC	CCGCTGGNCT	ATTANCTCCC	CNNCCCGTCC	NAATAAATGG	720
	AANATGGTGG	GGTTTAATAC	AAAANGGNCC	GNTGCCGCGA	ATGNACTGGA	TTAATTTCAA	780
	AAACCTCCAA	NTACCCCCAA	NTGGN				

1294RP

	GATCCGGAAT	GTCGCTCAAG	CTCCGCTGCT	TTCGGCTGGC	CTCGCTGTTT	TCTGTGGAAT	60
	CGTTTCTGGT	GGTCTCCTTC	TCCCATGTTG	ACCTTGGGTT	CAGCGTCTTC	AGCTGGTACA	120
50	CCTCGAGAAG	CTTCGAGTTA	TCGAATGCAA	ATGGGTTTAG	CATCTCGACC	ATATTGCTG	180
	CGCCACCTGC	CTGCCCTTTT	GGCCTTACAT	CGGGAGTCCA	ACTTCAACGT	AATGCTATAG	240
	AAAACGCCAT	TGGCCTCGCC	GTCTTATCAC	GTGACTGTTT	ATTGAGCTCG	ACAGCTACTC	300
	GACTAGCACT	GCTGCTGCTT	TAAGTGGGCT	ATACACTTTA	TATCGTTTCA	TTACTTTCTC	360
	CGTGGTCCGC	GGATGGGTGG	TGCTGGCTTG	TGTGCAGACT	CACTCTTGAA	CAGAGGAGCG	420
55	TTCTTAAACA	TGCTGGTAC	GACAAAGAAC	CTTACGTGCG	AGCCTCCGCA	CGAATACATG	480

EP 0 866 129 A2

5	GTCCATATGT	GTCACCTGGC	CGTTCCGTGC	CGTCGCTGTC	ACGTCTCTTA	GCTGGCAGTC	540
	ATGTTGTCCT	CGCTGCCCAC	CAACTTGCCC	CGATAGTTTC	GCCGGTCGTT	ACTCCAGCAN	600
	ACCGTGTNGC	TINGGCTTCC	TTCACACTTA	CAGGAATCCG	GAANTGCCAG	ATCNTACTTT	660
	TTGGTTTGGC	CGTTTCCNTT	CCTGACANAA	ANTGGTTTAT	ATTTTGCCCG	AAAAGNTTTA	720
	ATTTTACATT	TTCNAAACAA	CATANGTTGC	NTTTTTACNN	AACC		

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1294UP

	GATCTGGAAC	TCCAAGTTCC	TGATGTCTCG	CTTACGCTTC	TCTCGCTGCT	CATGAATCGA	60
	CTGCTGCTTC	CACCGAATGA	ACGACCGCTT	GTCCACATTA	GGATGTACCT	CGATGTCCGA	120
5	GTCATCCGAG	ATTTCTATCT	TGTCCCACTT	TGAGTAATCG	ATTGCCATTG	CACTACCTTG	180
	TTTCGTTCTG	GCTTCACACT	TGTTGTCTTT	AGATCTTCTG	GATCCACCAA	TAAGTATAT	240
	CAAAGATTCA	TATATGCAAA	CGTCCAACCT	AATAATGTTA	CACATAAGGA	AGGACCAAGG	300
	CAACGCCTGC	CCAGTTCTAG	CAACTTCTGT	GTGTCACTCT	CAACGATAGA	AGTCTGGTCT	360
	CGAGATGTTG	AGACCGTACT	CGGCCACAGC	GCTGCTGAGG	TCGTTGACGG	TCAAGGTGAC	420
	CTTGTTTCGCA	TTGGTCTTTT	CGTTTGTGTT	GTGCTGCTGC	TGGCTGATCT	GCTGTGTGCC	480
10	GGGCTGCTGC	TGACCGAGCA	TCAGTTGTGC	GGCGCGGGCC	TGGCCGTGTT	TGGAGTTATG	540
	GACGCGAATG	AGGAGCGGAT	ACGGAATACT	CGTAGGCGTT	CGGCCGCNAT	GTCGCTAACG	600
	AACTCTGGTT	GCCAACGCGA	AGAAGGCCTT	GACCCGANAT	CNGTGCACNC	CGAACCCTCC	660
	TGGTCANTTA	TTATCCATCA	CACNTCGGGA	AAAAGGGGGG	GGTTCTCTCT	AAGTCNAAAA	720
	CNCTTGANGT	CTGTCTCTGC	GGTGAATCGG	ATTTCCAAAA	CTTCTTTTNC	NGGGTTTGCC	780
	CCNGCGGGCC	CCNGGGGNGA					

1295RP

	GATCTTTCTT	TCAAATTGGG	ACGAGGTGCT	TAAGTCATCC	TGATCCTGCA	CAATCACGTC	60
	CATATTGGCG	GAGATCAGTG	CCGGTTTGGC	ACCAGAATCG	CTGCCCCGCC	AGGTGACTAG	120
20	CAATCCGAGC	TCGTTGACAG	TTTCCACCTT	TAGCTTACAC	CAAACCAGAG	GAAAGTCCCG	180
	CGACAGCTGC	TCGTGCAACC	GTTTGAACCT	CTTGATATGT	TCCGTGTCGG	ACTTCACCGC	240
	TGTGCAGCAG	CCGCTGTCAT	CCACCACCCA	TGCCGAGGGG	ATCTGCACTG	CACGCTGTAG	300
	CTTCTCGACA	GTGAGATTGC	TGAGCGTCTG	GTTGTGTCAG	ATTTGCTGGA	GGTGGTCTCC	360
	AAAGCCCCCC	TGAGGTTTGG	ACACGTCCCA	GCACGATGGC	AGTGACGCCC	CAGTCACCTC	420
25	CGAAGAAACA	ACAGCACTCC	GCGCTGTCTG	AGCAGAAAAG	CAGGCCAGCA	ACGCCAGCGC	480
	CGTTGCAAAG	GATATCGGTT	GCCCCAAAGG	CCAAGCTGCA	AACATCATTC	TGGTGGTTCAG	540
	CGACTGCTTT	TCCCACGAGA	TCCGTGGGGA	CCATGCGCCA	GATGGCGCCC	TTAATATAAG	600
	CCCCTCCTCG	CCAGCATGAC	TTCTGCCAAC	TCCCAGAACAT	TCTAAATGGC	CAGCTGCTGC	660
	TTTGATGGTA	CCCTNCCGNG	CTNGCGCCAA	AATTNATATA	CCATAATCCC	CNTCCTAAAT	720
	ATNCTTACAT	ACCACGCCCC	AAAGCGCTCC	CCGNAGCNCN	CCCAGCCCCC	CACCTTCNCC	780
30	NNAAGNANCC	GNTGNG					

1295UP

	GATCAACTTC	AGTTCTGCGC	GTTTGTGCGA	TGGAGGCCCG	CCAACGGCAG	ATAGCTTCTC	60
	AACTGTGGCG	GTACCCTGCA	CGGGCTCCAC	GACCGCTGTG	CAGTGGAAC	GCTCGTAATT	120
35	GTTCTTGGTG	TAGTGCTTGA	AGTACTCCAA	AGACCACACG	AATGCGAGGC	CTGCGAGGAT	180
	ATAGAAAACC	AGCGTCCCGT	ACCTACCGAT	TGCCATGGTT	GAAGCAAGGA	TTCCACTGCC	240
	GTAAGTACTC	AATTATTGAG	TGCTAGCAAG	CTGATGTTGA	TTGTGTGATA	TCAACGGTAA	300
	TCGGTTCGTT	AGGAACCTTT	TCAAGAAACG	CAAAAGAAAT	GCGTGCCTAG	GTCGAGCAGG	360
	TGACAACCTC	ATATTACTCA	TAACAGTTAT	CTATCTAAGA	AGCGGCACTA	TCGATATACT	420
40	ATCAGCTTCG	TATACACATA	TATATCGGAG	GTTTATAATC	GCAAGTTAGC	TATAATTGCC	480
	ATCGAGGTGT	AATACATCGA	AGATTGTCTA	CGAAACTACT	CTGTCAACCA	CACATCAGCG	540
	TATGAACAAT	AACAGCAATA	TTATGACAGG	CAATTGCATA	AAAGTATTCA	AAGAGGGTTA	600
	AACAGTTAAA	TTCCGTAAAG	GTTTCAGNGAN	TATTCCTGTA	CACCCCATAC	CGAATCGCCC	660
	TGCACCAATT	GTTACATGTT	TCANAGATTC	TCCGGGACTT	CATATGNACC	ATGTTGCCCG	720
	CCCNAACTCN	CATTATGTNA	ATGCTTGTNT	TCCTGACTCC	CCCGCTTGTC	CCAAATGCCA	780
45	TCCCAGGGTG	ANAGGTGCTC	GTGATCTC				

1296RP

	GATCCATTGT	GCGTTTGGAG	GTCACGCCAC	GGACGTGGAC	ATGTACGTGA	TGAGCTTCTGA	60
50	CGGGCAGCTC	TTCATTCTGT	CGGCACGCAA	GAAGCTTGAG	TTCCCGACGT	CTCCGCGGGA	120
	GAGTTGGGCG	TACCTTTCGT	ATTACAGCGG	ATACAAATTC	GAGCGCATGG	CGCTCCTGGA	180
	CCGTCCGGTG	GCCGAACTC	CGCGCGAGGT	TCTGGAGAGC	CGCGGCAAAC	AGGTCGTCCG	240
	CAACGGTCCG	CAATACAGGA	CTGTGATGAG	AACCGGCGTC	GGGGAGCACA	AGCTGGTGTCT	300
	CGGAGCTGAG	ATCGACGGCA	TCATTGACTT	CCGCGAGCCT	ACGGGCGACA	ACCTGAAGCA	360
55	CTACGTGGAG	CTGAAGGTGT	GTGAGAAGAA	CCGGAACCTC	TCAGAGAAAC	TTTTCTCTTC	420

	TTGGCTGCAA	TGCTTTCTGG	TGGGCATAAA	CAGGGTTATT	ATTGGATTCC	GGGATGAGAA	480
	ATTCCTCCTG	AAGAGCGTCG	AGGAGTTCAG	TACGTCAGAG	ATCCACACCC	TGTTTAAAGG	540
	GCACGGAATA	TTCCATGTAT	GTGTGTGACG	CCATAGATTG	TATGGTGCTC	CTTACAAATT	600
	GCTATNTGAC	TCCCCCGGGC	CCTGAAAAANA	NTTCAACTGT	TACAGTCTCC	TGCNNCATGG	660
5	TGCTTACTTT	TGCCCCACTG	CCCAACAAAA	ACCCCCAATG	GGANAAATTN	TCCCTNGTTG	720
	GTCCCCAATT	GGNGNGNCCC	CCANATANAA	AATTCCGNAT	TATTCCCTTG	TTTCCTTAN	

1296UP

10	GATCGTACGG	TTGCTGCTG	CGGTTTACCG	ATATGGATCG	GTTGTTTGCA	GTTGGCGAGA	60
	GCACGGTGGT	CGGTGTCTCT	GGCGACGTCT	CGGACATGCA	ATACCTACAG	CGCCTGCTCC	120
	AGGACATGGA	GATCGAGAAC	AACTACGACA	ACAGCCACGC	AGACGGCGCG	GAAGCGCTCA	180
	AGCCGAGCTA	TATTTTTGAG	TACCTTGCCCT	CGCTCATGTA	CCAGCGCCGC	TCAAAGCTGA	240
	ACCCGCTCTG	GAACGCCATC	ATCGTCGCCG	GCGTCGAGGA	CGGCCAGGCC	TTCTGCGTT	300
15	ATGTGGACCT	CAAGGGCGTG	AAGTACTCCG	CCCCAAGCTT	GGCTACTGGC	TTTGGCGCCC	360
	ATATGGCCAT	TCCTCTCATG	CGTAAAGTCG	CAGATGCCGA	AAAAGACTCG	CCGGCGTCTGA	420
	CCTCTCAATT	GCGCGAGCGA	CTATCCTGGA	GTCCATGAAG	GTGTTATTCT	ACCGCGATGC	480
	GCGTAGTTCC	CGTCGCTTCT	CGCTTGCCAT	CATCGACAAT	GATGCCGGTG	TTCAGCATGG	540
	AGCAACTGGA	AGTGGAAAAC	ATGACCTGGG	GTTTCGCCCA	AGGATATTCC	GGGCTATGGC	600
	NCCCAAAATNT	TTTGAATTAC	CNNGGCCGCA	ACGCCGCACC	CTGTTTACTA	TCTTGTTCGC	660
20	GGNTGTCNCC	CAACCGCTNG	GNTATCCCAT	ACNTTCAAAA	NGCNTAATCA	TCTGCCCTGA	720
	ACCCCNCTGT	TTTNGTNGAN	ACCTTCNCCC	CTTTTCNCGA	TTTCCCGGAT	TGNCAAAAAC	780
	CCTTTGAAAA	AACATTNCCC	NTTGGNAAAT	CGATG			

1297RP

25	GATCTCCTCG	ACGCTGGTGA	CCTTGCCGGC	CTTCACAAGA	CGGCCCAACT	TGGTCACTGG	60
	CACCCAGCCC	TTCTCCTCGA	CCTCTCTTCT	GCCCTTGCGG	CCCTGACGGC	CCTTGTTTCT	120
	GGCGCCGAAG	CCGCCCTTTC	TTTGTTCGCG	AGCTGACATC	TTGCTATCGT	CGGAATGGAA	180
	CACGGAAAGC	TGGGGGAGTA	ACTTTCGATC	GACGCTGCTG	ATGTAGTTAC	GATACAGCTC	240
	CGGCCGCGCG	CTTGCGTGCT	GAAAACCTGC	CCACGGTCTG	CGTCACCAGA	AAGGAGGTCT	300
30	GGGTGCTACC	GCTGTTTCCG	GCCTCACGAC	GTGTCTGGGT	TTTCACTGTA	AACCCACACA	360
	TCAGACAAAC	GCAGTCCCGG	ACGGCTCGAA	AGCAAAACCC	GCGTGAAGGA	GCAACGCGGA	420
	AGCTGCGGCG	TCCGTGCCGA	ATCTCGTCAA	AAACAGGGGT	CACAAAGGGA	TTGGCGCTGG	480
	CGCCAGGACT	GCTACGGGGG	CATTGGCCCC	GGCGGCAGCC	CCGAGCAATG	GAGCAACCCC	540
	CTTCGCGAGG	TACGGCTCAC	ACTGCGGTAT	AAAGGCGGGC	AGAGCGGTGG	AAGCAGACAG	600
	TGACACACAG	GAGAGGACAG	ATGTCCGACN	NCAAAATGAC	AATCCTATCA	ANAGGNGCGT	660
35	CGGGGCCAAA	CTATCAANAG	NTTCGAAGTT	CCAAACTNGC	CAGATCAAAA	GGCCCCAAAG	720
	GGAAAAAACT	TCCCCCCCCAC	GACCCTTTGN	CATTTTAAAC	CGCCNG		

1297UP

40	GATCCAAAAA	CAATGAAC TG	TTTACAATGT	GGAAGCCGTG	ACACAAGTGA	ATGGCGCTCA	60
	GGACCGCTAG	GAAGGAAGTC	TATGTGCAAT	GCATGCGGTA	TCTGGTACAT	GAAATTAAG	120
	CAGCGGTTTG	GGGAGGAGGA	TGCTGCGGTG	ATTATGGAAT	ACCGGAGATT	AACTAATAGG	180
	CACGATGATC	GCAGGGTGCC	CAAGAAATTT	GAGGTCCCAT	TGCCGTAGGT	CGAAAAAGTG	240
	AAGAGAGCCA	TAAGAGCTCG	TGTTGTGGAG	TATTTGAATG	ATGTTGAAAT	CCCGGTTAAA	300
	ACGAGGAGGC	GGGCGTTATT	ACATAAAGGC	AAGCCGGGCA	GTGCGTTAAA	AACAGAGATG	360
45	AAAACCCCTG	CCGCATGAAG	CACTGGAAGG	ATGAAACCAG	TTTGTACGCC	GGAAGGACAA	420
	TACCGGCGGG	TAGGAAGGTA	GAGACTATGC	TGTGGCATGT	AAGGAACGTA	CTTTTATTTA	480
	TCTAACATAA	CTAGGGTTCT	TTTGACCTGN	TACCTTTGTA	TTATCCCTTG	AANAAC TGAA	540
	CCCCCNCCCT	TTAAAAANTT	TTTNNNTTGN	AAATAAATCC	CCTTTAAAGA	ACCCCCCCCN	600
	NAANCAAACC	CTTNTNCCCT	TNGCCCAAAC	CCACCCAGAA	ATTTTCCCN	CNTTNCCGAN	660
	ACANCNGTTN	CGAGATTCCC	CCNTTTNCGC	CNAAAAAANC	TCCCCCCGAN	TNTNTNCCAN	720
50	AGNGCCCTTT	TNCNCTCCCC	NCCNANAATC	CCCAAATTAG	AAGGGGTNTT	CNCCCNNGCT	780
	CCCCGAGATC	CAAAA					

1299RP

	GATCTCCAC	ATTGAGACGG	TAGCAGCCCA	CATATTGCGC	TTGAACGCCA	TTAAACGGCG	60
	CCATTGCTCC	CATAGAGCTT	TCAGATTTCC	TGTTAGGCTC	CAACTCAACG	TCATACTGGA	120
5	GTTTAAATCG	AGTGGGTGCT	GTTGATATCC	AACTTGGAGG	CGTTCTTTT	GTCCTCGTAT	180
	CGCTTGAATA	GCCGCCCAGG	TCCCGTGGCG	AAAATCCATA	TATATCCATA	TTGGCCACCC	240
	AGCTTGTAC	ACATAGAGGC	AATAGTGCCA	GTAATGCCTC	GAGCCGAAAC	CATGCAGCTC	300
	CCCAGCGAGG	AGGCGCCCCG	CAGCGTCGCG	TTCCATAGAC	GGCAAGCCCG	GCGAGTGC GG	360
	CGCAGCGTCA	GCACGCAGTT	CCTCCCTGTC	ACGGTATGTC	CCCAGCCGGC	GGTGCGCACA	420
	CCCAGATACT	AACACAGCAC	AGACGCTGTA	TCAGCTGATT	GTCCAACCGG	CGTACTATTT	480
10	CACGTTTCTG	GCGAATGTGC	TAGTGACGCG	GTTGCGCGAG	GGCGCGGCAG	TGCCCATAGC	540
	AGTGGCGTTC	TGGATGTGCA	CGGTGGGCCT	GGGCATTCCC	GCCC CGCTG	CCATTGTGTC	600
	TGCCCGACGC	GGTGTGGCAG	GGTGTGCTGG	TGGGTGCGGT	GTGCTGCCCG	AACTACCACC	660
	TGGAGTACAT	GGAGACCTAC	ATTGCCAGCC	TGCTCGTGAC	GGGAGAGGGG	GAGTCCCTGTT	720
	TTCNCCGATG	GGCTCCCGGC	GGTGGGCGGT	TCC			

1299UP

	ACGCTTTTGG	TTTTCGGCGT	GATGGTGGGT	GGTGGTATAG	ACGATGTGAT	CTCCGGCTGC	60
	AATTGTAAAGC	CTTCTCCTCC	GGAGATATCC	CGCACGGAGA	AGTCGTCTAA	ATTTAACATT	120
20	ACGTTTCATGT	AATCACAGGG	CACCTTTTCA	AAGACACAGA	CGATCATGCC	ATTCTTACGC	180
	TTTGCCACACA	TGGACGCCCA	AATGAATTTT	TGTGTATGCG	AGGATGCTGA	CGATGCAGCT	240
	GAAGCAGGAG	ACGACAGCGA	TGTGACGCCCT	GGTTGTATGA	CGCTACTAT	TTACCTGTG	300
	AATACTTGTT	CTTGGCCCTC	TGTAGACATA	ATCTTGTAA	GGACAAAGCT	CCTGCTGTG	360
	GTGTGTATCA	GGTCAAGTAA	AGTAAGCGCC	TTAAATGCCA	ATTGGAGAT	ACCGAAGATT	420
	AAGCATGCCN	AATCGTTAGC	CGCCCTAAAC	TGCCATGGGT	GATGCTGGGA	ACAGGTAAAT	480
25	ATGGCCTGAG	GTGCTGTGTA	CTTACCTGAT	ATAAAAGTAT	GCAGTATGCG	GGGCGCTTCG	540
	TACGTTCTG	TGTAGTCTAT	CGGATCCTGG	ATAGATGTTA	GTTTCATCGGT	AAATGGTTGG	600
	AGATAATTTT	CGTCTGCGA	GGCCTGTATA	TAGTCTCTG	TGTTGAATAT	TCATGAAATG	660
	GTTGGGCTAA	GCTTTCAAGC	AGCTGCTTCT	TTAGTTCTTG	CTCATTACTG	ACTTTCTTCG	720
	CAGGATCTAC	GCCATCCGCG	TTGGTGCTGA	C			

1300RP

	GATCTCTCTG	CGCGGTGCAC	AAATGACGCA	GAAACAGGCA	TTCACGGAAT	TGAAGAGGCC	60
	TCAACTGCCG	CCGATCGCTA	CAGGCGCAGT	GGGACGACAT	CCTTTCTTTG	GTGCGTATGA	120
35	GGATACCTAA	ATAAGCACAT	ACAAAACGTT	AAATATGCAT	AAGGAGATAT	ATGCGAAAGT	180
	TAAAGTGTTT	TTAGTGGCCC	TCGGCCACAG	TTGCGTGTTT	CAGCGATAAT	GGGAGACCAG	240
	CCCGGCACGT	GATCAGATAC	GGTTGTAGTG	GCCATACGGG	CTTGCGGACG	AATCTACGGG	300
	GTATGGTGCC	TGACGCTGCG	CCGGCGGCGT	CTTACGCTGA	GTTCCCCACA	GCCGTTCTCT	360
	GTA CTGGTTG	ACGTCTTCGT	CGTGCAACGC	CCCTCGTTTG	CCGTAGCGGC	CCCGACTGCC	420
	CCCCGCCCTC	TGCGCCTCGA	GATCGTAAGA	CTCGTTGCTG	CTGCTCGAAA	AGCCCTTCTT	480
	GCGCTCGCTG	TAGTACTCGT	CCTTGCCGTA	GTACCGCGCG	GCCTCCGGCG	TTACTACGGG	540
40	CTGGTATACC	ACTTGTGGCG	CGGAGCATAT	ACTTGTGCAC	GCTGCTTCTC	CTCGCGCCCG	600
	CCGCTGGCGG	TGCCGTCTAT	AGCAGCAGCA	CGGCCAGCAC	AAGAGTCGCA	GATTCCNCTC	660
	ACCCCCCAT	AAACNCCGAN	TTACACCCCC	TATCCNATAC	CCAATTGACG	CTACNCATCC	720
	CNCTATACCC	CATCNTTGCA	CNCGGTACCT	ACTTTTCCCN	AANTGACCCC	CACNTNC	

1300UP

	GATCGAGGAG	TTTCCACTGG	AGGTGGCGCG	CTACATGACG	CTGCTGCGCG	AGATAGACGC	60
	CAAGTGCGTG	CACACGGTGC	CGGAGCTTAA	CGCGCAGATA	GGGCGCTTCC	TGGCTGGCTC	120
	GCGGCAGCCG	GGAAGCCCGC	AGCTGCAGAC	CATCAACCGG	CTCTTCCAGG	ACCTGATGCC	180
50	GTCGCTGGAG	GAGAAGATGC	ACGTCTCGTC	CATTGCGTTC	GAGACGCTCG	ACCGGCTCGT	240
	CGCGCGCGTC	GAGCTCGCGT	ACGAGGTCGC	GCTCAAGAAC	CAGGAGATCC	CCGACAAGCT	300
	GCGCCTGGGG	AACGACAACC	ACCTTGCCAT	GCACCTGCAC	CACGAGCTTA	TGAAGAAGAT	360
	CGAGTCCAAG	CAGCAGAGCA	AGTCGCAGCA	GGCGCTGCGC	TCCGAGTCCC	GCCGCGAGGC	420
	GATGGCGGGC	AAGAAAATGC	ACGTGGACCC	GCCGCGCGCG	CGCTGCTCT	CAAAGGCCCC	480
	CGTCCC CGNT	GGCCCCCGGG	CGCCCCCTGG	CCGCCAAGCG	CCCGCGCAAA	CTTTCCCCCC	540
55	CGCCCCCGGC	GCNAGCGCAA	GAAGCCCAGG	AACAANTACT	CCGCCCGCCC	CCNAAACAAC	600

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AATTTGGGA	AGGCCTCTTA	CTGCTACTGC	AACCATTCNC	CCTACGGGAA	AATGTCGGTT	660
GCGAANGGGA	AAAATGCCNC	TCNATGGTCC	CTCCCCTGGA	TCACTCNAAA	CCTTACCGAN	720
GGGAAATGTT	CTGCAANAAT	GCAAAAAAAC	CCTACATACA	GNCCGGTTAC	TANNTCCCCC	780
CCNCCTNCN	TGCCTTNCAA	TGGGTTCNC	NT			

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1301RP

5 GATCCGCGAG ATTCAATCGTG GACCCGCCAC AGGCAATTAC TATAACAACA TCCTGCGGTG 60
 TTAAGGACC TAACTCACGC TCAAGTATTT CAGGATGATA TCCTAGATGA AGAGCTGCGC 120
 CACACGCTGG TTCGGTTACA ATATTGCTCT CTTCCGCAA AATTAACAT GTCTGTACTA 180
 CAGCGAGCTG GTCAAGCACA ACAGATTTTG TCCTGTATTT TTGGGCGTAA CTCAGAGTAA 240
 GATCCGTCAC GAAAGATGTG CATAAAGAAG TAGCAACGCT TTTAGGATT CCGAAACGT 300
 TCCTGCCAG CAGCAAAGAT CTGTGCAAAA CCTCGCACC CTCTGTTTCC ACTGCTACAA 360
 CAGGGATAGA GTCTGCCAAA CCATGTTTCT CCAGCCCAT TACAATCCCA TTATATAACC 420
 CCCC GCCACC TACGCTGCAG ACGATACCTT TCACGCTCTC CAATTGCACG CCTTGGAGAT 480
 10 GCAGTGCTTC TACTACTTCA TCTACCATG TTGCATGCC TCCCAGATG AGTGGTTGTC 540
 GAATGGATGT GCATATATCG GAGCGACTTT TTCTAATTCA CATTCCCAT CAACTCCGGA 600
 CCGTAAGTTA TCATCGCTCT CTTTCAATAC ACTTCCCAT GANATCACAT CNGCCCCCGT 660
 TGANCGGTTT CGCTCTACCT CCNCCGCCAA TTNNTTCNGN CCTACNCGGG CAGGTNTCTT 720
 NTTNCGTGA CCCGTGGTGC TGCACCCNTG CNTGCNCCGA CTCCNAAAC NNTTGGNTGC 780
 NNGAAG

1301UP

20 GATCATCTGC GTGCGATACT GGCAAAAAAT GAGAGACAGC ATGATGAAAA TATAGTTAAT 60
 AAGATATTGC ATGATATAAG CACAGGCGGG TTTCGTGAA GAGGAAAGGG TGCATTGAT 120
 CTGGAAATGA GTGAAATGA AGACCAAGAG TTACAACAGT TTAGACAGAA AAGACGAGAA 180
 CTTTTGAAAC AAAAGATATT GGAATATGGT GATACTAGCA AGCTCGTATC TAACCCCAAG 240
 TCATACGCCT TTTTTCAGAC GATGGTGGAC GATGTTACTG AAGCATCATT TGGAAATACA 300
 TTTGATGCCA ATATAGATGA AAAACAGAT CCATCTGCTG CAGGTCCGAA AATTGTCATA 360
 TCAGAACAAT TTGTAAAGGA AACCTGTCA TTCTTGTCGA GCAAGAGTGG CGACTCAGAA 420
 ATCCCTGCAG AAACATAATC TATTTTCATCC AGCACAGTTG AACGTGAAGA AATTCAAGAC 480
 25 TTCATACATT GAAGCAAAAT AGTAACATTA ACATTTGAAA GGAGTCTAGA CTTCTGCTC 540
 AGATGGCTGA CTCAGCAGTG AGATAGAGGT GATTACNGCT TTCTTTANAT ANATTCCNCN 600
 GCCGCNAAAT TTTTATATGA ACTACTTCAC AANANTTTTA AAGTTGGCCC CAGGGGGGCN 660
 ATCTTAAGGG AATAAANATN GCGTCCAAGC CCAATACTTT TTTNGGAAAN NGTNGNGGTC 720
 CCCCNAAG GATTTAAATT CNACCAACTT NTCCNCCANN ACCCCCCCCC TTNTTTTCNG 780
 NG

1302RP

35 GATCGAAGAG CTTCTCGCTG ACTTCGAACG GCACAAGGTA CCCAAGCTCC TGTAAGAGT 60
 TATGAAACTC CGTAGCGGAA AGCGTGAACG AACCCTTAAT ATCATTTGCC ACATATATCA 120
 TGCGCCACTT CTTACCGCGC TTGTATAACG AAGTAACTC AGACAAGTTT ACGGTACCAA 180
 AGCGCGTCGC GCCAACAGG CTAATTAGCG CGTCCACCGA ACTCATGCAG AACTGCCAAT 240
 TGTCATCATT CTGTAGCAGA TGCTGTAGCT CCTCTGCTGT GAGACGCTCC ATCTTCCGGA 300
 CGTCGTGATT CATGAATAAT TTCTTTGCTG TTATAGCATC GGGGTCTTCA TTAGGAACGG 360
 TGGCGGGCTT GGCCTGGGTA TGGTTCCGGT GAGGCTGCTG AGCTGGCTGC GGCCTTGCAG 420
 40 GCAAATTATA GCTCTGTGCG CTCGGTGGTA TTGGCTTCCC GTGGCCCGGC AGGCCAGGCG 480
 GGCTGTGGA ACGCGAGGAG GATTTCCCTG AAGCTGCCCA ACGCCATGCG CAGGCAACTA 540
 CTATGTGTAC AAAAATTGCC GTGNTCCTGC AAAACCTTTG GTCTGTACAG AACCANCCCC 600
 ATGGCCCATG GAACGGNNTG GNTTTTTCGC CCAAATTAAN CCCTGGANAA NTGGGNAATT 660
 TTTGGCCATN TTTTCCNATT AAAAANGGNG GGGTNNAAGT GCNAGGNGC CCATNTNGGG 720
 GGNAAANTC CGCGCTTTT TTTTNTCAT AANGGNCCNC NTTGANNNCC GCCCCNNNN 780
 CCCAC

1302UP

50 GATCAACAAC ATACTTCTAA AGACATCAAT ATACGCCCGC ATGTCTCCGG ATGAAAAACA 60
 TGAATTGGTT GAGAGGTTGC AGTCCATTGG ATACCAGGTT GGCTTCTGCG GCGATGGTGC 120
 GAATGACTGT GGTGCCCTTA AAGCGGCCGA CATTGGTATA TCTCTATCCG AAGCGGAGGC 180
 ATCTGTGTCT GCGCCATTTA CATCCGCTT GTTTGAAATC AGCTGTGTTT TGGACGTAAT 240
 GAAAGAAGGC CGTGCCCGCT TGGTCACGTC CTTGCGCTGT TTCCAATACA TGAGCTTATA 300
 TTCTGCCACA CAGTTTGTTA CAATATTGAT CTTGTACAGC CGTGGATCTA ACTTAGGGA 360
 55 CTTCAGTTT TTGTACATCG ACCTCTTCTT GATCGTGCCG CTAGCGGTGT TCATGTCTCTG 420

5
 GTCGAAGCCC TATGAAGTAT TGGCCAAAAA GCGGCCAACG CCAATTTGGT TTCTCCGAAG 480
 ATATTGATTC CTTTGCTCGT GCACATCGTG ATTTGTTCGT GTTTCAGCTT GTCCCGTGGC 540
 TCGCAGTCCA GCATATGAAG TGGTACCGGC AGCCAGTCGT CGCGACGACG AACATGTTGC 600
 TTCCCANGAN NACNCAACCC TTCTTNGTC TCCACTTCCA TAAACCTGG TCCAATCNT 660
 GCTTCCGGTN GTCCNCCCN NCCNCNAACC NAANTTCGAA AATTTTGGT TATGGCANTT 720
 CCCCCTTCCC TGNCCCTCCC GGTGGANNAT TTCCCCCCCC CGAAACAAC TGGCNNTTT 780
 CNCTCCCGAA GTTNTCTCCAT NTC

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 GATCAGGTGG CCTTTATGGC CATACTTGTT GGACTCATAG TATATCTCGG CGACTGCACT 60
 ATTACTGGAC TGCTTGTCAA GATCTTGCGC ACCCATCACG CCGACTATAC TACATGTCTC 120
 GTTGGGCTTT GCGTCGCTAA CCGGCAGAAA AGATACTTTT ATACTTTATA ATACCAGTGA 180
 GCGCGCCATA CCACGTAATC CATCTTTGTT GCCAAATAAT TACAATATC CTTTATAGCTA 240
 CTGGAATTGG GCTTATCCTT ACAGTGTAC ATCAATTTTC TATCGTAATT CGCTATCTCC 300
 GCTCGCAATC ACTGCACTGC AAACCATTAT CGTCCTGATA GATAAAGATT ATAGGGTAGC 360
 GATCAATAGT ACCGGTAAAG GCGTGACCAA TATTCTGCTG GCGGTGTTTA GATGGCCGAG 420
 ACGCTAGAAT GTGGGAGCAT GCTGGTTTAG CGATATGGGA AGCCTTCACT AGAACCTGCG 480
 CACTAGTAGA GCACAGAACG TTGAGACTTA CAGCTGTTCG AAGTATAAGT TGTAAATTTTC 540
 CAAGGGTGGC AAGTAATATC AATTGATTCTN AAATGACTTA CCCCTACGTT GAACTGCTTA 600
 CTTTAANTTG GGTCCGGGCC ATCAAGCCCT GACACTCTTG ACTTTCCCCC ATGAAAAAAC 660
 TCCCGGGTGG GTTCNANCCC CATTNCCCAA ATACANTCCA TANGTCCTGG CCTTAACCA 720
 CTTGNTCCGG AGGATTTTTT TNCCAANAAG ANNNNACTTT TNAATTTNGC CAC

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30
 GATCTAAGTC CTCTCCCCCA AGCGGTGACG CAAGTGGACT GTCTGTGCTT CGGTAAATAA 60
 AGTTATCGAG ATGGTCCACA AGCTCATCCA CCTCGGATAT ATGTGCGCTG TGAGTAGGCG 120
 CAGAGTCACG TGCGGTGTG AACTGACAT CAGACTTTCG GGACGGGCTT CTTAGCTCAG 180
 GGTCCAAATC AATGGACACC TTTTCCAGCT CTGCCAGCGA GCGCAAGAAC TTTTGTCTA 240
 ATATATAGTC GTTAGTTTGG ACCACGCAAG AAACCGGTCG TTGCTGGCCT CCTGACGCTC 300
 TCCCGTGTAC CTCGGCTGCG CTGATGACTT TGCCAGTGGA TGGGTGAGCG CTCTTGGAGA 360
 TGACTTGATC GGGCGACTGC CACTTTGCCA ATCGAGGATC GTCTACAGTT GTAAACGGGC 420
 GCACCTTCTT TTCTGTAGGT GCTCGCGCTG CTGGTACTGG ACTCCTCCTG GACTGTCTGG 480
 GCGTTACTGG ACCTGTGCTT GCTGCTGTTA CTGGAACCGA AAAAGAAAAA TGACTTCCCC 540
 TCTTTTCATA TGACATTCCC NGTTGTGANA CNTACTATTG GCCCCNAGAA AATAANTTAG 600
 GNGAAATAC ACTCNCTATG TTTGCCATATA TTTCCNTAC CATATACAGC CTGCTGATTG 660
 CCAGTTTTAN AANTTTAAGT GCGTTACCTT ATATGTTGAA NCCCGTTATA TGAAGAATAA 720
 CCCCCAANT TTGCAANGAA CCCCNGAGGC ATTGNCTCCT TCANCANNAT TAAGNACATT 780
 TTGTCTTTTC AAGNACTTTA TAAGNCC

40 1304RP

45
 GATCAATGAG CGTGGCTACT ACTGATGCTT ACTGCAGTGC TGTGTCAATA TTACATATCG 60
 GTGGATAGCT AGATAAAAAAT GCTATACATA TATCTGTGCG CATTGTGCCA ATCTATATCT 120
 ATTTGTGCCG ACGTTGCGGA CCAGTAGGAG GTTGTGTTCC GCGCGGTGCG CAAATTCCGC 180
 TGAGATCAAG CCATTGCTG TGCTCTTGCC CTCCCCTAGA TGGTAGGTGC CACTTGTAAT 240
 AAAACCGACG AGATCTTGTA CGCGCGGCAG AGGCTGATCG GCGTCAATGG TCCGTTTGCC 300
 CGCAGCATTG TATTTCTTGG AAGCGACTGC CTGCCAATGG GCGAGATGCT TGACAGGCAC 360
 TGCATACAAG CGGGCATGTT CCTGAAATG GCCGCGTTCC AGGGCTGTAC AGACAACGGC 420
 GATCACGGGA AGTTGGGTGG TCACAACAGC CAGTTGGACG GGCAAGCCTG TGTCCATAGG 480
 AGGTTTGGGA AAAAGAGACA ACTGGCTTAT TGTNAAGGTC CCGGGGANCT NCNAAAANAA 540
 TCTTGGTGGC AATACCAACN CCTAAGGATT TCANCGNGTT CCCCAACTTN ATTNNTTTN 600
 TNGCNCCCGT TTCAAAATCA TATNGGTGGG TTGCNGGCGN GAATNTTCTT TTCNATTTCA 660
 AACCAACGNG GGGGNGCCNT TTGAGATTTG GANACNCCC TCNAAANANA NTTGTCCCCT 720
 TTCNCCNNAA AACAAAATTN NGGAGGAAGA GGTTTTANCC CNNTATATNC CCCCNCN

1305RP

	GATCAATGTA	TCCATTATAC	CCAGCTTTTCG	CAGCGACATA	ATATATTGAC	TTGATTTTAA	60
	AGCGGTAGAA	CTTTACGGGG	CTAGGGCCGC	TAGGTATCCA	AGGTTTAGCA	TCAGGATGCA	120
5	CGTCTGCAAA	GCACTTCTGC	AAGGCTGGAA	TGGGCTGGAG	TACTTCGAGC	TCACCCGCGA	180
	AGTTTGACAG	AGGTGCTTTC	ATGGGGTCTT	CAATCGATAT	AGACGCAACT	GAGAAAAGACA	240
	CGTTGTATTT	GTTTTTAGCG	TTTACTTGTT	GTAGTGTCTG	GTCGACCATC	AAAAAATGG	300
	GCTGGCCGTC	ATGCTCTACT	CCCTCACATC	TGTCGGGAGA	AATATAGTAC	ATTCATAATAC	360
	CATATGGAGT	ACCGTTTTGA	TTGATTGTTG	TCAACTGGAA	AGAACTTTTCG	TCTTTAATTA	420
	ATTTCTGAG	TTGCACTGCT	GCTTGTGTTT	CCTCCTGCGA	CGCTTGCGCG	AAAGCCGAAG	480
10	TAAGTAGTGC	CAAAAAACAT	GTAACATAATG	AAAAAATCGA	CTTCATTGTT	GCTATTGAGT	540
	GCCAATAGGC	GAGACTCATC	CATATGTNAT	GAAAGCGTTT	ATANATCNTT	GTINTGGCTT	600
	GAAAGAAATTA	TTATACTTTT	CCNGGCGGTT	ACATTATCTT	CCAACCAAAT	TGTTTCCTTT	660
	TNGANAGGNA	ATCCCCAAAA	TTTTTNAAT	TAATTNGTCN	NCGCANCGGT	TTTTTCCCCG	720
	GNGGGGAAAA	NAAAGCNGGN	NACCCGCCAA	ANCCGAATAA	AGGATTTCCTA	TNAAAACCCA	780
	ATTNTCCNAA	AC					

1305UP

	GATCCCCAAG	AAGAACATCA	AGATCCACGG	GTTCTAGGCG	CTATGTACTT	TGTGTAAGTC	60
	AATACATATC	CTCCTCCTCC	TCCACCACCA	CCACCTCCTC	CTCCACGTCC	CTCTGCGCCT	120
20	CCGCATAGTA	CCTCACACAG	TACGGGAACA	GCTCCTCGCT	GAACAGCCTG	GCCAGCTCGT	180
	CCGCGTTGGC	AAACTCCTCG	CCCGGCCGCT	CGCCTGTCCA	CCGGAACCCAC	GCAAAGAACC	240
	TCCCGTCGTA	GCGCTTCGGC	CACTCCATCT	CCACCGCCGC	GCTCCGCACT	TCCCCGTCTT	300
	CCCCCACCCT	GAAGTCTTTC	CTCAGCTCTT	GCGCCCCGAG	CTTGCCCTCC	ACCTCCCCGA	360
	ACTCCACCCT	GATCGCAAAAG	TCCCACGCCC	CGGCCCCCGC	CCACTCCACC	TCCACCCGCC	420
	GGATCGCCTC	CAGTCCCGCC	CAGTCCCGCC	CCCGCACGTA	GTTCCGCGAA	ATCCCCGTGC	480
25	TGCGTCAGCA	CGAATCCCCC	AGAAACCCGC	GATCCCCTCG	ATCGCCTTGC	TGCGCCGCGC	540
	GTATACCGGC	CCCAGCGCCG	CTGCCGCTCC	ACCTCCAGCG	CCCGGTCTCT	CCGCTCCCCG	600
	NCCGCTNGGA	NTCCGGAAGN	GCTCCACGNG	CGGGCCTGCN	CCCGTTAGTC	CCCTGCCCGC	660
	CATTTAGGNG	GGGNNCGGCC	TTNNTTGTTT	NNNGAAGGNA	GNGTCCCNGT	TCCNNGGCGC	720
	GNTNNGTTT	TGGGNNGGAG	NACGGNGTTT	TTGGANCNCC	CANTCNCGGA	NTCCTGGNGC	780
30	GAANGGNNGT	TNCCNCCNNN	TTGAGCCCCC	CT			

1306RP

	GATCTGATAT	TGGGTAATTG	CAACCTTTGC	ACCGCTTTGA	AAAGTACTTT	AGGAAGTGGT	60
	ATTTGCAATA	TAGTTTCATCA	TTGTAGTGGA	AGCACGAGGA	TACCTTACAC	TTGGTACCGC	120
35	AAACCGTGCA	GCAGAAGTGT	TCCTCGTCAAT	ATAGCTTACC	AAATGTATTG	TAATACACGC	180
	CGCTCAGTGG	CTTATTGCAC	ACATAACACA	ATAGCTTGTT	CCGCGTGAAA	TAATCCTGCT	240
	GGCATAGCAG	TACCACTTCA	GACGTATGCG	GGAGCTCATA	AGGGAAGAAC	TTCGGGCGAC	300
	ACAAAGCTCC	ACAATCGTGA	CAAACCAGAC	AGTTTTCATG	GTAGTAATCA	CCAAGCGCCT	360
	TCAGGGAGTT	CTGCGTGATA	ACCCCTTTGC	ATTGTTTACA	GATTTTGGCC	GTTTTTTGAG	420
40	ATGAGGTGGC	GGTTTATGCT	CCGCAGACGT	TCGCATTACT	TGCTCCGACG	CACTGTGTCT	480
	ATGGTTGATA	TGGTCACTAT	ACGTCCAGCA	ATAGCTGTGC	TTCTGTATAT	TAGTCATGAA	540
	AAACAGTAGC	ACTCCCTATC	TTACCCCTGC	NGATCGTATT	GGTACCGCCA	AATNGTTAAC	600
	CCATTTTCCA	AGAACATTCT	ACCNCTTCCG	TTTTTGCCCC	AAGAGAGGTN	TGCTATATTT	660
	GCCAAACAAA	GCCCAACTGA	AATTNAANAA	ACCCTTTTTT	CCCCCTTTTN	TTCTCCCCGA	720
	GGAACCTTTT	CGGCAANTTT	CNCCCTAAAT	TGTNTGGGGG	NTGANANCCN	AGAAAANC	

1306UP

	GATCATTTCA	GTGGATGGCG	ACATTTCATAT	GGATATCAGT	TCGACTTTTG	TTTCCAGTCT	60
	TATTCCACTG	ATTTTCAGGT	TACAAGAATT	GGGAAGGGGT	CTCCATTTTG	TAGGGACGAA	120
50	CAATTGTAAG	ATGTCACAGG	AATTCAGAGC	TCAGGTTGAA	ACGAAAACCTA	TTATCTTATC	180
	CCTTCCGTGA	GGGGACGATA	CCCTACAGAT	GATTATCCAA	CCCATCTCTT	ACGAACTGTC	240
	ACTACATACA	GTTTTCACTG	ATTTTATTTT	CATATCTAAG	GTACAAAGCT	CGGAACTAG	300
	GGATATCGCA	ATTATTGGGG	AAATTAATAAT	TGGATATCAA	ACAGCCAATT	TTCAAGTGAA	360
	ATCGTACAAC	TTGAAATTGT	CGGAGACGCT	GCTAACATCA	AAGCTACGGG	GGAGTTGTTT	420
55	TCGAGCCGTT	GAACTTTATT	GTTCTGATAG	TGACATCAAG	TTGCTTTTTG	ACGAATGTCC	480

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5	CCCCCCCCGA	AATGAATACC	CGCNATNTNC	ATTCTTNAAC	CGAATTCCCA	AAACCCNTTN	540
	TNAANTAATC	CCTTTAAAAA	TTNATTTTTT	CCNAAGNTTT	ACNCCCGCNA	ATTTTTTTTCC	600
	CAAATGGGCC	CCTTANATGA	AAAAANACTN	CACCCCCCCN	NCGAAAANAA	ATTTCTNCTTT	660
	GGAAANTNNN	AAACGAATTA	TTCTNCNCCCT	TTNTCCCCCC	CCCGAAANAC	ANTNTTTCCT	720
	CCCCCCCCTT	AGGAAAANTG	TTTTCCCCNA	TTTNANANTN	TCCNCCCNCC	CCCNNAACNA	780
	AAATNTTAAA	NCACCCCNNTN	TTNTNG				

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1307RP

	GATCCCTTTA	TCTCATATTA	TAGTCCATAG	TACCCCGTGG	ATGCCCTACCA	CACAGAGGTC	60
	CCTCTTCTGG	ACCTGAGACC	TAGATATCTT	GCGATATCAT	TGAAAATATC	GTTCAATTGC	120
5	TCCTCCGTGA	GCCCGTTAAC	TTCCGCCTCG	ATATCAGCAT	CGGGTGTTTC	CGAGATGTGG	180
	AAGTTCTCAA	CTTTGCCCTC	CAAAAACTCC	TCAAACCTCT	CTTGTTCTCT	CAGTGTCCGT	240
	GGCAACAAC	CATAAAATTT	CGCAAGCTTA	TACAGCTTCA	CATTGTCTAG	ACTTTTGAAG	300
	TCGCCCAACG	TGAGAGGGAA	TACGCCGTCC	TTACAGTCCG	GAATCTCACC	GTCCGCGTTC	360
	GGCAATGGAG	CCAAGAAGTC	CTTCTCCTCC	GACTTCGTCC	AATTCACTAA	GCGCCGCACC	420
	GACCGCTCTT	CCATCGTGTG	AAGCTGGCCC	TGAAGCTCCC	CCACTAGCTG	CACTAAGTCC	480
10	TCATTCTGTG	CGAAATCCGT	TGTATCAAAC	TTGCCGGCGC	CCCCTTTAGG	AAGGAACTTT	540
	TCGTCTAAGT	TTGCCATGTC	ATGCTTTTGC	TTGCTGACCT	GTAGCTCCAG	CACCGACTGT	600
	CCTGTCTTGG	TGATTAGGAC	GCTCTGCCGT	TTAACTAGCG	CCTGTAGCTC	CTCAACTGTT	660
	TCTTCAATGC	CTCGTCTGAC	ATAACGCACT	TCAAATTTAG	TAGAACGCTT	CTGAATATTC	720
	CTACACCAA	CGCCGCAGAG	AGAATGGTAA	AGA			

1307UP

	GATCCACCAA	AGGGTATTTT	ACTATATGGG	CCTCCGGGGA	CAGGTAAGAC	ACTTTGTGCC	60
	CGTGCCGTGG	CCAACAGGAC	CGATGCTACA	TTTATCAGAG	TCATTGGCTC	CGAATTAGTA	120
20	CAGAAGTACG	TCGGTGAAGG	TGCTAGAATG	GTTAGAGAGT	TGTTTGAAAT	GGCCAGAACA	180
	AAAAAGGCAT	GTATTATTTT	CTTCGACGAA	GTGGACGCAA	TTGGCGGTGC	TCGTTTTGAC	240
	GATGGAGCGG	GTGGTGACAA	TGAGGTCCAA	AGAACTATGT	TGGAACCTAT	TACGCAACTA	300
	GACGGATTCTG	ATCCACGTGG	TAATATCAAG	GTGATGTTTG	CTACCAATAG	GCCGAACACC	360
	TTAGACCCAG	CATTGTTGAG	ACCCGGTAGA	ATAGACCGTA	AGGTTAGAAAT	TCTCTCTTCC	420
	GGATTGGGAA	GGCCGTGCCA	ATATTTTCCC	GCATTACACAC	AAAGTCCATG	AGTGTGAGGC	480
25	TGTTGATTAG	ATGGAATTGA	TTCCCAGTTG	GTGTCCAAC	CCACCGGCGC	TGACTANATC	540
	TNGTTTGGCC	CGAGGCTGGC	ATTTTGTCAA	TCCAATTCCC	GACCCAGGTT	ACCTACAGAA	600
	ANGACTTCCT	TAAACCNGTG	GATAGGTCTT	CCACGGCTAT	AAAAATTAC	NCCCCTTCCC	660
	CGTTTTNTGC	AAACCCNAAN	CNNTCNCCCC	CCTTGNGGCG	TTTTTTTAAA	GGNTTATTTA	720
	TCCCAAANNG	TNTTCTTTTT	ACNATACTAN	TGTTCCAATT	TCTATNAAAT	NTTNTCCCCC	780
	CCGTGAAANNC	CTNCCCCGTT	NGCACCCCTA	T			

1308RP

	GATCTGTCTG	CTGGTACACC	GATGAACGAA	ATAATTGTGA	CCGTCACGGA	CTTCGAGAAT	60
	GCACCTCGGA	AGATAAAGCC	TTCCGTCAGC	GATAAAGATA	GAATGAAATA	CAATAAGCTA	120
35	AACAAAAA	TGGGCTGGAA	TGACGAAGCA	GGCGTGCAAG	TCGAAGAAGA	AGCATAGAGC	180
	AGCAAAGTTAA	ATAGGCACAG	CTATGTACAA	ATAACCAATT	TCAACTTGTT	CAAAGTCGTC	240
	CGCGTCTTAC	AGATTTTACA	CATGGAGACG	GCGGAATTTA	CTTGTTATAA	TGCCCTCTCC	300
	TGCGAACGTT	TTTTCGAATC	TTCCAGACAT	ATTCCGTATT	TCTTCTTTT	CGAGAAAGAA	360
	ACATATGGTA	TTTCTCTATT	CCTGTAACCT	GAGCTTAGCA	ATTTCTGTGG	ATATAGTTCC	420
	GCAAAGAGGT	AGATCCGTGG	CACCTCTGAC	AAGAACGAAG	TTATTCTTCA	GAGAAATGAAC	480
40	ACGGCCGGAT	ACATGCCCAG	AATGTATATG	TTCATAACT	TGCGCTCCAA	CATCAATGGA	540
	ATGGATAAGA	GCCAGCGTAA	CAAGTCCCAT	ACTAGTATAG	TCCAGCGGAA	TGCTTCAACA	600
	TTGGAATACC	CGCACATGTC	ATATCCGGAG	CTCTTTGATT	GATATAACAA	CCCCCNCCCT	660
	NTTNTGCCNC	AAAATTCCCC	CTGATGGTAC	CCCTAANGGT	TCTTGCAAAA	GCGGAACCCT	720
	ATCCCCCTGGG	AGCCNAAACC	CTTTACGAGN	AACNNATTAT	GGCCCGGTNT	TTNACGTCCC	780
	TNNCCTGTCTN	N					

1308UP

	GATCACGTGG	GCCGTAAGTC	GCAGAGAAAC	TTGCAACTGA	ACTGCCACTG	GGGCTCATGC	60
	ACCACCAAGA	CGGTAAAGCG	CGACCATATC	ACCTCCCACC	TGCGTGTGCA	TGTTCCCCTG	120
50	AAACCTTCA	GCTGCTCCAC	ATGCAGCCGT	AAGTTTAAAC	GCCCCGAAGA	CTTGAAGAAA	180
	CACCTGAAAG	TGCACATGGA	GGACACCATG	AAAGAGCGTT	CGCGTGCGGC	GCCGGGCTCG	240
	CGTGGTGTTT	GCAAGACAGG	CGTTAACAAG	GGCTCTGCGC	TACAAGAGAA	GGCGGCTACG	300
	TTACCCAACC	TGACTGTGGA	GAGCTTTGTC	AGCCAGGAGA	TGCAAAATTA	CTACCCCTAC	360
	TACAAAAGCA	GACAGCACCT	AGACGAAACA	CTGTGCGACA	TTATTCTCCC	GCCCCCAGC	420
55	CGCTCTAGGT	TGGTACTTTG	GCGTCCGAAC	CGCCAAGCTA	CACACGGAAA	GCAGTGTCTT	480

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5	CTTCACGACG	CTGTGCGCAGG	ACATGTCTCG	TCGCTTGCCT	TCTCTTGCTC	CTTGCAACAG	540
	CCCCCGGCCT	GCGGTTAAGA	TGGTAATGCT	TCCCCCGCCC	CAGAACAGCA	ATATGCACGC	600
	CGTGCCCTAG	ATATCCCAGC	GATGCCCCGA	CTCCCTCCCT	TTGGTGA CTC	TCCNGGANCG	660
	AATCCCANCC	TTTGCCCGAG	ANACACTTCC	GACCCNCTCC	ATATCCCTGC	TCTANCTGCC	720
	CNCCTCACCG	CTTCTCATA	AAATCGCATT	GTTGCCCGCAN	CCTATCCTCA	TCAAGCCCCC	780
	TGATANACCC	TGNAAAAAGAC	TGANTCCCCC	CCAAACC			

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1309RP

	GATCAATTAT	TAGAGGCAAT	ATCAAAGAAG	TCCCATATTA	CTGAGGAGAA	CAGGGAACAG	60
	CCTGGAGAAA	GAATGCCGCA	GACGTACAGA	TACACGCTGG	AAAATCAGCT	TGCCCAGTGA	120
5	GTGCTCGAAC	AGCCGATAAG	AGTATTGACA	GTGGTAGCGT	GCAAGAGTCA	ACGACAAAAT	180
	GAACAGAACA	TCATACTTCG	GGCGCGAGAT	GTTGAAGCTC	GACTTGGTCC	GCCCCGTGGAC	240
	CTTTTTTTGAA	GAAGTTGCGC	CAGGATCCCA	CGGCGGCCCT	GCGCGACGCA	GCAGGGACTG	300
	GTCTCCAGCG	CGCCAGCAGC	AGGGAGCTTG	TCACCACGCT	CACAGAGCTC	ATCGCCATAC	360
	CCGCGGCGGC	AGCCATGGGC	GGCAATTGTA	TGCCCCACGG	AATGAGGACG	CCCATGCTGA	420
10	CTTGGGAGCC	ATGAGAGAAT	TGTACAGGAC	TGCCCCAGAA	ATGTTTCACT	TGACGCGGTT	480
	AACGTGGCGC	GCGCGAGATT	CGATGGCATA	CAGAAATGCG	TTTAGCGGCG	GCGCCCCGAG	540
	AATGTCCCAA	ACCACGATT	CCGCGCGTTC	CGCACGAAGT	CACTGTTGCC	GGACAGCGAA	600
	ATACCGAGTT	CNCTTTTACA	ATTGCCACAA	TTTCTTTTGAN	GCCGTCTCCC	GATAAGGCAC	660
	ATATNGTTN	TTTTTGCCGC	ACTGCCGCAA	NGTNCCACTT	GCCCCCTGG	TACTTTCCCT	720
	GAACATTTTG	ACGGATNCCC	AANCGTGCAA	ACTCTCCNC	CCCGTGTNN	CCCATACCAT	780
15	CCANTTTTTC	GCCNC					

1309UP

	GATCAGGACC	GCGGTCNCTG	ATTCGATTGG	CCATGAGTTT	AAGTATGACC	CAGAGGGCCG	60
	CCCTGGTGTA	TCTAATCTGA	TAAACATCGT	AGCTGGCATC	CAGAAGAAGA	CTATCGCGGC	120
20	GGTGGAGGCA	GATATTGCTG	GATTTAAGGA	CCACGCAACT	TTTAAAAACT	ATGTTACAGA	180
	CATCCTAGTA	GCTGAGCTGA	GGGGGCCAG	AGAGGAGTTT	GCCCCGTATA	TGAATGATAA	240
	ATCATAcata	TACGAGGTTG	AGCGCAATGG	GGCTGAGCGA	GCAGGTGCCA	TAGCTGCTAA	300
	AACCCCTGGCA	GAAGTCAGAG	CGATAATGGG	TTATTAGTTA	TATTTCAGATT	CCAACCTTGT	360
	CTATAGACTA	GCAATAATTA	TAAAGATACA	TCAAGAAGAC	CAAGAGCAGA	TGCGTAACTG	420
25	GTTGTCACTC	TTTGGACCTG	CCGGATATCA	GCACATGCAA	CCAATATCTG	CTTCAGCAGT	480
	CCTCCCGCTT	CTCGTTAGCT	ATTGTGCCAC	CTTGATTCTT	CCATCCGTTA	TACAGCCAGC	540
	TCAGCACATC	ATCCATCTAT	TTATTTTPTA	GGNTACCACC	ATCTNTTTTC	CNATGAAAN	600
	ATTTGGTAAT	CATTGTCCCN	TTATTTTPTA	GGNTACCACC	ATCTNTTTTC	CNATGAAAN	660
	CGTGACAATC	CNCCNGTTTT	TCNACCCTCC	CTCCATNAAA	TNTCTTTCAT	CGTGGGTTTC	720
	GGATCAANCC	CTNNGGNTCN	TCCCCTNCGC	CTCCATCCNG	GNATTTACAC	CCNTTNTTTT	780
30	CTCCCCCCTC	ATNAANC					

1310UP

	GATCCAAAAA	AATTTTAATA	CTGAAAAAGA	AATGCCACAA	CTAAGCTCAG	CTACCTTAAA	60
	GAATCGGGAC	CAAAGCTGTA	AGGCAACAGC	TCCTCCAATG	TTGCTGCAG	AACCTTGGAC	120
35	CCGTGCGCGT	TCATCATAAT	CACCGTGAGC	TTCTTCGGAT	CAACGAACTC	GCGCAGGACC	180
	TGCCGGCAAA	TCCCACACGG	GGTCACGAGC	TCGGACGAGT	CCCCACTCAA	TGCGATGCAG	240
	ACCCAATTTC	TATGCCCCGC	TGTTACCGCC	TTTACGACCG	CTGTGCGTTC	CGCGCAAATA	300
	CCGGCTGGGT	AATGCGCATT	CTCGACGTTA	GCGCCGACAA	TATACTCGCC	TGACGCTGTC	360
	AAGATGCAGC	AGCCACGCG	GAACCTGGAG	TTATGGGCTG	TACGAGAGCT	CCTTCGCGGC	420
40	TAGTGCTCGA	GCAACC GCGC	CCTGATATGG	CTCTCCCTGT	GTGCTTGGCA	TTGGCTTCCG	480
	TGGCGTCGCC	TCCTAGGTAT	TGGGGTTCCC	CTAAGTACTG	GCTGCGAACC	CTTATGTTTT	540
	TTGCAGGGGA	ACGAATTGCG	CCCGAACC GG	GTGAATCCCG	GGAACATNCA	ANTACCCNCT	600
	TTTGGNTNNC	GGGNAAAGGG	NNANNTTCCN	NNCTINGCNC	CGGCNGGAAN	AAANAATGTT	660
	AACCATGTGG	ANTAAACCTT	TAANATGANN	CCTATGGCCN	GTTTAACTTT	ATCCCCCNC	720
	CCCCCCTTTT	AAANGTNNNA	NCCCCGCNT	TNTACCTCTA	NNCCNGCGGG	GGNGCANNAN	780
45	CCACAAATNN	TNTGTTGNGC	GCNGNGCGTN	NCTAATATGG	AGCCTNGGGN		

1311RP

	GATCTTATCG	TTCAGCGTAC	CGTCTGCAAG	AATCTGAGAC	ATAAACTTGC	GCTGCGACGA	60
	GTTCTTGGTA	AATTCCTTCGT	AGTACTGTGC	GTGTGCGCT	TCCAACGCTT	CCTTCCCCCG	120
50	CTTGACAGC	AGCTCCACCT	TTTCCGTGGA	GAGCGGCTCT	TGCTCGCGAG	AAGCCTCCCG	180
	GTCTAGCGGC	ACCTCGTGCC	AGGGCATGTC	CGCAGGCACC	AGAAGGTTGC	CGCTGCGAAC	240
	CGAGCGCAGG	TCATCGACCA	TGCCGCGCGC	AGGTTCTCTC	CCGGCGGACT	CGGCATCGAA	300
	CCCCGCATCG	GACTCGCCCC	CCTCTCCGCG	GGACTCGGCG	GCACTCGCTGT	CCTCTCTCGG	360
55	TTGCTCTTCG	GCTTGCTCCT	CGGCTTGCTC	CTCGGCTTGC	TCCTCTGCTT	GCTCTCTCGG	420

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5	TTGCTCCTCC	AGCGAATCCT	CCGGCTCGCT	GCTCTCTGCT	GCTGCCGCTG	CCGCTGCTGC	480
	CGCCGGCAGC	CCATGTTGCG	AGCAGCCCGC	TGACGTCGTT	CTGCAGCCCG	GCATCGCCGT	540
	CTCCTTCGTC	GCCGCTGAAT	GCCTGTTGCG	TGAGCTCGTC	TGCGTTCGCT	CAGCCCTTCC	600
	ACAGCGCCAA	GTGTTCTTT	CTNAACCCCC	CANNGCCAAT	NGTTCNCGG	CNTCATCCCC	660
	CNTTNTTCC	CTGGTTTCCC	CTTTGGTNGN	CCCCNGGNAN	ACTTTTTCCT	TGGCTTNCNN	720
	CAATTCCTTT	TTCATTGGT	TTTCCCCCA	AAATTTTNAN	ANNGGGTTAN	CTMNTCANNN	780
	NGGCNGNNNA	GAGAAACCT					

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1311UP

	GATCTTCTGA	TGCATATTTT	CGCTCTCACC	TTGCGCGTTA	AGTTTTTTCCA	TGTAGATAGC	60
	TCAAAGTCAT	CATCCCCGTC	ATCTTTTTTCA	GTGTATAGAT	TCTGTGATAC	TTCTCCTTCT	120
5	TCCTCTTCCT	CTTCTTCCTC	TTCTTCCTCG	TCTATATGAT	CTTCGCCTGT	CAGTTCATTG	180
	TCTATTCCAT	AATTGGGTTT	AACTTTTCGGC	TTGGGCTCCT	TTTGCTGGCT	ATGATCTTCC	240
	TGGATACGTT	TCTGTCCATC	TGCCAATCCC	GTTTTCTCAT	CAGTAGCTTG	CGAACCGGGC	300
	ACAGTATGGA	TTTGTTTTGA	GCTAATTGCA	TTACTACCGT	CACGATCTTC	AAGAGGTCCT	360
	TTGCCAGCAT	GACTTTCGGA	AGATTTCGAG	CGTTTACCTG	CAGGCGCACT	CTTACCCCGT	420
	TTATCTGCAG	GAATGTAGTC	CTCATCGTCT	TCATCTTCCT	GTATCGTCTG	TATGCCTCTC	480
10	CTCACCAGTC	CGCCCTTACG	CTGTCCCTAC	ACTCTTCATC	ATCCTCCTCC	TCATATCTAC	540
	CTCTTTTCCA	GTCTTCTCCA	CTCATACTAT	CTCTACCACA	TATCAGGATA	ACGTATAATG	600
	TGTGTACTTT	TTTGGATAGC	ATCNCTGGCC	CTAGGAANGC	TNGGGTTCGG	AATATAATTT	660
	AACATCTTCC	CAATCACAAA	TINCTCAGTA	ACNGTGGTAA	ATTNAAACGN	AANTTTTTTAA	720
	CTTTCATAC	GGTTTANGNC	CCATGGCTCT	TGAAANCGGA	AAAATCCGGG	GCCCCCTTN	780
	GAACCTTGTTT						

1312RP

	GATCATTCTC	ACCAGTACAA	ATGTATATTT	ATATGTAATT	GTCTCTCTCT	GCTTTTGCCA	60
	TATTTTTTTA	TTTTTTGTGG	TGACAGCGTG	CACTGACGCT	GACGCGCAAG	CCGCAGGCGC	120
20	GATTCTTCGC	AACTTTTCGT	CAACGCGCGA	CAGACAGTCA	GAAAGTAATA	GGAAACAATT	180
	AAATACGTTG	TTATGTTATA	TGAAGTTATA	CATAAGTGGC	TGCCATCAGG	TTATATATTG	240
	CTTTAAATAA	CCCATTTCGT	TGGAAACCTC	CTCTGTGAAT	GCCTCGCTCA	AACCGGGATG	300
	GTTCTGTTTC	ATCTCGGGCA	AATATTACTG	ATAATTGATC	TACAGCGTCT	TTTGTCTCTT	360
	GAGTCCGTGC	TCTATCACGG	ACGCGTTCGT	ACTGTAGCGG	ATAACATGTT	TAAAGAAGTT	420
	TAGTTCCCTC	TGTGAAGGAG	CAGCAGCTTT	GAGTGCCTTT	TCATCATAAT	ATTGTTCAAG	480
25	GTAGGAGAGG	AGGTAATGTT	TGTCTCTGGG	TTCTTTGAAG	GGCTGGATAA	TAATGACTTG	540
	ATTGTGACTC	CTGGTGATGG	TACATTTAAC	ATGCCAATCC	CAGTTCCTCA	GTTAGATTCT	600
	TACCGGTTTT	GTTATACCTT	GTTTINATAAG	GGTTACTTTG	CNCCCNACT	TGCCAAGAAA	660
	TCATCTTATC	CCTTTGANAG	GTCACCTGTC	CCTTAATTGT	AAACCTACNC	CCTTTACAAT	720
	CTATGCTTAT	ACCCNGCCAT	TGTCCCTGAA	GGATTTTNTT	ATTAACCCCTG	CNCACATCCC	780
	TTGGCTGG						

1312UP

	GATCAGGCAA	AGGATTTCTA	CTCGTATGTT	GGCAAGAACC	TGTCACAGAA	ATCCGACAGC	60
	AAGTTGCTTC	CTCGGAGGAT	TCAATTTGAA	CTTCAGAGGT	TTGACTATTT	TCACTCTCTA	120
35	CTCCAGTATG	TTGTAGGATG	TAACGCTCGT	GATTTTGCTG	TGTCACCTGC	GAGGTTTCAA	180
	TCTTCGATCG	ACCCTAATAA	TAAAAATACA	AACATGCACC	TCGTGAAGAA	GTATCGTTCC	240
	CATTTCTTAC	CATTTAACAA	GATAAAGAGC	CAACAGCGCA	TAAGGCTTTC	TAAAGTGTC	300
	AACATATTCTG	ACTTGAATGA	CTTCTACCAA	CTTGCATCAG	CTACCTCAGA	ACCAAATAAG	360
	CCCCTCAAAG	AAGGACTCTT	ATGGTCTTAC	AGGAATAATG	GATGGCATAA	ACAGTGGGTG	420
	GTAATAACAAG	GATCACAGCT	CTCAGAATAT	TCCGATTGGA	AGACGAAAGC	TAAGGTGCTC	480
40	AGCCGACCGG	CCATTAATTT	GACGTTTGTT	TGTGTTAAAC	GTTCCGAGAA	AAAGCCTAAC	540
	GGATTTGATA	TCATAACTAC	CGACGGCGAG	GCTCGTTCTT	TCCAAGCAGA	GTCAGAGGAT	600
	GAAATGAAGC	AGTGGCTGTA	TGCGCTTCAC	TCTGCTGTCTG	GGATAATAGC	CATTGAGGAG	660
	ACAGATGAGA	ACAAAGATCC	ATTGTCTATT	GTCCGTAATG	CGGATCCGTC	AAATAGTGCA	720
	TGCTGTGACT	GTCGGAGCGA	TAAGCAAGTG	AATGGATATC	TCTGAATAT		

1313RP

	GATCGTGTCT	TGCTGACTTG	CATGTCTAGC	TCAGTTCTTT	ATTACCCGCC	TCATGTTGAA	60
	ATTTTCCAGG	AACCATCGCA	CCAAATGTAT	CGATGATATA	GATTACATCT	ACCCTTCGCG	120
	AAGCCTGGAA	GGAAGCTAGA	CCTCTAATCT	AGTAGCTTGC	CATGTACATC	CCGCCATCCG	180
50	ACCCGCGAAG	ACCAGCCAAG	GTGACGGCCG	GCCAGCTCTG	CGAGCTGTGC	CACGCGCGCA	240
	AGGCGCTGGT	AAAGCGCCCC	AAGAACCCTG	AGAAAGTCTG	TAAACTGTGC	TTCTTCCATG	300
	TATTGGAAC	CGAAATCCAC	AATACCATTA	TGGAGAACAA	GCTATTCCAG	CGCGGGGAGC	360
	GGGTGGCAGT	TGCGCGCTCC	GGTGGGAAAG	ACTCCACGGT	GCTTGCCTAC	ATATTGAAGC	420
	TGCTCAACGA	AAGACACGAC	TATGGTCTCG	AGATTGTGCT	TCCTGAGCAT	CGACGAAGGG	480

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5	CATTGTGGCT	ACCGAGACGA	TTCCGCTAGC	TACTGTGAAG	CGCAACCCAG	AGCAATACGG	540
	TTTGCCCCCTG	AGATTGTGTT	CCTACAGGAC	CTCTACGAAC	TGGACGAATG	ACGAATAGTG	600
	CCTGCGCCCN	GGAATGCNCA	ACACTGCNCC	TTACTGCGGG	TTTTTTCGAC	CCAGCGCCTG	660
	ATTCCGGGGG	GGNAATGCTT	GAATCCACCN	NTTTGTTAAN	GGCCATACCC	GAAAAAATGC	720
	CNAAAGNGCC	CANAAATCCT	GGCCGGGAAA	TTTGGCNAAT	CNAAATAACN	CTTTTCCCCA	780
	AANAGGTCCC	GNTAANNNTT					

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1313UP

	GATCAAAAAA	GATACGGATG	TTATGCTTGT	TAAAAATATTA	TATGCTATAG	TACAACGTAT	60
	CGCGTCAAAAC	ATAACGCATG	AGGACTATAT	TTTTAATTCA	CTAACTTCGG	CGAAGCATCT	120
5	CCGGAAGAAA	TAGCCTCCTG	TATGGGGCTA	AGTCCATAGG	CGTCGGTTCCG	GCTCATCTCT	180
	GGAGACTTTA	AAGAATTAAG	TCCGAAGGCT	AGGCTCCCAT	ACCCCAAAGG	CGAGTGGGCA	240
	CTTTGTTTGA	GAGATCCTTC	TGACATAGCC	TTTCTTAGTG	ACAGTGGCGG	AACATGGGCG	300
	CGGGAAGGAA	TACTTTGTCC	GTGCAATGAA	CCCTCGGATA	AAGGCCTACT	TAGCCCGTTT	360
	TTGAAAAATG	TGACAGTCTT	GTTCTTGATA	TCTAGCTTGT	ACCTCGTTGG	AGTGGGTTC	420
	TTTGCAAGAC	CAGTGGGTTT	TTCCGAAAAG	CTTCGCGTCT	TCCCGGAATG	AATTCTGAGT	480
10	CCTGGTAGGG	AACATCCGAG	ACTTCCCAAA	AACCNTTTCN	CTNTCCATTT	TCNAAAAAAT	540
	GGAAATCNNC	CCGGCCATTA	TNGATCTCTT	CCCAAATTAC	NNCNCNCCC	TCACCTTTGNG	600
	ACTTGGGNAT	ANAGANCCCC	NTCNNACCCC	TCCAAANAAA	AAAAATTCTC	NTNGTGCCCC	660
	NTNATTTCCC	CCCGGGGCCN	NNTTTTAATT	CNGGGGAATT	AAATTTTGTA	TCCNNGCNGG	720
	TNGAAGCANG	TTATNGCCCC	CCCTTGACCC	ATNTTTNACT	TNTTAATTTT	TCCCNNNNCG	780
	GNTGGAAACT	TTGCCNAAAG	GCANGCTTTT	TGAACCACT			

1314RP

	GATCCATAAA	CTATCTTCTC	ACTCGCCGGA	TGCAAAGTAT	CAAGGAATAG	GCGACAATCG	60
	GTAATGATTG	GCTCGAGCTC	ACGCAGATAT	TGGCGCACTT	CTGATATCCG	TGGGTGTGTC	120
20	GATGCATGAT	GCACATGAAT	AAAAGGAAGA	AGCTTCGAAA	GAGGTACACG	GCCCGGGTAG	180
	CGTGTGATGA	GAGCTGTTAG	TTCCGGCTTCA	ACATCAGCAA	GTTTCTCTAT	AGGGGACGCA	240
	GGGTGCTCAA	CATCATTTAT	TAGACACTCC	AGCAGTTTGT	CTGAAAAAAA	GGTGTGCATG	300
	GACAAGTGCA	CCTCATCCTT	TGAGATGCCG	CGGATAACGT	CCCTCAGCGA	CGCCAGTCTC	360
	ATCGTGCAAC	TCCGTGCAAA	AACTCTTGAT	TGATAGCGTA	ATGCAGTCAG	AAGAAGTCGT	420
	TAAAAGCACT	TTCGATGCCC	CAGTGAAACC	TAATCCTCGT	CCGATATAAA	ATCGAACGTC	480
25	TTAGCAACAA	TCTTCCATAT	CCGGAAAGTG	TTTTACAAGC	TTCTTACGAT	TTTCCACTCC	540
	TCGATTGAAT	ACTCCGGCCN	AAATCTTTTA	CCATATACAC	CCNNTNCNGG	GCTTTTGCAC	600
	GAATTCNTTA	TTTGTTGAAG	AACTGGACAC	TTTGAAACTT	TGCACATTGC	NGANTCCGAA	660
	ACNCTTTTCN	CNCCGAACCTA	ATNTNAACCC	CAATCCTGAC	CCAATACACT	CCCCCCCCAA	720
	CATGACCCCG	CACANGATTN	TTTTTTCCCN	AGAATTTNTT	NAACTNTTTG	CCCCCTNANA	780
	CATTNTAAAT	C					

1314UP

	GATCTTGCTG	CAGACAGATG	CCGCGGAGCT	ACCCTTTTGA	ATCCTTATAT	AAACCCTTTT	60
	CCAGCTGTAC	CGCAGTAAAC	TCCCCTTGCT	TCAGGAGCTC	CAGGCTGCCA	CGCACACTCG	120
35	AGGCCTACAC	GCGTGACTGC	ATTGGCTTCT	GTGCGCACAC	GGAAGTCTTA	AACGAACCTC	180
	AATCCCATCC	AACCAGTTCT	GCTAACGTAG	CTACTTCTGG	CCAATCGCTC	AGCCCCATAC	240
	CGTCGAGGCA	ATCTTTCCAA	GCCACATAAA	CGAAACCTAC	ACAGTTACTG	CGCAAGGCAA	300
	GTGCCAAAAG	ACCACAGGTT	CCGCAGTACC	AGAGCAAAAA	GCTTACCTGT	CAACACTTCG	360
	AACATTCGCG	TGGCCTTAAC	CATATGCCAC	ATGAAGCAAT	AGACCCCTAA	AATAGAAAGC	420
	GATTGGCGCG	GAACAGACAT	TCCTGGTGTT	GTACTTGGAA	CTCACATAGG	GGCTGCACAC	480
40	GTGCTTAAGT	CCTCGCTTGC	AGCTGAGGCC	ATGTGCCCCC	CATTAGTGAC	CCACGTTGAT	540
	CTCGAGCCCG	CAAATGATCG	TCAGCGTGCA	TCCGACTTGG	CATTGCAAGG	GATGTTGATC	600
	CCCTGANGGG	AGGCTTGCAA	CAGCGCCNCC	CTTGTTTCNC	ATCCATAGGC	TGTGAGGCC	660
	GGAATGATCC	NCTCTCCAGG	GGAACNCCCT	CCCCAACGCC	CCATAGGGCC	CNCCCTGGGN	720
	TNTTGCCCGG	ANACTCCNAA	NCNNGGTTTA	AANNTTTTTT	TTAAANGNCC	CAGTGGTNTC	780
	AAGGCCCCCN	NGCCTTTTTT	CANCCCGCAN	TTNCTNAATT	TTTGNCNGCG	GNA	

1315RP

	GCGGCCGCTC	NNCCAACCTAG	TGGATCTTCA	TTTGTGGCCC	GGCCGACAGG	TTACCACCGC	60
	TTTTCTCTCC	CGTCAGCATC	TCAACTAGCT	GCTGTAGCTG	GTACTCCCTG	TCGCCGCGGA	120
50	ACACGTTGCA	CTTGCTTATT	GCTGTGCATG	AAAGATCGTG	CAGCTGAAC	ACATTACCGT	180
	AAGTGATCAG	CCCAACAAGC	GCGTTGGGGG	GCAGCAACGA	CAGAGAGGTG	ATGATCGAAT	240
	CCTTCAGCGC	CTGGAGGTTT	TCCTCCTCCG	CGGTTACGTC	CACGACGTAG	AAGAAGATCG	300
	GCGCCACCTG	CACCGGCCGA	TTTGTGATGT	ACTCAACCGT	CGTGGAGTTC	AGTTCCGCGG	360
	GCATCGCCTC	CTGAGACATG	TTCCACATAGT	GCTGCGGAAG	ATGGTTCCGC	GTCCCCGCAC	420

AGAGGGGCACG	CCCACACGTT	CGACCGCACG	TCGATCTCGC	AGTACGGGTT	CAGCACCCGC	480
CTTACAGTGT	TGGCCCCACC	CACACACAC	CCGGTTTGTT	ACGAAAAACA	CCGCCAGCT	540
CCC TCCAATC	TCTTCCACC	CGGTGTGTAC	AGCATCCCN	CCGGCNCAC	GTTCTTGTT	600
CNCGTTCCCG	TCCGGGAAGC	CCGGGAAAAAC	ATTCCACGA	NAAACGCACC	CCNTTTAGTT	660
CTTCC TCTCT	NTTTCGAANC	CACCTCTGAA	CCGNGANCCA	CTTTTANNCC	CCTTTACCCC	720
CTTTGATCCC	CNCCGAACCC	CNNAATGGA	ACCAANNAGC	CNTAAACNN	TGCNAAAAAC	780
GANTTGCCCCN	TTTCAAGGTC	CCATCTCTTG	CCCCCCGNGA	ANAAAANTNC	NCCGCCCNNA	

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1315UP

	GATCTTGCGG	AATATCGGCT	CCCAATCCGT	ACCCATCCAC	TTCGACACTA	CCGACTGCAC	60
	CGCCAGCGTG	TTCATCGGCA	CAAGCTGCTC	TCCTAGGCTC	AGCACC GGCG	GCACCACAAA	120
5	GTAGAACC GC	CGCGTGGTCT	CCAGCTGCTC	CCGCTCGTTG	CGGAACGACA	CGTAGTAGCA	180
	ATACGAGCCC	GGTACGTACA	CATCCACATC	CACGCAGCTG	TCCTCCAAGA	AACCTGCGCT	240
	CAGCAGATGC	TTGTAAAAC T	TGTTCCGCTG	GAACCTCGTA	TTCTTTTCCG	GCGGGCAGTT	300
	GGTCCACACT	AGCCCCGTCC	GTGTACACAG	CGATCCGGCG	GCTACCACCA	ACCGCACCCG	360
	CAGCCCCGCT	TCCTCCCCAG	CGTCTCGGCC	AACAGGTAA	CATGGCAACG	TGAGCACACC	420
	CTTTCCAACC	TCTCCTCTCA	CCGGCTCCCC	GTTGTCGTCT	AATCTCAACA	GCACGGTTTT	480
10	CATCGCTGTT	TGCGCCCTTT	GCTGCGATCT	AAAGGAAGCT	TCGCTTGTC	TGCAGCTGCT	540
	AGCCTTG GGA	ACTGCCATAG	TCCTTTGACC	TTGACGCCGT	GTTAAATAGT	GCATTTTCAGT	600
	ATACACAATT	TGACTTACGN	NCTCCCNCG	TGCTAACTGA	GGGANATTAC	CCNAAACCCG	660
	GANGGGANNA	TAAACNGNTNA	NAATTTNCCC	GGTNGCACNC	NTGCCNTATG	NTTCCNTTTT	720
	TGGAAANAAA	CCCTNNGGNN	GGTNGGTTGN	NAAAAATTGA	AAACCCNGGN	TNAATACTNC	780
	NTTNACNTTN	TCGGAAAACA	AAANTNCGGC	CCCCCCGN			

1316RP

	GATCCAATAT	ATGCGATGGT	CTGAAGGGTT	GTCCACGTGA	GTAGCTTAGC	GAATACTTTG	60
	CCAAGGCGTC	TGCGACATCA	AGAAGAGTCT	CAAGATAATA	ATAGTCCTTT	TTGGGCAGTA	120
20	AGCGAAGATT	GTTCTCGCC	TTTGTCATTT	CTGGCCGGTC	CCTGGACCCA	TTTGGTGCGC	180
	TGTTGAAAAA	GCGCCAAAAG	TACTTCAAAA	TGACCGATTT	TTGACCTGG	AAACCTGCCT	240
	GGAGAGAGAA	GTCGTGCAGC	AACGTAAATT	CACTGAGAGA	CAGCAGTGTT	TCGATAATTG	300
	CAGATTCTTG	ATTCTCCTTC	GTTAATTTTG	GGTACAATTT	AGATGAGCTT	AATAAAAAAT	360
	GTAGTGTCTG	GACAGATGGC	GATTCAGCCA	ATAAATAATG	GCTGATGGAT	TAAATGATGC	420
	CAGCTGCGCC	AACCTCATCTG	CATTGCTTAA	GGAACGCATT	GATTTTCAGAC	TATAGTTATT	480
25	GGCAGCATCC	ATGTACTTTG	TTGTACTCGA	TCAGGTCCTT	CACTGAGACA	CCGTCAGAAA	540
	CGCTCACCGT	CTCGTCAATG	AGTTAGAGCC	ATCCATAGAT	TTCCCCGAGG	CAGTTCCCGC	600
	CATGAATTTT	CACCCACTTC	CCCCCCGGTC	CATACCGCAA	TTTGAACATT	CCCGGTCAAT	660
	ACCTTCTTCC	TCCCCCGGNT	NTTCCNCAAN	AGGGAAGTTA	NATTCCTGNC	CTTTTTTTTN	720
	AAAACCCAAT	TCNCACCTTT	TCNNGGAANT	TTTCCGGGTT	GAGNAAAANT	CCNACNCCCG	780
	GTNGCCGGTT	TAATTNCC					

1316UP

	GATCAACACT	CGTACAAACG	AATATAGTCA	CATGACCAGA	TAATCGTCGT	GACTGGCACC	60
	CATACATCGG	CACCCATGCA	CCCACATGAT	GGTTTTCTTG	GCGGGTGGGC	CGTGCTGGGC	120
35	GGGCTCCCCG	GTCTACGCTG	GGCGGTGTAG	GCGGCCGGCT	GGGCGGCCAG	GCGGAGCAAT	180
	GGGCGGAGGA	ACAGCGAGCG	CGCCAGCAGC	GGTGCGCAGC	TGGAGCGTCC	GGCATGTGTG	240
	GAAAAATTTG	AGAATATAGC	ACTGTTATAC	TGAACAGTAT	ATAGAAAGAG	CACTTCCTGT	300
	AGGTTTGAAC	ATACTATACA	AGCTCCCAAT	CATCGACGAT	GGCTGTTGGT	AAGAACAAGA	360
	GATTGTCAAA	GGGCAAGAAG	GGTTTGAAGA	AGAAGGTCGT	TGACCCATTC	ACCAGAAAGG	420
	AATGGTACGA	CATTAAGGCC	CATCCACCTT	CGAGAACAGA	AACGTCGGTA	AGACCTTGTC	480
40	AACAGTCCAC	CGTTTGAAGA	ACGCAGCTNA	CTTCTTGGAA	GGGCNNTTTC	TTCAAGGTNT	540
	NGCNTTGGCC	AACCANCGG	TTCNTAGGAT	TNNCNCTTCC	NAAAGGTTC	ATTANAAATT	600
	TACAGGTCCC	NGGGCAAAAC	CCTTTNGACA	CCTTCCCCGG	TTTGGGATTC	CCCCCCCCNA	660
	CATTTTAATT	CAAAGGNCCA	AAATTGGCN	ACCTTAATTA	NGGNATNTCC	TNTTNAAAACC	720
	NGNAAAAANN	TNTNTAATTN	TTTNNCCTTG	CNTNCCCAA	AAAATTTNCC	CATTTNAAAA	780
	ACNTTTTNNC	CNTCCCCTCN	NTTNAACNCC	NAAGGTTTTN			

1317RP

	GATCTTTATC	TTTCGATGAT	ATCTTTCTCTG	AAGAATCGAC	AAACACCTGG	TCCAGCAAA	60
	TGGAAGCTAA	GTCTCTCCAA	TCGGATGCCA	AATAGTTGAC	ATACCGCGCA	TTTAACTTCA	120
50	CTAACCGGGC	GGCACCAATA	TCCTCCAGAA	CTGTATTTAT	TTGCTACGC	TGAACGATTT	180
	GTTCAATCAG	CGTAATATTC	GTCAATACAA	AGAACCCAAT	TCTCTGCATC	TGAGGTATCC	240
	TTTATGTGG	AGCTCCGACT	TCGGGCTCTA	AGTTTGGATT	TAGAATCTTT	TGGGCCTTGC	300
	GCTCTAGAGA	TATGGTTAAG	TAATCTATAG	CATCGCTGAA	GAAGCAAGAG	AGCAATTGCT	360
	GTGCATTCTT	CGGTGTCATA	GATATCGTCC	AAACATTTT	TGATTTCATTG	GGCAGCCATG	420

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	ATTCGCGAGT	CATCGATTGT	ATAGTAGCAA	GGCAACCAGA	CTTGTATTCA	CTAAACTTGC	480
	GTAGTCTGGA	CATAACATCA	ACTGTGGCCT	CCAGTTACAC	CATTATCAGT	GGTAACTGAG	540
	CCCAGAGAAG	CGGTTTTTGA	CCGATGTACT	TGTNTCNATC	TTTTTGAACA	NGGACNCGGA	600
	AATTTTCATTT	CANGTCNGGC	TNCNCNCTCC	CAAAACNGTT	CCNTGGTTCT	NGTAAAGGTT	660
5	TNNCCCTAAA	AATNGGGNTT	CCCNNGTNAG	NTCCCCCCCC	AATTCNAACN	NAANACCCNA	720
	TTTTTNTAAT	TCCCCCNCCA	AAATTCAATT	ATACCCCCCN	TTTTNGGTAT	TNTAAATTTN	780
	GGGGGNCNCN	NTTCCAAAAA	GGNGCNG				
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1317UP

	GATCGTTCTT	ATATTTGTTA	AAGAAGAGTT	TTCTTCAAGC	ACTTTGAGCT	GAATAATCTT	60
	GTCAAACATA	TTGTCAGGGC	TCCGCTGGTC	GTTAAACCGC	CGAAACCTCT	TGAGGAACCC	120
5	ATCTAAGATC	ATAATTGCCT	TTTCTGGCTC	CGATAAAGCT	TTAATAGATT	GATGGTTGTC	180
	GCCTCTTTCT	GCAACGCGGG	ATTTAGTTAT	TTCTCTAACG	GATTCCACAT	CCTTGTAAGT	240
	CAAAAATGAT	AAACACACGA	CTTTGACTGC	ACTGTTGTAC	GGAATATAAT	TCTCCTTCAT	300
	CTTTTCCAAC	CATTGCAAAA	GTGTTTCCG	CTCGAACGGC	ATATGATTGT	TTCTGTCCAC	360
	AATTACAGCT	CTTGAAGTAT	CCTTTGTAG	AAACTCTAGC	GCGTCACGCA	TCAATTTGCT	420
	CTTATCCTTA	GTAACAATAT	TATCATTCTG	TATGTGGCCC	CAGGACTCTC	CAAAAATATT	480
10	CTTCAATGCC	AGCGCGACTG	TCGTCTTTCC	ACAACCAACC	GTGGCCACAG	GGAATGAAAA	540
	TGAACTTGGT	ATCTCGTCCT	ACCTTATCGA	GCTCCAGATG	CATACTGGTC	CCCCCNAGCT	600
	CCTTTATATC	CTCCGAATTT	CCATAATATC	CAATCCCAAA	ATCCCCAAAT	CNTTCTTAGG	660
	AAATTTTCC	NNNACTNGAA	ATCCCCTTAC	CTTGTTNTATA	CCCCCTGNAA	ATTNGGATN	720
	TTGATTCCNG	CCAGGGANTA	CNATCCCNA	TTTTTNTTTG	TGANNAACAA	NGCTTTTGAA	780
	TTTTTGTCCC	CNCCCNCTGT	GNANTACCCN	CCCTCCTCCC	CCCTTNTTN	TTACN	

1318RP

	GATCGCCTCG	TCGTTCCGCC	GGCTCGTCAG	GCTCTGCGCA	AGGAACTGCC	CGAACCGACC	60
	AACCAAACT	GGCATGTCTT	TCGCGTAGAT	GAAACCTGCT	TGCTTGCTGT	CCACCGCATC	120
20	CCACACGTTG	TTCAGAATAC	CCTCTGCCTC	CGTCATGACT	CCTGAGCCGT	GAGTGCAGTT	180
	CCCAAGGCTT	TTGTTGTGCT	TGGCAGTTGA	AACGACGCTC	GCAGCGGCAA	AACAACACCG	240
	GCCCCGCGGC	AATTGCTCAC	GTGCCTCCTC	GCGCCACATA	AGCACGCACA	CCCTGACCCG	300
	ACACGCACCC	TGCAAAAGTAG	GTCATCACCA	AAGGGGCACC	CCGCCTGACC	GTTCGCTGCG	360
	TCGAGCAGCC	GCCCCGCCAG	CGCCAACGGC	CACCAGCATG	CGCGTTCTCC	GTAGCCGCGG	420
	GCGCCGTTGG	CCATCGCCGA	AAATACCTCG	GTTTGGCCCC	CTGATGCCGT	CTGCCGTCCG	480
25	CCGCGCCCGC	CCGGCGCCCA	GGCACCAGTG	CCTGGTCAGG	GCGCCCGGGC	GGGCGGGGTC	540
	GGTCACGTGT	GCGGTTACCC	GGGCGTCGTT	TAGATCGAAG	GTTCTAGGTC	TGTGCCGTGC	600
	TGCCCCTTGT	TGTGCTACCG	CCAACAGTGG	GCGCGGCGTA	CGCGGCAGGC	ACCACGTGGC	660
	AGTGGCTATC	ACGTGAAAAG	AGGGCGGGTA	ACGGTGGTTC	GCCGCTGAGA	CACATCGCAA	720
	CTATTTACAG	GGCACTTAGG	NGTTGACC				

1318UP

	GCAAAAAATG	AGGTCCGCCA	TGCGCGGCGG	CTCGCGCCCG	TCCGCGACCA	AGCTCCGCGG	60
	CCCGTCCGCG	CCCCACAGGC	ACCAGCTCGC	GCCTGCGCGG	TAGCTCGCGC	CCATCGCGCA	120
35	GTCGCGCACC	GCGCCCGCGC	GCCGCAACGT	CCACATGTCG	CGCACCACCT	TCTCGTCCAG	180
	CACACCGCCC	CCGCACGTGG	CCGGCGCTGG	CGCGCCCGCG	GGCACCTGGC	GCTCGTGCGC	240
	AGCCAACCTCG	CCTGTCTATGA	ACAACGCTGT	AGGAATGCCC	ATCTTTGCC	TTTCCGCTCG	300
	CTGCCGCTGT	GTGTGTGCTA	TACGCTGCCT	TATATACCTG	CCAGGAGAAA	TGTCTGCTAC	360
	TATCCCCGCG	AAAATATCCA	TCCGATGCGA	ACGGCGGAAC	TCGCCGGAAA	CCTGGAGCCC	420
	CGCCTCTGTC	GATCGTATGG	AGAAACAGCT	AAAATCGCTC	AGCTACTCAT	CTCTGGCGCT	480
	GTGGTTACCG	GTCGCCGCAA	TGCGGCGCAT	GCCCAAGTCC	GTTTTTTCTC	TGTGGCGGGG	540
40	CCAGGGAGAG	CGGGGCGCAG	ACGGCCAGAT	TTTGTGCACG	GCAGACCGCG	TTGGCTGTGG	600
	TAACGCGTAT	GAAATACGGG	GAAGCGGCGA	TTACCAGTGG	GTTTCGCTGT	CAGGGGTGCC	660
	TGGGGCGCGG	GAACGCGGTT	ATGGTCTATA	TTACAGAATG	TGTACAAAGG	AGTCACGTGG	720
	GGGGGGTCGC	GGGCNGGACA	GCTGCCTCTG	TTTCTTCC			

1319RP

	GATCTTCCTG	CCTTTTGACC	TCTTCATTAA	TCTTCTCCTT	TAACCTCTTT	TCCGTGTCAA	60
	GAATGTCTGT	TAGCAGTTCC	TCTTCTCTGT	TCGGTTTCTT	CCTGTTCTCT	CTGCCAAGAT	120
	GCAGCATCGA	GTTTGTGCTG	ATGGGCAAGA	AATTAGAATT	GATATCGCCG	ATCCCTACGA	180
50	AGAAATCGTA	CGGCACAACC	TTAATGAGAT	TCTCGCACCA	GTTCCAGACA	TCACCTCTAT	240
	CGTCAATGAC	TACGACCATC	GACTGGTCCA	TCGGGAACAG	ACGCTCGAGT	GATTTTTGCG	300
	TCAGCGAACC	GTTTTTCATG	CGTGACAAAA	TTCTATCGCC	AAAGAGCTTC	CCATCCGGGT	360
	CAATTATCTT	GGCAATCTCT	AGCGCATAGG	CTCGAGTAGC	CATGGTGTAT	ATATGCAGCT	420
	CGAAATGCGG	CGCGATCTTC	GCAAAGAATT	CCTTCAGGCC	TGGCCGTAAT	TTACAGTTAG	480
	TACCAACACT	TGCGCCGTTG	GTTGGCTTTT	GGCCCCCATA	TAGAACGGCG	GCAGCACAGC	540

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	TCCTCCATCC	GANAGANAAA	AACTGCNCAT	CCTTAGCGCC	CCGTATTTCGG	GTTTGTTTNG	600
	GTTCCCTTTG	ACCACTCCCC	CATGGTGGGT	TCACACCCGC	NATNGATTCTN	CCGTCTGGTT	660
	CAATTTTACC	CCCAGCATNG	CTTGCGCNCN	TCCNNNCAAC	TTTGACTION	CCNCTGACCA	720
	AAATCCAAC	TGCNTTGGAC	CCGATTGT	TTTTNTTTG	AAACGNNANT	TCCTNGTCNN	780
5	CTTGGGNCCC	CNCTTTCCCN	A				

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1319UP

	GATCATCGGC	ATGCTGGAGA	ACCCAATTTT	CCAGTCTCAG	ATGAACGAAA	TGCTCAACAA	60
	CCCGCAGATG	ATCGACTTCT	TGATACAGCA	GCACCCGCAC	CTGCAGGCAA	TGGGCCCGGC	120
5	GGCGCGCGAA	ATGCTCCAGA	GCCCCTTTTT	CCGCCAGATG	CTCACCAACC	CCGACATCAT	180
	TCGCCAGATG	TCTCGCCTGC	AGATGGGCAT	GGGCGGTGCG	GGCGCCGAGC	AGGGCACC GA	240
	CTTTCCAGCC	CCCGGCTCCG	CCGCCACACC	CGACGCCGCC	GCCCCCTGCG	CGAACCCGTT	300
	GGCTGCCATC	CTAGGCTTGC	AGCCCCGGCG	TGCTAACCCG	CTGGGCGCTG	CGCCCCGAGA	360
	CCGCGGCCCT	GCAATGCCCC	CTCTAGACCC	GGCTATGCTC	TCTTCCCTCT	TCGGCGCTGG	420
	GCGCTGCCAG	CCCTGCGCCC	GCCGAATAAC	AGGGCTNCCC	AAGNANGNGN	TANCAAAACA	480
10	ANATTCGCCC	ANGCTNAATN	AATTNNGGCN	TCTCCAACCT	GAANAAANAT	TTCCGGGCTT	540
	NAAGCGCNCG	AAGATGTTCT	NTCNNGGGCG	CCCTTNTATT	CTTTNTNTAA	GGNAAANTTN	600
	TAGGTGNNGA	NTTNTCTGCT	NCNNGGGGCG	NCGTGCGCGT	TTTTNTTTAT	TCCCCNTTNT	660
	TTGTNTTCTC	CNTNCTGNIT	TGCNACCCCA	CNCAATTTTT	TTTNGGTGGG	GGCTNCCNTN	720
	TTTTCATNNN	TTNCNANNAC	GNCGNFAATT	ATANTTGTNT	ATCACGTCCT	NTTTNTTTTT	780
15	NNCCNACNGN	TTGGGTTGCC	CCTTTNANNT	GAGGNTGGTG	TAGGGAAAGA	AAAT	

1320RP

	GATCTTTTCA	AGAAGTTTAA	CAATGACTTT	AAAGCTAGCA	TTGATAAAGT	ACTCAAGAAA	60
20	CCTAACAGAG	CGGAGATGTA	TGATGCTCTT	TTGTCAATTA	ACGTCCATTG	TAACAATATC	120
	ACCTCGGGAT	TGAATAGAGC	TATCTCCACT	GGTAATTGGT	CGTTAAAGAG	ATTAAAGATG	180
	GAACGTGCTG	GTGTTACCCA	TGTCTTGAGT	AGGCTTTCTT	ATATTTCTGC	TCTGGGTATG	240
	ATGACAAGAA	TTTCTTCGCA	GTTTCGAAAA	TCTAGAAAGG	TTTCTGGTCC	TAGAGCTTTG	300
	CAACCCCTCG	AGTTCGGTAT	GTTGTGTACA	TCCGATACGC	CGGAAGGTGA	GGCCTGTGGT	360
	TGGTTAAGAA	CTTAGCATTT	ATGACACATA	TTACCACGGA	TGATGAAGAG	GAGCCCAATA	420
25	AGAATCTTTG	CTACTTACTG	GGCGTTGGAG	AACATTACAT	TGGCTAAANA	ANGGCNCCCT	480
	TCCTTTTAAA	TNNNGGGGGT	TTTATTTGGA	AAGGGTACTA	CCCCCGGTNC	ACAAAATCCC	540
	CCCCGNGTTT	TTGTTCCCCC	TTTTAAACTN	TANAAAAAAC	GNGTAAATTT	CCNNATTTCT	600
	TTTCCCNNTN	TCCCAANNNC	CTCAAAACTT	NTTCTTTTGC	AAGGAGGGGG	GAAATTTNTN	660
	ACCCCTTTNT	TTTNTNGGAA	GAGAATTTTT	GTCCCGGNGG	CCCCCAAAAA	TTTTTAAGGG	720
	GAANTCNTTA	NATTCCCNAN	NGGGGNTNNT	AATTTTGTGN	TTTTTANAAAA	AAANCCCCCC	780
30	CCNCCGNNA	A					

1320UP

35	GATCATGAGG	GAATCCTTGG	AAGAGGATGA	CAAGAAGTCC	GACGATGAAG	GTGACCTGTC	60
	TATTCCAGAT	GCGCCTTCCT	CTGAGGAGGA	TTAGGCATAT	AATGGGTCGT	TTATATGTAC	120
	ATTAATTAAC	ATTCCGCTTT	AGCTTTTPTA	CTCTTATCCT	TACGGTAGCT	CACCCATATC	180
	TGTAGCCCTG	CTCAGTTATC	ACTAAAACGA	GTGCCAGGCC	CTAGTACTAT	ATAATCCCCG	240
	GTTTCGAGCT	AGAAACAAAT	TCTGATTCGG	CTGGTTTGCA	TGGGAGTACC	GCGATGCAAG	300
	ATCCAGATAG	CACTTTAGTC	GAGGAAAGGT	TGGCGGCTAC	GCCAAAAGTT	ATCAACAAGG	360
40	TCAGCAAGAA	AGGTTCAAGC	CCCCTTTCAG	TGTTTAAAGT	TAAAGAGGGG	AGCCTATCCT	420
	GCCNAAANTG	CGCCAGGGTN	CNTGAATTTN	GGAGAAAAAA	NTGCGTTTTT	TCCGGAAAAAG	480
	CGCCCCNTGA	NNCCAAAATT	TATTNNGGGAC	CCNCNACACC	NCGAGAAATT	TNNTTNAAGN	540
	GCGCCCTTTA	AAATNCCCAA	TNTCTTCNAA	ANNATTTGAG	GNGGAAAGAC	ANTTTNTPTN	600
	AATTNCGCGG	GGGGTNTTTT	TTGCCGCCCC	GGNGNTCNTC	CCNCCTCCAC	NANTTTNAAA	660
	NATAGGAGGA	ANGGGNGGNG	GCCANATTTT	CACCTTTTCNN	AGTTNGANNG	CCNGNAAANA	720
45	GNNTGGATGN	CCACCAATNC	GGGTGNTNGA	AAANANTNCN	NACTGCTTGT	ACACAAATTT	780
	TTTTGTGCCG	CNGGTGACAG	AAAAAAAGAN	GGATTTTTTN	ACAACCNNAA	AAANAAAAAA	840
	AAAA						

1321RP

50	GATCACGTCG	TTCTTGGAAT	TTCTATCGTC	GACGGTGCTG	TTCTTCAGCC	GGGAGGCGAT	60
	ACGGCTGGCG	ACGCTGCGCA	TCAAGACGGG	CGGGGACGGC	GGGCGCGGCG	GCGAGATGTC	120
	TGCGGAGCTG	CAGACGGCGG	TGAATTTTGC	AAACATACCG	ATGTGCATCG	GGGCGCCGCT	180
	GGCGGTGGTG	CTGGCGGTGT	GGCAGTACTC	GAACCTCAAC	AGCTACTTCA	CGCAGCTGCC	240
55	GTCTTCTCG	TGGTCGATCT	ACCTTGTGCT	GCTGTCGATC	CTGGCGGAGC	TCGCGAGCGA	300
	GCCGCTGTAC	GTGGTGAACC	AGTTCATGCT	GAACTACCGC	AAGCGGTGCG	AGTTCGAGGG	360

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	TGCGGCGGTA	GCAGCGTCCT	GCCTGGTGAA	CTTCGCGGTG	ATCTACTGGT	ACGAGAAGTG	420
	GTTGAATGGG	CGCGGCAGAC	GTGCACGACA	GCTACAGCCA	GGAGGCATCG	CGGTGCTTGC	480
	TTTTNCCCCG	GGGAAGGTTG	CCCCCNCCAA	AACTTTNCCT	GGCCCGNTCT	ACTTGAANAA	540
5	CTTGCGNCTC	TGGGCCCCCA	AAAACTTTTT	TCCCTTTTNT	TNACAAGTTC	CTTTTCCGGN	600
	NATTTTTTAC	GGGNTTNTTC	CNCCCGNAAT	TTNTTGCCCC	TTCCNAAGGT	TTTTTCCCCC	660
	TNTTTNTTTA	NCCCNCCTTN	NCAAGGGGGA	AANNTTTTTN	CTTCCCCCNC	CCCGGGAGAA	720
	ANNGGGGANT	TTCTTTTTTT	TTAAAANGGN	NCCCCCCCCG	ANGNNTTTNN	CCCCCNAGAA	780
	NATTTTTT						

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1321UP

	GATCGAATTC	GATTTCCTTT	CGGTGCAAGG	AAACAGAGCC	TTCGTTAAAG	TGGGATACGA	60
	AGACCGTGCC	CAATTTTCGT	CGGCCCTTTC	TACATACATC	TCAAGCGAGG	AACTTATCGG	120
5	CGTGCCATTA	GTGGTCCATA	TATTGCAAGA	ATGTACAAAG	TTAGAGAGGA	TGAAGGTTGG	180
	GGAGGACGAT	GAGCTATGGT	TCAAAAGGAG	TTTGGAGGAA	NAAGTANCGG	ATTCCAGTTG	240
	TAATTAGCTA	CAAAAGCGGA	ACGGGTGACA	CTAAAATTCC	ATGCGCTAAC	TTTTCCACTG	300
	AAAGAAGCCA	CATGAAGCTT	TTATATCTTC	TGGGGCTCCT	CTGGGACGCT	TACACGTCCA	360
	GAAGTGTTC	CCAAAATTCC	TCGACGTTTT	CGAGGTTTTA	AGAACCGATC	GGTCTCCGTG	420
	CTTGACAGAGA	GGTGCATTTG	ATGGGGCGAA	AAATGGTTTT	TCAACCGCCG	AGGGTCGTTG	480
10	TTCAGGAGCT	TTGTTAGTTC	GAAGTTGGAG	CGCCATTCCA	TTGATTGCC	CTTGCTCTTC	540
	CTCCCTNGCA	CTTGCCGCTT	GCTGCTATGT	TTACTTACTA	NAAGCACCGA	NCCACACTTA	600
	TCTGGTTTTT	TTTTCTTATC	CTGANACTCC	CTTGAATTAT	TGCCCTCCTT	TGACTTTCCC	660
	CCTGTTCCAC	GTTNGTTACA	CNTTTGCTTT	GAATATCTTT	CCTTTCCGAA	GCACCCATNT	720
	TTATAATTAG	TCCTATTGAC	CCCCCCCACC	TGGTTTTTGT	TTTCCTCCCA	ACANGTTCTC	780
15	TTCTCCACTN	AGNTTTGTAT	ACNGAATGTC	NACCC			

1322RP

	GATCCAGGAA	ATAGTACAAC	GCCCTTGGAT	AATGCCAGGG	ATTCTGACT	CCTAACGAAA	60
20	AGCCTCTCCT	CTTCTAATTT	CTTATTAAAG	TAGTTAGCTG	CAAACGTGTA	CAAATCCCCC	120
	GGCCGTCTTT	GCTCCACTTC	TTTCTGGAAT	GCGTCCAGTA	GGTCACGGTG	TTCTGTGAT	180
	AAAACCATCG	AGTAGTTTGT	TGTGTGATGC	AGAAAACCTG	CCTATAGCGG	AACCAAAATG	240
	CTCTAGTAGT	GTGACGGCAC	CGTTTTATCC	AGTTTGCTAA	GCAGCTGCCC	TAGGTTAGGG	300
	AGAGTAGAAA	GTGTCAATGG	ACCCGAATTT	CCTTCTGCGC	GCGGCGAACG	ACGTTAAATG	360
	TGATTACCGT	GATCACGCTA	CTGGGGCTAA	CTACCAATTG	AGACAGGCTA	GTTGTGCAAG	420
25	CCTGAGGAGG	TCTCCGAAAA	GCTTGATGTG	AGGATACTCG	TGTTCAAGTA	TCTTGATATG	480
	CTGTATTGAT	CTGTCCGTGA	GACCTCGAGC	TCTTCGTCCG	TCAATGCCCC	GCGCCTAGAG	540
	AGCTAGGTTG	ACTCCGAGTT	CTACAAAATT	TCNAAACNCC	TTGAAAATTC	NCAACATTGT	600
	TNTGGACCAT	CNANTTCCCC	NCCTTCGGAA	NNAAGCCCTC	CANCCTTTTT	TNACGTTGCT	660
	NACTTNCCCN	CTGAAAAAAC	GTTCNATTTA	CCCTNTTNTA	CNCGGCAGGA	AACCCCCCAN	720
30	TTCTTTTTTC	ATNAACCGGT	ANCTNAAAGA	ATTTTCNNGC	CATGNGGTTT	ANG	

1322UP

	GATCTTCACA	ATCGACGCCA	CGTCCATCGC	GATGTTCCGC	CGCACTGCCG	TCACTGTGAG	60
35	ATATTCTGTAC	GGAGAGAGCC	GGTACGTGTT	GATCATGAAG	TTGCGCACAT	CCTTGTACGC	120
	TTTGGCCGTC	TTGAACCGCA	CCGAGTCGTT	GAAAAAGTCG	GGCAACGCGC	GACGCTCCAG	180
	CTCATGGATC	TCGTTGAACT	GGAACCACGA	GGCAAACGAC	GGCAGCATCA	CCGGGTGCGC	240
	CTGCTTCGCT	AAGAAGCGCG	CCGCTTGTTC	CTCCAATTTT	TGCGCCTCCT	GCTCGTAATC	300
	GATCTTGGGT	TGTTCTCTGCT	GCTGCTGCTG	CTGTTGCAGA	TGTGGCAGCA	CAGGTACAGA	360
	TGGATTACAG	GTCCTCGTGT	TGCCCGACGA	AAGCGTTCCA	TCGCCAGCGT	TGTCAATATT	420
40	GCCATCTGG	ACATCCATTG	GCTCGCTCAT	CGTTATAAAG	AGTATGCCAC	GCTACTTTCC	480
	CCGTTTAATA	GCTTTCAAAC	GCGTCTTCGC	TCTGCTACCC	CGCTTAANTC	CACACTGGTT	540
	TNTGTTTTTC	NCCATACCCA	AAATTTTAAA	ACCCATTTTT	CCACATCAGC	CCCATATCCT	600
	CCGTTTGGTN	GNNGAAATTT	GAAACCCANC	CCTCGCCTGG	CGGAAAANNC	TNCTTATGGA	660
	CCCCCTTCCC	NTCTTTCAAT	CGGTCCCCTT	NACCAAGNNT	TTAGCCCCCC	GGNANANGAC	720
	CAATTNGGTC	CTTCCGTCNC	TTTCCCTTNT	TAAATTGAAA	AAGGTTNCCC	TTTGAAAATT	780
45	AACCCNGCCC	NCNTCCCCCC	GANAAATGGT	TTTTTTGT			

1323RP

	GATCAGTTTG	CAGGGACCAT	GAGCAGGGCG	GGCGACGAAA	GCAGCTCTCC	TTCGTACACC	60
50	TCCGTGACAG	GGCTCAACAC	GCCCTCGCAG	GCGGACGACG	ACGAGGAAGA	GGAAGATGCG	120
	GCACCGTTTT	ACATCCATCC	AGATTTGAGG	ACATCACAGC	TCTACTTTGA	GAAAGTGATC	180
	GATGAAGAGC	CCCTCCCGGC	GCCTGTTAAG	CGGGTGTTC	ACATTAATCC	GTATGGAGAG	240
	GAAATTTTCC	CTGTGCGGAA	CTCTCGGTCT	ATCCACCAGC	TGAAGCGATG	CGATATGCTT	300
	GTGTATTCCA	TCGGGTCTCT	AATTACCACC	TATTGCCATG	GTGATCCTCC	GGTACTTGCG	360
	AGGTGGTCGT	CCAAGGGAAG	ATGAAAAAAT	GCTACTGATC	NCNCCAATCA	ATTNNCNAACC	420
55	TCCGATTAGG	GGGGGGGGNT	TNTTTTTTTT	ATTTTAACCC	CCCTTTGGGG	TGACCCGNNC	480

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5	NAAAAAAG	GGGGCTTGN	NNNTTTTTT	TNGNCCCCGC	CNCCTNTTCG	GNAGNTTTTT	540
	TTTTCTGGNG	GGGGGGCCCC	CCNNNCGGAA	AATNTTNTNC	AAAAGGAAGN	ATTNCCCCN	600
	NANGGGGANT	TTTTTTNTTA	NNAAATNNAA	AAAAAATTNN	TTCCATTCCC	MNAATTTNNN	660
	NTTTTTNNNN	CTNTTNCGGN	TTTGNAANTT	NACCCCCCNC	NANAANTTTN	NTTTTTTCCC	720
	CCCCCCCCC	CCCGGGNNNN	TNCNTTTTTT	TTNNNGATN			

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1323UP

	GATCCGTTTT	TCCAATATTT	CACCGTCTCTG	TAAATCAACA	GTTGAAAAAC	AATGGCGTGC	60
	TTAATCGACG	AACGCAGCAC	AACCAGCAAT	AGGCTTCGAA	GCCGTTCCAG	AGGTGATATC	120
5	GCAAAGTTGC	TCGAGCACTA	GAACGGACTG	GGTCATTATA	TAGGTGGTAG	TAAGAAGTGG	180
	GTAGAAGGAA	GGGGACTATG	GTACAGCGCG	GGCGTGGAGG	CAGGGACGCC	GCAGTGGGTG	240
	CCGCTCATGG	GCATGGGCAT	ATGCGGCAGT	TGTACGAGTT	GGTTTACAAC	CGGGGGGCGG	300
	TGGGGACGTA	GACGTTTACT	GCCGGACCTG	CCGCGGCACG	GGACGCTTGA	CCCGAGCAAT	360
	GTTGTGTGCA	CGCTAGTGGA	GCTGTACCAC	TCGATTCCGG	GCGACATCCC	GCTGATTAG	420
	ACGCATTCTNA	TCGCCGGTGG	GTGTNTCTGA	NCNAAGTTGG	ACCCNGGAAC	CTGATTGTTT	480
10	TGTGGCNAGA	ACACATNCCC	TTGTTGGTGG	ACCCACCCGA	NAATTAAACC	GCCCCNCCAA	540
	GACNAGCCGC	CCTCCCCCCN	GNGCGTTTGG	GTNNINGCCA	TTNGTCCGGA	CNTCCAAGAA	600
	NTTTACTNGC	ACCGNCGGNG	GCACCGCCGN	CGGGGCACCT	NTTTCAACNC	CNTTCCCCCC	660
	CNTGGGGGGG	NCCCCCCTTT	TGAAAAANNG	TGGGGGGGAC	CGGTTCCGGT	CCCNTTCCCC	720
	CCATTCTNATT	TTTNTTTANA	NANNAACCAAC	CCGCCTCCCT	TNNCCCCACN	CAAANNNTNGT	780
	TNGTTAANCT	NCCCCNTTAT	TCTNCCCCCC	CGNCNCNTAT	TCCNACCCGN	CNGT	

1324RP

	GATCCTACCG	GGATGCACGA	CGCATACAAG	TATATCAGGG	ACCTTGCCGA	GGAAATGGGA	60
20	CATAAAATTG	AAGGACCAGA	TCACAAATTGG	TCGTTCCCTTA	TCATAGCCAA	GATATATATA	120
	TATATCTGGG	ATAATTACAG	CGCTTGGTAT	GTATACCTCC	TACATACAAA	TACTTACATA	180
	CACATAAATA	TAATACAGCT	ACTTGTAAAG	CGAGAAAGGT	TACTTCTGGA	GAGCCATTAG	240
	AGACGCAACG	AATGTCAAAA	TCAACCTCGG	GCGGACTTCA	TTGATATCTT	CAGGAACCAA	300
	CCAGATTAAA	GCACCAAGTT	TTCTCGCGAT	AGAAATTGCC	AATTTAGCGT	TTGCATACTT	360
	CTCTTCCTCT	GTTACGGCCG	GGAGTAACCA	AGTCATAATC	CACATATCCT	GGAGCTAATC	420
25	CGTTCAATAC	ATCCAATAGG	AAATGGGCAT	TGCTCAACGA	AGCATCCCTG	GAAAGACATA	480
	TCCTGCTCGA	TTTGCCACCC	TTGGCACTTG	CCTTGCGCCC	ACTTTAGATC	TGACATCTGA	540
	ATNCTCTACC	AAACAAACTN	TGAGGANATN	TGTTTGACAA	GTTTTCTGCN	CCTCACTGCC	600
	AAACTAAACT	AAGGTCACAC	CTNTTTGCNT	CCCCAATTCC	AACCCCTTNN	GCCCCCCCCA	660
	AAAACTTNA	ATTCCCAAAT	TCANNCCCTN	TTTGGTTTCC	CCCCCAATNA	NCNTNAATTT	720
	CNNCCNTNN	CTGGNCCCGG	NNGAAACCCN	TGAAATAAAC	CCCCGAATAC	CTNCNTTGCC	780
30	CGAAC						

1324UP

35	GATCTTAAAG	AGGCTCAGTA	TGCAGAGGCA	GTTTCCAGAA	GAAGACAGGC	TGGGCTTCGA	60
	AATCCCTCAG	CTCCCGCCGT	GGAAGAGTCC	GCAGATGAAG	CAACACACAC	AACAGGGCCA	120
	GCAAACGCCG	CTGCGGCGGC	CGCGCTGCAT	CCTCGGTGCC	CCTTATGAAC	CGAGCAGGGC	180
	GTCGTCCACT	GGTGCAAGCC	AAAAGCGCGA	CTACGACTAC	TCCGTGTTCA	ATGAGAGCAG	240
	GCTCTTCACT	GAGAGCAAGA	TAGACCAAGT	CTTGAAGAGC	GAGGCCGCAA	CGCACAAACG	300
	CGTATTCCAC	CGCGACCGTC	CCCACGACGA	CAGCTACCGC	CCCGACTTGC	AGCCGCTCTG	360
	CTGCGACAGC	TCGGACGAAG	GAAGGGAGAG	CCCCGGCGCG	CGCAGAGCGC	GCCGTTGAGA	420
40	ACGCCCCGTT	TGGTGGGTCTN	AGCATCCCCC	GGANATNCNT	CCCAGAAAAA	ANTNTTTTCGA	480
	ACACGCCGCC	CGCCCGCCCC	CCNCAGAACC	TCCCNNTAGC	GAACNTTNNA	AGAAGAATNT	540
	TNCCANTTTG	CGNCCCTNCT	TGGANAATGG	TGGGCCNGCT	TNACNAAACG	CTAGGTTGNC	600
	GCGCCGAAAA	NCACTTTGCT	TNACCGCATN	CTCCCCNGAA	AGANAGANAG	NTCCCCNCAC	660
	TTTTNCGCAA	TTTTNTCCCC	CGCGANAAAG	GTTCCCGTTN	ANCCGANGGG	NGGCGCANNA	720
	ANAAACCTAC	NCANTTTTNA	CATTCCCCCC	CNTTTTTTNC	AAAAAAGANA	ATGNNTTTTT	780
45	CACCNTGACA	ANTGATNNCT	TTTNTGAAGG	GNGGNAGTAC	CCCCCGCTTG	CCTNTCCTCC	840
	CCTTAGANCT	NCNATTTTGT	TTTTNT				

1325RP

50	GATCAATGCG	GGAGTGGCAA	AAAGCGACTC	AAGGTGAACG	TGTTTCAGCA	CTGTTTCATGA	60
	TGGGGGGTGG	TCATTTTGCC	GCAGCCATCG	TATCTCACCA	ACGCATAGAT	ATCAGTGGCA	120
	ATGCCAAGAG	GCATGGGAGAA	TCGTTACAGG	AACAGGCCGT	GCACTTTCTT	GAGCACAAAA	180
	CGTTTTCACG	ATACACCACG	AGGCGGAAAC	AAGGAGGTTT	ACAATCGGTT	ATGGATAACG	240
	CCAAGGGGAA	AGCAAATTCC	GCAGGCTCTA	CGCTACGTAG	ATACAATGAG	GCGGCATTAC	300
55	GGAATGACGT	TCAGGACCTG	TTAAAGAAAT	GGAGGCCATA	CTTGGAACGC	TGCGAACACA	360

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5	TATTTATTAG	GGCCAAAAAT	GTTGCGGACA	GGAGCGTATT	CTTTACGGAA	AATACCCCAT	420
	TGACCAAGGT	TAGACCCGAG	GATTTCGGACA	TTCCCATTTCA	CAACCCGTAG	ACCTACCACA	480
	AATGAGCTAA	GGCGAGCATG	GTGCGAGATA	ACATACTTGA	AGAAGACATT	GAAGCCCAGC	540
	CATCACATCG	GAGCGGCATA	CTCCTAAAGC	GACAATGATC	CACTGCCAAT	AAGCGACGTT	600
	GTACGCAACT	TAACCCCGNG	GNAACCTTA	NCAGGAACGG	CTTCTTTCTT	TGGATTCNAG	660
	GCCCCNNNT	ATTCCCTNIT	CNAAAANCNT	NTTTCCCCAA	CCTCTTTTTA	AACCCCGGA	720
	AAAAANNNTTN	AAACCCNCNC	CCCCCCCCA				

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1325UP

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GATCGTGCCA	TGTCTGATGT	GGTATTTTCGA	TGCGGGGCCG	GGTGGGAGTG	CCAGCTGGAC	60
TACGAAATCA	AGGACGAACG	TGAATTTTCA	GCCGCCCTAG	ATACTGTCAA	GGGTGCGCTA	120
GCCCCCGAAA	AGAAGTCGCC	CTGCCGCACG	ACCGTGCAGC	CTGGGCCTGG	AGCAGGCGGG	180
AACAACACGC	CGACACGCGT	ACCTCTGTCC	AAGCTCTTTG	TAGGTGCGAA	AAACACCAAG	240
TTCAAGCCAG	TGATGCGCTC	TGCGGATGCC	GCTATCGCGG	CAGGCAGTGC	CGCTTCGGGC	300
CGCCACTGTG	CGCTATTCTGA	TAAGACACAG	ATAGATGACC	CACCTGGTCAT	GAACAAAGCC	360
GGTGACGACG	AAGTCGAAGT	TGTAGTCGAT	CCTATTTTGT	CAAAAAAGCT	ACGCCAGCAT	420
CAGAGAACAG	GTGTTGAATT	CATGTATGAC	TGCGTCCGGG	GGCTCGCAAG	GTCCGAGAAG	480
GACGATGATA	GAACAGTGAT	GATCTTGGAA	TATGATAGTG	ATGTCAAGGG	TTGTCTGTTG	540
GCGGACGAGA	TGGGATTAGG	GAAAAACATGC	ATGACGATTG	CTCTGATCTG	GACGCTACTG	600
AAGCAGCATC	CCCAGGCCAT	CGTCTGTTCC	datGCTCCGC	AATTGGGGGG	TTTGGTTTGC	660
AGGGTTTTTT	GCCANAAATT	CTCNTGGTAT	GCCCCGGTGA	CTCTGATTGG	CGACTGGGAA	720
AANGATTTTCN	CCNATNGGNN	GCCGANGAAT	AAATTGGANC	CTNGAANCCN	ATTGCNAANT	780
ACCCCCCAAA	ANAAAAAATG	N				

1326RP

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GATCGAATTA	AGTCAGATTT	GATTGCGATG	GCTACTAACG	AACGTGCATT	GTCAGACGGA	60
CCGAATCAGG	TACACATTGA	AACTCGTGAG	TGGCTAGTGC	AGACAATCAT	AAATGAAAGT	120
TGTGGCTGGA	GCAAGGGAAC	TGCGATGCCT	TAACTTTCTC	AAAAACTCA	TGGGTGGTCA	180
AAAATCAATC	TATTCAGTAT	ATAGTATATC	AAAACATTAA	ACCAAAGTAG	GCGCCAGAA	240
TATTGCCAAA	ACATPGCACT	GGAGTATTAG	TATGTCAGAGA	AGTAGCAATG	GGCGGCTAGC	300
TGGTTACGTG	GCAATTCACGG	ATGACTTATA	GAAGCCCAT	AATCATCTTT	TAGTGACAGT	360
AAGATCAGAC	ATTAAATAAC	GTATCGAATT	TTAGGGGAGA	AGTCATCACA	CTTGCATTAG	420
TATACCGCAA	TAATTCGCGG	ACCACATCAG	TTAATACTGG	GCAATGGTTT	TAAAAAGCGA	480
AACTGGGTTT	ACATTTCAGT	TGTTTTGCAA	CATAGATGTC	TCTCCTCATG	CTGCTTCTCG	540
GTTGAATAAC	CATGCTTCAG	TAGGCACCGT	TCCCAGTATT	TGGTAATTAG	TTGCCAGACT	600
CCTTTATAAA	GGATGACCCG	AATATGANCT	TCCATTAAAC	TTGCCNGGAA	AANANATTTG	660
GCANCCGTAN	ATATTTTCCT	GCCAATTGAN	ACCGTTCTNT	GAACCCCTNC	TTGGGGNCCN	720
GCTTCCCAAA	AACGAANTTC	CCCGGTNGNT	NTTTTATAGG	TNCNAAGAAA	AANA	

1326UP

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GATCAACAAG	CGGTTTCGCG	AGCTGCCGGA	GAACCTGCGC	CTCAACGGGG	TGACGCCGAG	60
CGGCAAGCCG	CGGCTGTTTG	TGTGCCACAC	GTGCACGCGC	GCGTTTTCGC	GGCAGGAGCA	120
CCTGATCCGC	CACAAGCGGT	CGCACACGAA	CGAGAAGCCG	TATATCTGCG	GGATCTGCCA	180
CCGGCGGTTT	AGCCGGCGGG	ACCTGCTGCT	GCGGCACGCG	CACAAGCTGC	ACGGGGGGAG	240
CTGCGGGGAC	GCGCTGCTGA	AGAAGGGCTC	GCCGCCGCGG	CAGCGGCTGA	GCCGGGCGGT	300
GCGGCGGCGC	AAGAGCGCGG	AGGGGCTGCG	GGCGGCGGGC	AAGCCACGGC	GGCGGCTGTC	360
GTCTCTGCG	CAGTCCGGGG	AGAGCTACGC	GTCGGTGCGG	CCGCGCAGCG	CGGGGGGGGG	420
CGAAGAAGGT	GCAGTTCTCG	ACGCCGCGAG	TGCTGCCGGT	GGACCTGACG	CAGGAGCCGT	480
CGACGTTTAC	GGCGCTGGAG	GCGAACGGTG	GTTGCAGGAC	GTGAACAGCC	TGTCCGCGCT	540
GGACGGACGC	CGGAGGAGGG	GAGCTGCAGC	CCGCGTCCGC	GCTGTCTGTT	CAGGCCACGC	600
ACACGCCGTC	GCTGTTTGCC	CACCTTTCCC	NGTTGGCCGT	CCTTACGGGA	ACCTGCTTGN	660
CGCTTTTGCC	CCGAATTGCA	GGTTCGAAGG	GCTTNCCTCC	CGNNGGCNCN	CCGCCCCCCC	720
CGCATCCCCC	CCCGTNNCCC	AAAATTTCAA	GTTAACCCAA	NAACATTCCC	TTTCTGCCT	

1327RP

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GATCCAAGCG	TCTGGAGTAT	GCTAAACGAG	CGTCTCATGC	CAGGAACAAC	GTATTATCTC	60
GTTGAACGCT	GTCCTCGAGC	CTCGAGCCAA	ATCTGACCGT	TTTTTTGCTA	GAGCATACCC	120
AAAAAGAAAC	ATCTTGATGC	GCTAAACAAC	ATGACAATGA	TTAGCGCGAG	GATGCTTTTC	180
ATGTTCTAAA	TTCATGCTCT	GAGGTCCGAG	TCGGTGCCGC	ATGTAGTCCT	GCCGGCCGAT	240
TATATTGCGG	CGTAGCTGTG	GTGAAACATC	GGCGCTAATT	GACGGATAAG	CAGCTGTGTA	300
CCTTATTTTC	ACTATTTCTT	TTCACATACC	AACGACTAAG	GTTGATTCCA	AGAGGTACTG	360
ACTGACCCAG	TGGACAGCGT	AGTTATCGGA	GTAACCTGGC	AATGTCGTAC	GGGTTCTCGG	420
GGACGGAGG	AATGGGCTGC	TCAAGGCCGA	CGACGCCGGA	GCTGACGAAG	GAGCTCAACA	480
TCCCCAAGGA	CGTGCGCAGC	GCCATGAGGA	AGTCGCTGTC	GTACGACTTC	CTTAATGTGC	540

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CTGGCGGGGA	CGAGCAGGCG	AGCCCATCGG	GACGCCGACG	ACAGCGACAG	CTGAGGACGG	600
CGCCGACGGA	ACTGGAAAAC	CAAACCGGCG	AANGGGCCCN	AGGGCNGNGG	ANCAANGNCG	660
GAAAGGGGGA	ANTTTGCCGA	NTACCNCTGT	TGGCCCNCCC	CCGCGGTTC	GANTTTGGGT	720
TGNCAAAATC	CCCTCCTCAC	TTNCAAACCT	NCTGAGTNN	AGT		

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1327UP

10	GATCGGAGGC	GTCGCTGGAG	CGTGCTCTTG	TTCTGTCTCT	GCTTGGCTAC	GCCCGACTTG	60
	GCAGCCGCGG	CGCTCCTGAG	CGTCTCATAC	TTGCTGCCCTG	CTACTTGCAT	GGTTTCTATC	120
	GTCACGGTGC	AGCAACTGGG	ACAACAGCAC	CCAGCAACGG	TTGCATTTAT	ATAGTGTCTA	180
	CCTGTACGAT	AGGGGACTGA	TCGCTCTGCG	ATGCGTATCT	ATCTCATTGC	GGAAGGTCT	240
	CGAAACGAAA	AGCGCCAGTC	GCTGTGAGC	GACAATAGCG	AACCACAATG	ACACAATAGT	300
	GCGCGTCGGC	GACCCGATCC	CTGCATGAAG	ACCGAATGCT	CGAGCAGATT	CTTGTGCGGG	360
	CGTCAGCGGG	TAGCGCGGCT	CGTCGTGTGG	CGGAGCCCGG	ATATGCGATG	GCACCGGATG	420
15	GCGATGTGCT	CGGCGCTCGG	GATTAATCTA	GCTCTTCGGA	GATATGCTTC	TGTAGGAGGA	480
	AGAGGGCGTA	GGGAGAAGGC	CTGGACGCGG	GCTTGGGGAG	CTCTGCAACG	TTGCGGGGGC	540
	GTGCCGCCGT	AGGCGGCGGC	ACACCGGGNA	AATNCNCNGN	GANCCTNGTN	CCCTCCNTTC	600
	CNCCCCCAA	ACTTGCGGGC	NTTNCCCNCC	CGAATNNCAA	GGNNGNCCCC	NAAATCCTNA	660
	ACCCCCCGNA	GGAAAGNNTT	GGCCTNTTGA	NCAAANNACN	CGCGTTNAAA	NTCCCGGGGG	720
	TTTGNGGCCC	CCGAAAANGG	GGATAAACCN	GGCNACNACC	TTTTGAAATC	GCGTTTCNTT	780
20	TTNCCCCCAN	ACNT					

1328RP

25	GATCTCTTCT	GCAAGTTTCT	TTATCGGAAG	CCCAGGCTCT	GGATTTCCTT	TCTCAACACC	60
	AATGGTATTG	TCTTCGATAT	CAGAGAAGGA	GCGCTTCGAA	TTTTGCGCAC	CACCATATGG	120
	ACTCTCTTCA	TTATTTTCGT	TATTTTCTCC	ATCACTTTTCG	CTTGCCAAAG	AAGATCCAT	180
	CGCACCCATT	ACATCGAATT	CTTCATTATC	AGCTTCTCCA	CCTGTTGTAG	TATTTTCGTC	240
	ACCATTATTA	TCTGTGTGCT	TATTGATTGC	ATCACGGCCC	ACACGGCTCA	TTTGATCAT	300
	GCTAGATGTA	TATGGGACAT	AATCCACCTT	TTCCAACAGA	GGACCGAATC	GCTCAACCAA	360
	GTATTGATTT	AAAACCAGGA	AGTTCTTTGT	ACTGACCTCG	GCATATTCCCT	GATCTTGCCC	420
30	GAAACGTGCC	GAAATTACCT	TAAATAAGTC	GAGCACGCAT	GAGTTGGCCA	TGTTATCAAA	480
	GTAAAGATTT	TCTTGTAGCA	GCTGACAAAT	TGGATCAAAA	AGATCTTAGA	TATGAGATAG	540
	TTGTGATAAA	ATTTCGATC	TACAGCCACG	ATACCCTTGA	TACCCGAAC	GCAGCCAGCC	600
	TTAACTGTAT	AATATGGATG	GTTCCATTAG	TTTCCAATAG	TCAATAGATG	CCATTTTCCA	660
	ATATNAACCC	CCCTTGACAG	CATAATATEA	GTTCCNTGTT	NTNATAATCC	CCCCATTTTA	720
	CCAAACCNGC	NCNGTTGATT	NCCCNCCCTC	CACCCCT			

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1328UP

40	GATCGGAGGT	ACATAAGTGC	TCTACCGACC	AACCCCGCTC	TCCATGCATC	AACCAATGGA	60
	GTGAAACAG	TTGACTGGCG	AGCAGGCCGC	CGCACTAGAT	GCGGAACCTCA	TGGGCCCAGA	120
	CGTTGGCTAC	TCGCTGCATC	AATTGATGGA	GCTAGCAGGT	CTTGCCGTGG	CGCAAGTCGT	180
	CGTGCGCCAT	TGGGGCGCCG	CACAGGCGAA	GAAAAAGGTG	CTTGTGCTAT	GTGGGCCCTGG	240
	CAATAACGGC	GGCGATGGCT	TGGTTGCTGC	ACGGCACTTG	CGGCTCTTCG	GCTATGACCC	300
	TGTGGTCTAC	TTGCCGCGGC	TGTCGGCCAA	ACAGCCCTTC	TACGCACAGC	TTGCCAAGCA	360
	GCTACACTTC	GTCGGTGTC	CAGTGCTCTC	CGAGGGCGAT	GACTGGCGTG	CGCATCTTGA	420
	GCCACGTGAC	ACGCTCTGCG	TTGTGGATGC	GCTCTTTGGC	TTTTCTTTTC	GTCCGCCGCT	480
45	GCGCGAGCCC	TTCGCTAGCA	TTGTCGCAGA	GCTCAAACGC	CATGAGGATG	ACATCCCAAT	540
	TGTCGCTGTC	GACATTCCCA	GTGGTTGGGA	CGTTTGACGC	AGGACGCTCA	CCCCTTTACA	600
	CTTATGCACG	TGTGCTGATN	TCTCNTGAAC	GCCCCCAAAA	AGCTGCTCCC	NCNCACATTG	660
	AAACTGGTTT	TTTACNCCC	ATTANTTTTCG	GNGNNGTTTC	ATCCCNAAAC	CCNGCCCCGN	720
	CCTCCNTGTT	TTTANTCCNT	CCCCGTATCC	TGNNCCCATC	CANANTGCGT	TTTTGANTTG	780
	CCATTGCNTN	ATCT					

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1330RP

	GATCTTGGAT	TTGACATTGT	CAATGGTGTC	AGAGGACTCG	ACCTCAAGCG	TAATAGTTTT	60
	CCCTGTCAAA	GTCTTCACAA	AAATCTGCAT	ACCTCCCCTC	AAGCGCAACA	CCAAGTGCAA	120
5	CGTAGACTCC	TTCTGGATAT	TATAGTCGGA	CAACGTGCGG	CCATCCTCTA	GTTGCTTACC	180
	CGCAAAGATC	AAGCGCTGCT	GGTCTGGGGG	AATGCCCTCC	TTGTCCTGGA	TCTTCGATTT	240
	GACGTTGTCA	ATGGTGTCAG	AGGACTCGAC	CTCAAGCGTA	ATAGTTTTCC	CTGTCAAAGT	300
	CTTCACAAAA	ATCTGCATAC	CTCCCCCTCA	GCGCAACACC	AAGTGCAACG	TAGACTCCTT	360
	CTGGATATTA	TAGTCGGACA	ACGTGCGGCC	ATCCTCTAGT	TGCTTACCTG	CAAAAATCAA	420
	GCGCTGCTGG	TCTGGGGGAA	TGCCCTCCTT	GTCTCTGGATC	TTGGACTTGA	CGTTGTTCGAT	480
10	GGTGTCAGAG	GACTCGACTT	CGAGTGTGAT	TGTCTTTTCC	GTCAAGGTCT	TGACGAAAAT	540
	CTGCATACCA	CCTCTCAAAC	GCAACACCAA	GTGTAAAGTA	GACTCCTTCT	GGATATTATA	600
	GTGCGACACG	TTGCGGCCAT	CCTCANNNTTG	CTTACCCTGC	AAAAATCAAA	CGCTGCTNGT	660
	CCTGGGGGAA	TGCCCTCCNT	GTCCCTGATT	CTTCNANTTT	GACATTGTCN	ATGGGTNCCN	720
	AAGANTCCNC	TCAATTNTTG	ANTTCTTCC	CCGNCAGGTN	TTGAANN		

1330UP

	GATCAGATGT	TTTGTGCTAG	TACGTCGCGA	TAGTACTAAA	ATTACCATAT	GCCCATCAGC	60
	ATTATACTAA	CTAGTGTGTG	TTTGCAAGTAA	GCGGTAAACC	ACCCATTACG	CCTGTTGTAT	120
20	CACCAGAATC	CAAAATGCGTT	TTTGAAAAGA	GGTTAATTGA	GCAGTATATC	GATGAGCATG	180
	GGGTAGACCC	AATCTCCAAG	ACAAGCTTGA	CTAAGGATGC	GCTAATTGTC	ATTGCCCCAGA	240
	CACCCACAGC	GTACGCGCTC	GCAAACGCAG	TAACTCGGC	TACGCTCAAC	GCCAATTACA	300
	GCATCCCAA	CCTTCTGTCA	ACACTACAAA	ACGAATGGGA	TGCCGTGATG	CTGGAGACAT	360
	TTGAGCTGCG	GAGTCAGCTG	GATATGTGCA	AAAAGGAGCT	ATCGTCAGCG	CTGTACAAGT	420
	GCGACGCGGC	TATCCGCGTC	GCGGCACGCG	CGAAACAGGA	GAATGATGAA	CTCAGACACA	480
	CGTTGACGGA	GCCTGACGGA	GGCAGTCGGC	GCGCAGGCTG	CCGATGCCCC	GCCCCTTCCA	540
25	GCGGAATTGA	TTACCGCGAT	GGCAGAAACG	CACAAGAATA	TGTGCAGCAA	ACGAAAGAAA	600
	GAAGGAAATG	AAAGCCAGGT	AGTGACGGCA	TTTGCTCCTG	GAACAGCCGG	TCCAAACGGG	660
	NTGCGAGGTC	AACCGGTTTT	TTGGTTACCC	GTTTNNNTTG	TTCCGGAAAA	ANAATTANCT	720
	NNCTTTTTAA	CCCAAAGGCA	GGGCCNTNTT	GCTGAACAAA	AAGGGTTTTT	GCTNCTNNAA	780
	AATTNGCCNC	TNAC					

1331RP

	GGATCATTCT	CAGGTATTAG	AGATTGCTGA	TGGGCACGCG	CTTTTTCTTC	AAGGAATTCCG	60
	ATCGGAGGCG	CCTCTAGAGT	TGAAACGAGT	TTATTATACT	CAGCCATTGC	TACAAGCATA	120
35	TAATCAATAG	CCGCAGCGCA	ACTCTGAAGA	TGATCTAAAG	AAGGAGCATC	TGCCTTTTCT	180
	CGTAGAACAT	TGAGAGCGGT	TGCCCTCTATA	ACTTCATGCT	TATAAGTGGA	AGCACTCGAA	240
	ATAACATGTG	ATAAAGGTGG	AGAGTTGGCC	AATGTGTTCA	AAGCTTCTAA	TTCTGAAACG	300
	GAAATTAGTG	CATACCCAGC	AGCTGCAGCT	TTATTCTTCA	AATGATCGAG	AGAAGGTGAT	360
	TCGGCTACTG	TTCTCAAATC	CAGAAGAACG	TTTGAATCAA	GGATTTCCAA	GTTTCTTTCA	420
	GATGCATGTT	TCTTGAGGAA	GCCTTCATCT	GGGCTCTCCG	TATATCTGCT	TCAACTCATC	480
	CATAGTAATC	AGCAGAAATG	ACAATCCATA	TATGGTTCTT	GGCTTTTCGT	TGTAGTTAGT	540
	CGATGGCTGG	ATTTTCCCAT	GGTAGAAAGA	AGAATATCGT	GCTCTTTCTT	TTCAAACAAC	600
	AAATATCATA	TGCCCTTGGC	TTTCTCCTGC	CAAAAATCCA	AAATTAGANA	TTTCTNATCC	660
	CCTTTAATAN	TTCCACATGT	TCCCAATTCC	TCCCATNANA	TNACTGTCTA	ACTGTTTGTG	720
	GCNNACCCAA	AAANATTCTT	TCCTNTCCCT	TTTCCCCANA	TGCTCCTTTN	CCAGTC	

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1331UP

	GATCGTGCGC	CTGCTCCACG	AGCGGCTGCC	CAAGGCCACG	CGCTCGGACG	TGGCCTGCAT	60
	CAAGAGCTAC	GTCTACGGCG	ACGGGCTGGA	CGAAACCCCC	TGGTGCGCCT	CCCATGCACG	120
5	CCCCCGGAC	TGCCCCGCGC	AGTCGCAGGA	ACGCCAGGGC	ACGTGCGGGC	CGGGCGACGA	180
	CGAGCTGCGC	ATCTTCACGC	TCTCGCAGCT	GCTGGAGGAC	CAGTCCGCGT	CCGAAGATGT	240
	CATCCCCGAT	AGCATGGATG	CGGGCGACGC	GGTCAGCCTG	GGCTCCCCGC	AGCCCCAGGC	300
	AGGCCTCTCG	CAGCACAGCT	TCTGCCCAGA	TTCCACGCAC	GCGTCGCCCC	TTGGCGCCCG	360
	CCGGTTAACC	CCCTTGACGC	GCGCGCCCGC	CTCCCCACTC	CCCGTCCGCG	TGTACACCGC	420
	GCCCGCCTCC	CCGCTTGACT	ACATTCCCGA	CAGCAAGGGA	TGAACCCCTA	CGTCCTCCAG	480
10	GGCCCCAGCC	AGGCCCCGAG	CCCCGCCCTC	CTGNTTGAAG	GTNNGAANGC	CACCCTNCCA	540
	AAANTTTAGG	GGTNGNGGCC	CNNGGCCGCT	CAACCGNTTG	GCGTCCGNAA	AANCCNNTGG	600
	CGGCGTNNCC	CCNNCTTTAA	GGCGGCNTCG	AACNCNGCNT	NTTTCGGGNA	GGGTTTCCAN	660
	ACNCAACNG	TNNNNCCCCC	CCTTTTTTCT	TCNAANAAAG	GCCTNTTTGT	GTCNNITCCG	720
	CCNGGNNNGN	AATTTTNTTT	TGTGGGGCTG	NNCCCTNAGA	AAACNCCCNC	NGGGNCNNNG	780
	GGGAAAAAAA	AANTTTTTTT	CCNTNGGT				

1332RP

	GATCTTTTAT	GTTCCTTTAG	AGCAAGGTCA	ATTTTCACAC	CACTTCTATC	ATCTTATATC	60
	CAGAATAATT	TGAACAAGAA	GGTACCGTCT	AGTGAACGAC	GTGATTTTCAT	GCCGGCGTCC	120
20	AAGGTTTCATG	AGTCATTACT	GAAAAATGAAG	CAGCACTATA	TCGAAAATAG	GTTGCTCGAA	180
	CTACAAAAAC	TTTCATCAGTT	ATTCGTGATA	GATAACGTGA	ATTTTTCCAA	AAAAATGATA	240
	AATGTCGAAG	AAAGAAGAAAT	CGTAAATCTT	CTAAATGACC	TAGATGATGA	TGCTAACTTT	300
	ACTTTTGAGA	CTGTCCATAC	TAATTTTGTG	AATAATGAAC	TATTCATGGA	ACTACATGAT	360
	CACAAGTCAG	TGATATCGCG	CGTTTGGACA	TTAGATACTG	CGGAGGATTG	CAATCGCATG	420
	AAGAAAAGGT	TACGACCATA	TACACTCAGC	TCCTCGACTA	TTTCAGGCTC	AAGTTGTCCA	480
25	ATATTGATGT	AGATCCAACC	GCCACTATGA	ATTTNAGTTC	CGAAACTCCN	TTGANCACTG	540
	TTACCTCCCT	ATTGTGTTTG	TTACNCCAAT	TGATCCCTCC	ANTTTCCGAT	TCGTGAAAT	600
	GGNGGAAAAC	CNNCGAAANT	GCNGAAAAAC	CTAAAAANAAG	GAANACCGTT	AACNGGGTTN	660
	GGAATGTCTA	TTGGGGGGGG	GCCNNANCTT	TTAAAGNNNC	TTTCNNGGGG	AANANNCCNN	720
	NCTCCCNINA	AANTTTTTTC	CCCNGGGNAA	AAANTTNTCT	GG		

1332UP

	GATCTTTTTT	AGACGCAGTG	TACTATCGAT	GAAGCATATG	ATTATTATAC	AAAACTTCTG	60
	TCCGATACTA	TTGCATTAAA	CCCGCTTAAT	AGAAACGAAT	TTTTGGAAAG	TTGCGACACA	120
	TTAGAGATGT	ATGGAGTCGC	TTCTATTGAA	AATGGCAAGC	ATGGCAAAAA	GGCCAAACAA	180
35	TTGGTAAAA	TGATCAAGAG	TACAGTTGAT	GAAAAGGAGT	TCCATGATGA	AATATGTNAG	240
	ATGGACTTGC	TTAAGAAATT	GATAATATAA	AAGGCTACGA	GCTTCAATAT	TATAATACGC	300
	ATTGCATAAT	TTATTACATT	AAATTGATAT	AGGTATATTT	TTCTTCGAAG	AATTAATTCT	360
	AATCATTTTC	ATGTGAAGAT	ATCGCCCTCT	GTGTTACCTG	CGGATATTTT	GACTCTTAGT	420
	ATATCTACAT	ATTTTGGCGA	GCCATTATTT	AAACTCGCCA	GCTTGACTCT	GGACCCAAGA	480
	GCCGTAATGG	CAGCAGCTCT	TCCTGAGCGC	AATTTCTTCC	AGCAATTGAG	GCACCATGTG	540
40	CCGTCTTTTA	ATTCCAGCAC	ATATAACAGA	CCGTCCCCTC	CAATAACCCCT	AACACAATTA	600
	TTCCCTTTCT	TTCCCATCAT	GTTTCCGATA	CTGGACATTG	CCTGAAATGC	AANTTTAACA	660
	AGCCTTATAC	CAGTGAAATC	NTGCGTTTGT	AAANATGCCN	TGCCAATTTT	AACCCGTGAG	720
	GTGCGTAACC	TGAACTTTTT	TTGAAATTTT	AACCCCCCA	ATNANNTTTC	NTTTTTGNAA	780
	CCCCATGCCT	TGTTTCNCT					

1334RP

5	GATCATAATC	CAGTCGCTGT	CGAGATACTC	GACAGGAATG	GACGTCAGCG	ATTTTCGTCTGA	60
	AGAGCGCCGG	AAAACCTTGT	CCGTTGGCTC	CGGCGTTGCG	GTGAGCGTCC	CGGGCGGCGT	120
	GCCACCGCTC	GACTGCAGCC	GCGCACGCTT	CCGCATTATC	TGGTTCATGG	AGAATAGCGA	180
	CGATACTGGA	CGCTTCATGA	TGCACTTTAA	GGCCACAACC	TCGGCCGTAT	CATGCTGGCC	240
	CCGCCGGCAC	CCGGCCACCC	GTGCCCCCG	CAGGACAGTC	CCGAAACGGC	CTCGTCCCTAA	300
	CCGACCCCTCC	AGCATATACT	GGTTCACCTG	CACGCTTTCC	CGGCCCCCTA	TCAGCCGTGT	360
	CGTCTTTTTCG	AGCAGAACCA	TCTCCACCAG	CTTGTATATC	TCCTCAAATA	ACGCTGCGTA	420
10	TGTTACTGCG	TCCCCGCGCG	AACCGCTCCT	CCCCAACACC	GTGTCCGTCA	AACGAGAGCT	480
	GCTACGGCTG	GAGATGCTGC	GCAGCAAGAG	AGAGTGCTCT	CCTTCATTGA	ATTGCACGAT	540
	AGTAGGGTAC	GAAGTCATGC	NCCCTATGCC	CTACACCATG	NANCTGGTTT	CTATTGTTNN	600
	TCNGGCCCCC	NATNNTGTT	CCAACTNTTN	TTANCTGGGC	CACNTTTTTT	TNTGGTTGCC	660
	CCCCGAACCT	CCTTCCCTTA	ACCAATCCTG	GCCCNCTTTC	NCAACAGGAA	ACCTTNTGAA	720
	CACTTTCCCC	NAAANGTNGC	GAANAAAAAN	TTTTTTTNNAT	TNCCCT		

1334UP

20	GATCCTGCGC	GGCTCCGGCG	AGCCGGACAG	CGCCGCCGTG	GCCATTCTGG	AAAGCGCGTC	60
	CGCCGGCGGG	CCGCCGGTGC	GCGGCCTAGT	CCGGGCTGTA	CAAGTCGCCC	CGAACAAAAAC	120
	GCTTTTTCGAC	ATCACTCTCA	ACGGGCTGCC	CGGGCCTGCG	CAGTACTACG	CCTCGATCCG	180
	CGCGTCTGGT	GATGTGTCCC	GCGGCGCGGC	GTCCACCGGG	CCCGCGTGGC	ACGTGTTCTGA	240
	AGACGCCGTC	GCGTGCGAGC	GCGCCAGCCC	GCTCGGCGCT	GACCTCTGCG	CGGGCTCCCG	300
	CCTGTTCGTC	GCGCCGCTCG	CCGTGCAGGC	GCTGATCGGC	CGCGGCTTCC	TCGTGGGCGC	360
	CGACCGCGGC	CACGCGCTCG	CCGGCGCCGC	CGCCGTGCGC	GTGCTGGCGC	GTAGCGCCGG	420
	CGCGTGGCAG	AACGACAAGG	TCGTCTGCGC	GTGCTCCGGC	GACACGCTGT	GGCAGGAGCG	480
25	CGGCTCCGCG	CGCTCCGCGA	ACATCGCATG	AACGTGTATC	TACATACCTG	CTACGTTGTG	540
	CTCGCGCCCC	CCGCCAAGCG	CTNCTCCAN	CCGGGGGGGC	CCCGGGGGCC	TTCCAACTCA	600
	CCGCCGGGGG	GCCCGCGCTG	GCCCCGAAAC	CCCCTTCCGC	AACGNCCAAN	AANNCCANN	660
	CCNTACNACN	CCCANPTANC	CAACACNTTC	NTCAACGGGT	TNNTNGCCCC	CCCCCGNCNC	720
	TTCTCCGGNG	TTTTTTTTTT	CCGGANNATT	NCTGNTCCCN	CCGTNTCCCN	CCTTATTTTG	780
	NNNGCCCCCC	CCCCC					

1335RP

35	GAGGCAACGG	AGGTGGCGGT	GGTATCAAAG	GTCTGGTAGT	CGCTATGTCC	TTTCCGAGCT	60
	TTTGGGGTTT	TGTGGTCTTG	CTTTTGTGTT	ACGCTAAGGT	TGGGCGCGGC	GAAATCACAT	120
	GCACTGGGCG	CGATTCCAGG	TCCGCCAAGT	TAATGGGANA	CACCGCGCCG	CTCAGCATAG	180
	TGCTGTGGGT	CCTCCTATGT	GATTGCGACC	CAAACGTATG	GTCCGCCCTT	GGGTGTGTCAT	240
	TTTCTGACGT	TGTTATTCCC	TCCGGGCCAC	TAAAACTGCG	CCTACTCTGA	TTCTCTGTCA	300
	GTAACGCAGA	GTAAGACACA	CGCTTGCTTC	GTGTGAGCGA	TAGTGTGCGA	CATAAATTAC	360
	TATGCGGGGA	NCCNTNCCAA	NTTTAACCTN	TGNNAANAAA	ANACCCAAAC	TNNTTCAAAA	420
	CCCAAANTTC	NATTTNNGGN	NCNGAAAAATN	CCGNTTGCGN	AACCCCGCGT	NNNGGGGTTT	480
40	AAATGGGGTT	TCCAAAAAAA	ACCCNCCANT	TTTCCCCCCC	CCCCCNAAAT	TNNTAAAAAN	540
	NCCTTTTAAA	AANNTNNTTT	NTGTGGNGNC	CCCCCCCCC	CCCNAAAAAA	AATCCCCCN	600
	AAAAAANCNG	GTNTTTTCCC	CNTNGGGGGG	AAACCCCCC	NAAAAANNCNN	ACNTNCNANN	660
	NNGGGNCNC	CNNCCCCCN	ANCNCNNTGG	TNCCCCCCTT	TNANAAAANG	GNCCCCCAAN	720
	CNTTTTTTTN	NNNNNNNNAA	AACNCCCTTT	TTCNCCCCC	CCCCNNAAAA	AATTTTNNNN	780
	NTNNNTTTTN	G					

1335UP

	GATCAGATAA	GAATTGAAGC	TCAGCGGCTG	ATGAGCGCAC	TGCTTCCGAT	ACGGTGGTCC	60
	TGTACCAGGC	TGATAAAATG	TGACACTATC	ACCATAATGG	GGTTGTAGCT	GGATACGATG	120
5	TCCGGATGCG	GATGGACTGT	TCTGAACAAG	ACGTGCAACG	TGCGAGGCC	ATAGTGGGAA	180
	ATCTAATTAA	CGTATTTTACA	TATCAGTGGC	GATGTGTCTA	GGTGCCGGCC	ACCTCGATTT	240
	CCTGCTACTG	GACAGCGCCG	TCATATAAAC	ATTATTTGTT	AGGGTTTAAA	GTTGCTTTGT	300
	GCGGTGGAAA	ACAACGTCAC	ACACTAACTA	AATCTAACTC	GAGCCAGCAA	GCAACTATGT	360
	TAAATAAGCC	GAACAGTTTA	CGATTCCAAG	GGCACGGTGG	AACCCCCCAA	GGCCCCGCTC	420
	CNANTCNTTC	CCTTACAAAA	AGGGAGGGGG	GCCCTACCAC	TACCGAAACC	ATACNGGTTN	480
10	NAAACAACCC	NAANCCCGTT	TTTCCCCCCC	CCAAAATTAA	ANANTGGGCG	CCCCCTGNNC	540
	NCNATTTGTT	NNNTNTNANGG	GGANAGGACC	CCCCCCCCGG	GNNNGGNTCC	CCCCNNTCNA	600
	AAACCANNAC	CCCCACCCCN	ANAAAAANGG	GGGGGGGGGN	GGAACNCCCC	GATTTTCTAAA	660
	AAATTTAAAA	ATTNNNNGAA	ACCGNAAAC	GGNGTGNNCN	TNCCNNNNNG	AAAAANGTTT	720
	TTGTNGNNNA	CANCCCCCAA	CNNTTNTNAG	NNNCCCGNNC	CCCCAAACNN	AAAANTTTNC	780
	TNGNANGGGG	AACCANTCCC	CCCCCNT				

1336RP

	GATCATGTTT	AACCCAGATA	CGAAAACTGA	GAAGCTAGAG	TGGATAGAAA	AGCTGCGAAA	60
	AGTAATAGAG	CTGAACAGGT	TTCAACAACC	ATGGGTTAAA	AAGTTCTTGA	ATAGCAGTGA	120
20	GAATATTCCTC	TGAAGAAAAAG	CATGACCACA	GGATTACATA	GAGTAACTTT	TGTGCAAAGT	180
	TTATCTGTAT	GTACAATTTTC	ACGTTATAAA	TTTTTAAAGT	ACTCGGGCAA	AATCGGCACT	240
	TGGTAGCGAT	AACGCACACT	CGAGTGAAGT	CCATCCAGTA	CATAAACATT	ATGTCAACTA	300
	CTTACCATTA	TTGCCATTGC	CAGATGAAGT	ACCCATGTTT	TGGTGATTGC	CTGACCCATT	360
	GTTACCACTT	GCAGCGCCCA	GGTTTGGGGG	AATCATGCCA	GGAAAGGGAA	AGGGCGGGAA	420
	ACCCCGAACA	TGGGTGGCAT	ACCCATGGGA	AACGCCAGGC	GGCTGCGGCA	GAGAACCGTT	480
25	GTTTTTGTTC	CGCCAAATTG	AAGTTCTTTG	GT'TTNCNNN	CCCCCGGCA	AAAANCTTAA	540
	CCCCGTCCCC	CNGCCCCCN	TCCCCAANC	TTTCCCNNTG	NNGTTGGAGC	CCCCAAACCC	600
	CCCCATATNT	TNNCTGCGCC	GGGGTTTNTN	CCCCCNGGGA	GACCCCCCCC	CGCNTTTGTN	660
	NTNTTACCCC	CACCCNCCCC	CCCCCGGAA	ANCCNGTNTT	AAAAAATNCN	AANAANNTNT	720
	GGCCCCCGNG	CTCCCCGGGG	CTCCCNTATA	CCCCCGGNN	GTAAATMNC	NAAGNGGNCC	780
	CN						

1336UP

	ATCGCCATTT	TAGGGATGAT	CCCATCACC	ACAGCTCCGA	GGCCCTTGTA	GAAAGCCAGC	60
	AAGCCCTCCC	CGCTGTAGAT	GTTGGCCCCC	GTGCGCAAAA	ACCCAGGGGG	CTTCGTGCC	120
35	TCGTTTCGCGC	GCCTGTAGAT	CTGCATGCGC	ACCTTGATCG	TGTCCAATGG	GTGGCAGCAG	180
	AGCGCCTCAA	ACAGGCCCGC	GGTCCC GCCC	GCAACTAGGT	TCACGGCCGG	GTTGGTAGAT	240
	TTCTTAGACG	ACATGTGGTT	ATCAGGGTAT	GGCTGCTGGC	ACACTGCGCT	GCACGGATCC	300
	GCTACGCTTC	TGCGTCGCGC	ACCTATATAT	ACAACGGGCA	CCGACGGCGG	GCCGCCCCGA	360
	CCTTGCTCTC	GACGCAGCGC	CAATAGGAGC	TCGCGCATAC	CCCCGGGCGA	ACGCGGTGAG	420
	TCAACCCGGC	CCGAAGCGCG	GGCCAATGGA	ACCGTCACGT	GAAAAGCAAA	GACTTAAAGT	480
40	ACTATGTAGC	TACACACTTA	GGCCTCGGCC	ATCTCGCGCA	GTCTGCGGAT	CGTGGAGCGC	540
	ACGTGCGGCG	GGCAGCCGTG	GAGACGTGTT	ACGCACCACC	GGCCACAGTC	NTCCTTTGCA	600
	CNAACCTTGCA	NTTCCCAAAN	NCCCGNAGCG	CCGCGCTTCN	CCGCCTTCTT	TGCCGCAAAA	660
	AGAACATCCT	TACCAACTTC	TTGTGTGCCCT	NCCACTTCTT	NAACCTGTTT	CCNNCACGAA	720
	NAANCCTACC	CCCCCCNTT	TTNCCGNAA	TCCNACCTTN	TNCNTNCTTT	TACCATTNTT	780
	NTTNAAGGG	TGN					

1337RP

	GATCTTAATT	TAAAAATTTA	ATTAACATTT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAAATAAAT	TAGTAAAAATA	120
50	AATAGAAAAC	CATAAGTTAA	TTGATTCTAT	AAGAAAAATG	GAATTTATTTG	TGGCATCTTA	180
	ATTTTATATA	TTTAAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATAAA	240
	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAAATTAA	TTTAAATATT	300
	AAATATACCA	TTTTTATTAA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
	ATTTAATTTA	TATAAATTAT	TTAATTTACT	TCATTGATAT	ATATAATTAT	TAAATGTACC	420

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	TTTCATAATA	TTTATTTTAA	TTAGTCTAGT	AATATTTCTA	TTTAATAGTC	TCCCTTTAAT	480
	TGGATATTAC	TACCTACTAA	ATATTTACCT	AATAATATAT	TATTAAGAAT	ACTTAAATCT	540
	AATAATTTAT	TATCTAAAGG	TATATAAATT	AATTAAATCC	TTTTTTATTA	TTATTTAAAT	600
	TATTATTAAT	AGTAAATTAT	ATTATTTATT	TTATTCACCA	TAATTTTTTTT	GATNATAATA	660
5	TATCCTTTNN	TAAATGGGGA	ATTTATNAAT	AATTANCTTC	NANGAATTTT	AATGAANAAC	720
	CCCCNTTANN	ATAAAATTAG	TTAANNNTGN	NCTCAAAANN	CCNATCA		

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1337UP

	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTTAATAATA	AATCTATTAA	TTATATAAAA	60
5	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCATTTCAT	TTAATACTCC	TCTAATTCAA	180
	TCTTAAAATA	TTCTTAATTA	TTAAATTATA	TAATAAAAGT	TAGTGGATAT	AGTTTAAATTG	240
	GTAAACATA	TGTTTTAGGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATTAT	300
	ATCATTAAATA	TAATAACTCT	TTAATTAGAG	TGGTACCACA	AGAATGCTGA	AAGCATTAGG	360
	GGTGTGTACC	TTAGCTCTCT	AATTAAAGTT	ATAAAATTAT	CTTAACCTAAT	AAAAATAATT	420
10	AATTAAATAA	ATAAATAATT	AATTAAATTT	AAAATGTTTA	AAAAAAGAAA	TAAATAATAT	480
	GTTATATTTA	AATAGATCAA	AATTTCAACA	ATTTCCATTT	CATTTAGTAC	TACATCACCA	540
	TGACCAATGT	TACATCATTT	AGTTTAATAG	GGTTTACTAA	TAACCTTTAN	CCTTTTACCA	600
	AANNANNGGT	ANTANTNGGA	AAAATTATNC	CCTTAATAAT	AACCTTNATN	AANNNATTTN	660
	ATATACCAA	ANNNTNTGAN	ATTTNAAAAA	ATATNGGCCG	AANCNNCNTA	TTTTGNGTAN	720
	CCCCNCNTA	CNCCNGAAAA	AANGNTTACC	CGTGTTCCCC	CNTATNNTGN	NTNCCCNAAA	780
15	ATAAAAAATG	NGCCCCCAC					

1338RP

	GATCAACCGC	AACCCGTCAC	TCANGTCCAG	ACCGTTATAG	AGACGGTCGT	CGATGGCACT	60
20	ACAAGGCCGG	CAAAATGCTTT	GCTTATGAAT	AGCACGGTTG	AGGTGATAAC	CGTTAAGGAA	120
	ATAGTGAAGG	AGACAGTTTT	CGTGACTGAG	AAGGTGACTA	ACTAACTCCA	ATGCAAGCAG	180
	AACGCTTTCT	GTCTTTTTGT	CCAAACCTAC	CTGAACACCT	AAACTTAGTT	ATTACAACAT	240
	GAGTTTTATT	TACACAGTAG	GGTGCCACAG	CCACAGGAAA	TATCCAAAGA	AATTAGCTTT	300
	GCCTTGATA	AAGATATTCA	TCCCTATTCA	GCGACCCCTC	TAATACGCAT	TCTCTAGAAA	360
	GTTCCTTGGC	TTTCATTTTA	AATCCTCGTG	CACCTCGTCC	GTAACAGTGT	CTATAGTATC	420
25	ATTCCGTATC	ATTTCTGAAT	GAAGTAGATT	CCATATCAAC	ACTTGCTTTG	GTGGAAAGCT	480
	CATTATTCTG	AGCAGTAATG	GCTTCACCTC	TATCCTGTTC	CAACATACTT	TTTTTAGCTG	540
	CCCGGATTAA	CCTCCCTGAA	TTCCCTTACG	ATGCAGTCGA	GACCCATGCC	GATTTATCAA	600
	ATTTATCTGT	CCTTTAAANA	ATTTTAAACC	TTTGACNCCC	CTATTATTAT	TTTTTAGCNT	660
	ATCGTAATGC	TGCCNGANCC	CCCNAAANGAN	ATGGGGTTTT	CCNTATTANC	CCTTGGTTCC	720
30	CCAANTTAAA	ACCCNCCCCG	GNCCCCCCCC	CCCCCACCN	GGTGGGANAA	T	

1338UP

	GATCAGGTTT	TCCGGTACGT	GAGAACGTAT	CTAAGGCACA	AAGGGCTTTG	GGCGACTGTG	60
35	CGGACGCTTG	AGTTGCNAGA	TACAGGACAA	AGCTGTTACG	GCGGCAACTG	GTGCANCACG	120
	AGCAGCCGAG	GAGCGATTCT	GCGCGAAGCG	ACGGTGAATT	CGAGCCAGCT	GGTAGCAGGA	180
	GTGCCGGATC	GTCTATTTAG	TTGCGACGGG	CGTCGGAACA	GGATGCACGT	AAACGTTGCG	240
	GTAACACGCG	ACGCTGACGC	GACGGCTGCT	ACGCCGATAG	CACGGGAGCG	CAAACGACGG	300
	CAGCCGCTGT	CGCCAGAGAT	GTCTTACCA	CTGCGCGGTA	GCAAGCTGCA	GCGGCGGAAG	360
	CAGACACTGT	AGGCCGGTCC	GGGTGCGGCC	AGTGGGACAC	ACACGGTGGA	CGAGCTGGCC	420
	GCGCAGCTGG	AGCGCGGCTG	CGAGCAGGCG	TCGGAGCGGA	AGCCGCCGTA	CTCGTATGCG	480
40	GTGCTGATCG	GCGTTGCGAT	CCTACAGTCG	CAGGAGGGCA	GCTGACGCTG	TTCGCNAAAA	540
	TACCGNTGNA	TTTCNCNCNT	CTCCCCTTAN	TAACCGGTGT	TTTAAACCCG	GGGTTGGAAA	600
	ANANCTTCCG	GACNACNTNT	TNCTTAAACA	ANGGTNTTGT	TTTAAGGGGN	GGMNNCCCCC	660
	TCAAAGGANG	GGCCTTTTGG	AAAATTAAGG	GGGCCNTTNA	NGGGGGCCTC	NCTTNNCCAA	720
	AAAGGGGGAA	TNATTTTNNG	GGCCCANATT	TNNCAAAAAT	TNTNCANTAG	GGGGNCTNNG	780
45	NNAANTTTNT	TCNCTT					

1339RP

	GATCATCGCC	TTTAGGCCCA	TGTCAACCTT	GCCCGCACCG	ATCAACTCCG	TCACGTCCGA	60
50	CGGGTTCGTG	GGCTCGAGCA	GCGCAATGTC	CACACCCTCC	TGCTGAAAGT	AGCCCTTGGA	120
	CTGGGCTAGA	AAAATCGCAA	TGTGGTATGG	CGCAGGCTGC	CAATTCAATA	GGAATGAAAC	180
	TTTGCTAGAC	ATCTTCGGTG	CAGTCTCCGC	AGCTACACCC	CATTGCATCC	AGGCTCATCA	240
	GCCGCTTTAT	ATACCGCTGG	GCCAAAGATG	ATTGAATACG	GTTCCGACAG	GGCTACTGGA	300
	ATACCCGTCG	CGCCACAAGC	CCGCCACTGG	ATGCCATGCG	CCAATGCGGA	AGCCTCCTAT	360
	GTGACATGTA	CTAACAGAGC	AGCTTCCTTA	TGCACCTTATC	GAGCCAAAAC	CAACATCTGC	420
55	GGAATCACAC	TTGACGGAAT	CCGGCCCCAT	GCGCAGCTGC	TGGAAACACA	AATCCAGCAA	480

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	CTAATAGGGC	TCAGTGGTAT	AACGGCCCAT	CGCTCTCTCA	ACGCCAAGTC	CCTCTCTGGG	540
	GAAAACATGT	GATCACGTGC	TACATATTCA	ACCCCCGTCT	TACCTCATAG	CTGCGCATGT	600
	CCAGCCCTGA	ACTGTTCCGA	CCTTCCGTCT	TCCNGAAANC	CTGATTGCCT	TGCTTTAATT	660
5	CCCCCTCTCC	NCCAACCATG	TNTCGCCCAT	TTACTTCCGT	TGCTTTTTTA	TTTCGTGCAT	720
	TGTTTTTNTA	AAAGNNCCTG	TTAANTAAAT	NCCNTCATTN	TGGA		

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1339UP

	GATCAGCGCA	TTTGTGCGATA	GTGGCTTTGA	TTCGAAAAAT	CCGATCATTA	CCATGCTGAC	60
	TATACGTCTA	CTGACCAACG	CCTTTGCAAA	CAAAGACTGG	GGCGTTAACC	TAATGTGCTC	120
5	TGCGCCAATG	TATAACTCGA	TATTTGGGTT	GATTGATGCA	GACCACCCAA	CTTGTCCTCC	180
	TAAGCAACAG	TCATCACTGG	CCGTAGCAAT	AGCTACCCTA	ATATACAAC	ACTCAGTGTT	240
	GGTAGTAAAA	GAGAACAACC	ATGACATCCT	AGCAATTGTT	GCAGAGGTT	TAAACAACAA	300
	ATACGGCTCC	TCTTCCTTTA	TCCTGCGGAA	CGAGGAGGCC	GCATACAGAC	TCCTTGTTGC	360
	TTACGGAAAC	TTAAGTACTG	TGGAAGGCAC	CCTCGCACAG	TTTGCTCCTT	CTATCTCATG	420
	GATAAGGAAG	CTGAAGAGCC	AGTATGGCCA	CATATCGAAA	TTCCAGGATA	TTTTAAATGA	480
10	TATTTAAAGA	AAGGTGTACG	TATATATCCT	ATTCTTTTCA	TCGCTGTCCC	GAGGCCTTCC	540
	CGGAAAAATG	GTGAAAACCT	CGCTCTTTGA	CACACAGCCT	TTGCCCTTCA	ACAGGATAGT	600
	TTGAAGGGAC	ATGTTCTGTT	GACAANNCTT	GAACCAGGGT	ACTGGTGNAA	AATTTNAANA	660
	TCTTTTCTCC	NCCGAAANCN	ANTTCTNCGG	AANTTAACGG	GAAAAAANC	CCCCTCNNNC	720
	CTTTNTTTAN	TAACCCCCC	CAGGNTTNTG	ACCTTGATTT	TTACAAAACC	TTTTTNTT	

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1340RP

	GATCGCCTGA	TATCGACAGG	CACTTTTGTA	TATTAGCAGT	ATTCTTGACG	AGATAATGCA	60
	GTCAACTCCT	ATATAGAAAC	CGGATACAGT	GGTAAAAACG	CAAATGTAGG	CAATTATATA	120
20	TTACTCTTCT	CGACACCACT	AACCTCTCGA	TAGCGGCATA	TCCTGTAAAT	TTGCATACAC	180
	CTTTTCCCAA	CTTTCAGTGG	TCTCGTTGGC	GTACTTTTACA	TGCATCTTGG	CCCATTCCCTG	240
	GAAGACATGT	GTGATACAAA	ATTGAGTCTC	CTGGAAAAAT	ACAAATTCCT	CTAAAAATGCA	300
	CTTTCATATT	AGCCAGGACC	TGTTTAGTTG	CTCAGCAATT	GTCCGTTTGT	CCCCTTGAAT	360
	TGTCGTCTGT	AGTTTATCAT	ATTCTGCACC	TTTAAACGTCC	GGATTACTCT	CCATAGATTG	420
	AAGTTTGTCC	ATATTTATTT	CCACTCTCCT	CTGCAAATGT	GCTATGTTAT	TCCCCGCCAT	480
25	AATTTTATAC	CTATCAAAGA	CCCCTTCAGT	GCTATAATAA	TATCTATGAA	GGTCTTAAAC	540
	TTACCCGATA	GGTGTTCCTC	CACTTCCTGA	CGCTCCTTTC	TTAGAGGTAT	CGGCCACGCT	600
	ATTGAGATGT	TTTTGATATN	NTGAAAATAT	GANATTTAAA	TATCNTGAAT	AGTGCCTCTT	660
	CCTATTGGGT	ANAANTGTIN	CNGAATTATC	AANCAATTCC	TCCATCACNC	NGCCAAGCAC	720
	CCNCCGTCTC	TCNAANACCT	GCNCNTNGCC	CCGTNCGGTT	NNNNNA		

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1340UP

	GATCTGCTGT	ACCTGAATGG	ACTTTGTCTC	CTGAAGTAGA	AATGTAATGG	CCCCTTCGGG	60
	AATACATAAC	AAACATAGCG	GAGACAAAAA	CAAAAGCGTT	ATACACGCAT	CTGCCGTTAC	120
	ATCACCGTCA	GCTCCTTGCA	GACCAATAAG	CCTTCAAGTT	AAATATAGGC	TAGCTATAAC	180
35	ATATTATGTC	GCTAAGAAGG	GCCAAATCGT	TGCCATCGCT	TAAGAATATC	GCTGAGGTGG	240
	CCAAGCCCCAT	CACCAAGGCC	CCCCCGCTCC	CCCTGCTTGC	GTTTGAGGGC	CCTGGGCTGT	300
	CCACATGTCG	CTGGTATCCC	ACCACCGTGC	GCACAGTGCA	CAATACCCCC	AGTAAGGCGC	360
	AGACGACGCT	GCTCTCGACA	GCGAAGAAGG	AGAGTGCCTT	TTCCGCAATG	AACCTGAAGG	420
	CCTTGCGGAA	CGAGTGCCGC	TCCCGAGGCT	CAGGGTCTCC	GGGCGGAAGT	CGGATTTGAT	480
	CGAGCGCATT	GTCGACTTCG	AGCTGAAGGG	ACCGCTGGGC	AGGCGCGGGA	CACGGCGGGC	540
40	GTTCCACAGC	CCGGGCACGA	GCAGCGCCAG	CGTATGCCGC	CCGTGGACAA	GGTCACCATG	600
	CCCGACATCG	CGCTTGACAG	AACGAACCCC	GTGCCACACC	CTGAGAAAAA	CTACATACTC	660
	CGGANTCCNT	CNTTGTNCCN	CCAAGGGGGT	TTCCCTCCCC	GTTACCNATT	CCNAAAAGAT	720
	TTTTGCCNCG	GAACCCANGA	AGAAACCACC	CGAACTCCCA	GAAGGGGGNT	TTNNNNANCCG	780
	AACCGAANCT						

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1341RP

	GATCACATCC	GATGCGAAAC	TCGTATATTG	TTTTCCCAAC	ATGATGAAGG	TGAGTGTGGG	60
	GCAGCAATTG	TCCGGTTGAC	GACTCCTATA	GGCCCGGGCA	TGCCACAGTG	ACCAGAAATT	120
	TGCAATGTGA	TTCATGATGC	AAATGGAAAC	CCCATCCAAG	TTTCACAGTC	GCAAAAGAAC	180
50	AGTTGGATCC	TGACAAGGTT	CTTCTGTTAG	GCAGCTCTAT	AGACACTCCG	GTTGCTGTTG	240
	CTGCGGATGC	AACGAAAGTG	TCCGCCCATG	CTTTACTCCA	GGCCCTTTTT	ACCTCTAACG	300
	AAAGTGAAGT	AACCTCTGGA	TGTATTACCT	TTTCAAGAGT	CAGAAACCTG	ACCAGTTTCG	360
	ACTAGTTTTT	TATTGAAGTC	CGTGCTGTCT	CAGTATTTGA	AGCAGTTAGT	CCCACGAATG	420
	AGAACTTAA	AGAATAATAG	AATGGGGAAG	ACTCAAAATT	TACGGCTACC	ATAAGACTCA	480
	CAGACTTACT	CGACTCGAAC	GTTTTCGTCC	GCACCTTGTC	CTGCGAGTCA	TATACAGAGC	540

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CCTGTATCGC	GTAAACACC	GGATGCGCTA	CAGCAAGGTA	CTCGCCTACA	AGACAACACC	600
CTACGTACGC	CGTTTCACAG	TATGCAAATA	ATNGAAGGCA	TTTCCTCCNG	ACTTTTTCAGC	660
NAAAGGNITT	ATNCGAACTG	ANCCCTGTCC	ATACTTTATT	CCCCCNANCC	CNGTTTTCNA	720
AAAANCAGNG	AACCATACNA	TGCGTTTAAT	AATGAACNTT	CACNT		

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1341UP

	GATCAGAGTA	GATTTAGTAA	AGAGGTAACC	ACCACTGTTC	CAAGAAGTCC	AGGGCCTTGG	60
	CTTGACCAGC	ATTGGTAAGT	GCTGTGGCTG	GAAATTTGCA	CTTAAACGGT	CTGAGCTCAT	120
5	CTGGTTTCGCC	AAAGACCTAT	GAAGTTTCAA	AACACCAACT	TTGCTGCCCA	TTCTATATTG	180
	AAATGTATGA	CAGATGGCAG	GTGCCTTACC	GTACACTGTT	TTATTGGTAA	CTGGGTCTAC	240
	ACCTTTTCACG	TTCACCTTTG	CCACATGGAT	CAACATAGAA	ATTAAAAGAG	AGCCAACCTT	300
	AGCCTTGATA	TTGTGCGGCC	AAAGAACTTT	AGACTCCTCA	ATTTGTGTAT	TTCTAAACGT	360
	GGTTTTTGCC	CTTTGGACCA	GCTTCTTGAA	TTCGTTACTA	TTGGCCCTAA	CTTCCTTAAA	420
	AATCGATTTT	TCACTCTTCA	ATAGTGCTTC	CGATCTGTAT	TCCATCTCGA	CAGCCTTACC	480
10	TATAGCCAGA	ACCGCTCCTG	GTTGTTCTCA	TACCTTCACT	GACGCTCCA	GTTAGAATTC	540
	CAAGCCTTTA	CCNATTCCCC	AAATTGTTTA	TGAANACACA	TTTCNCCTNG	ANTNACCCCA	600
	AAATTGAAAT	ANGGGGNCTT	TTCCANNCCN	TGAAANAAAA	TGTNGAACGG	NGTTTCAGTT	660
	AAGCCCATNT	ATCACTNNGN	ANCATTNNNN	AAAAANGCTT	CCCCCTCCC	TTTTTAAAC	720
	GGGATCTTNC	CAAAAAACCN	CCCCCTNAAT	GAACCATTTT	NCGAAANCCG	GAAGCCCNNG	780
	CCCTCNCCGN	CTANATTCCN	GCAANNCATN				

1342RP

	GATCCTGATT	TTGATTTCGC	CATTGCTGAT	GTTAATGCAC	TCAGTGCTGA	TGTCCTATAT	60
	ATCCAGCATG	AATTATCCTG	GTGGATATGC	GCTATCTGCA	TTCAACAAAT	ATGTGCTGGA	120
20	CAATAATATC	TCGAATGCGA	CCGTCCACCT	AGATGTCTTC	ACTTGTATGA	CGGGTGCAAC	180
	GCTGTTTGGA	CAGCTGCCGG	ACTCCTACGG	GATCATATAT	GACAAGACTG	AAGGTGATGA	240
	ATTATTGGAC	GCATGGTCAT	CGTTCGATTA	TGTCATTACA	ACTGATCCCA	ACAGCTCACT	300
	GCCTCCTGTT	ACAGGCTACA	AATGGGAGCG	CATCCAAACT	ACTGAGGCCT	TTGACCGCTT	360
	GGACCTTAAA	ACTATACCGG	AAATAATCAA	CTCAGAAGTT	GCTAAGGGAT	TCCCTATCTT	420
25	AAAAGATGCA	ATACTCTCTG	CAGACCTGCA	ACCTGTGAAG	GCTGCGTTCA	CAGATGTGAT	480
	CAGGTGCAGG	GATTTCAGTG	ATACATATAA	AAGAGTTGAG	AATTAATAGA	ACCAGCGCTC	540
	CGCTTACGGA	CAGTTTCCAT	ATAAATATTT	ATTTATTAAA	CTTAAAAGTT	CTGCGAGTTG	600
	AGGAGGAATT	TGACTGCTGG	AGATTCCGAC	ATACTGAAAA	CATAAAGTGC	ACATTTACAG	660
	GATTCCGGCAG	TTACTTGATT	CCCCNTCCTN	NNCCTTAAAT	GCCTGATCNA	ACTTNAACA	720
	TCCTATTGAA	CCCCCTTTGG	TGNTCCAANC	AAANTNTAA			

1342UP

	GATCGGGCAG	GCCGCGGAGC	AGCAGTCGCG	CGCCTTCAAG	GAGGCCGCAG	ACTTCGGCGC	60
	CATCATCCTG	ACCAAGATGG	ACGGGCACGC	CAAGGGCGGG	GGTGCCATCT	CCGCGGTGGC	120
35	CGCCACGAAA	ACACCCGTGA	TCTTCATCGG	CACAGGCGAG	CACGTACACG	ACTTCGAGAA	180
	GTTCTCGCCG	AAGTCGTTTC	TGTCGAAGCT	GCTCGGCATC	GGCGACATCG	AGTCGCTGCT	240
	GGAGCAGTTC	CAGACCGTCT	CCAACAAGGA	GGACACCAAG	GCCACCATGG	AGAACATCCA	300
	GCGAGGCCCG	TTACAGCTGC	TGGACTTTCA	GAAGCAGATG	CAGACCATCA	TGAAGATGGG	360
	CCCGCTGTCC	AACCTCGCCA	GCATGATCCC	CGGCATGAGC	GGCATGATGA	GCGGCATCTC	420
	CGAGGACGAG	ACCAGCCGCA	AGATGAAGAA	GATGGTCTAC	GTGCTCGACT	CCATGTCCCG	480
40	CGAGGAGCTC	GAGTCGGACG	GCGCTCTTCA	TGCACGAGCC	CGCCCGCATG	CTGCGCGTCG	540
	CCCCGCGGNC	CGGGCACCTT	CCGTCTTTCC	GAAGTNTGAA	AATATCCTCC	NTTGCCTCAG	600
	CCANATGATT	GCCCCGCNTT	GGCCCCANGG	GCCNANAACA	TTGGCGGCTC	CCCTGGCNTG	660
	CCCGCCNGCC	CCNGGNATGT	CCCCGCCCTC	CNCCTCCAAA	NGATNTNACC	NGCCCNANCN	720
	TCNNTTNNCT	CAACCCNCCC	NTGANNNCCN	CATAATGGCT	NNNCCGNNGG	GGNCCNGGGC	780
	CCCCATGCCC	CCATTAGGCN	AT				

1343RP

	GATCAACCAA	TGTGTTAAGG	AAATTTTAA	CGTTTTCCGG	GGATTTGGCC	ATCTTTCCCT	60
	CTAATTGGTA	GGAAACATAG	TCTGTAGCAC	CCATGATATT	AGCAAGTTTC	CGCCGAAGCT	120
50	GAAGCAAAC	CTTAAGCCTC	TTCACCTGTT	TTTCGGAACA	ACTAAACATT	GCGGTCCATA	180
	CCTGCCTCCG	AATAGCCTCT	GAAGGACAAG	CATTCATAG	TGTATACGGA	GCATACCCAC	240
	TAGTTGGTAT	CTTATAGTTA	TTACCCATGG	TGTCCTTGGT	GAGCTGACGA	AGAACAAGAT	300
	GGCTAGTGCC	AAATCTTTGC	AAATCTTTGC	ACCGAATCTT	TATGTAGCTG	GAAGATAATG	360
	ATTCTGTGTT	GTTGATGAAG	TCTTGGCCAA	TAATGCTGAT	GTTTTGGGAT	AACTGTATAA	420
55	ACTGCTTTCT	GACTTCGGGC	GACGCATATG	CGCCTGCTTT	TTCAAAATCC	TCTAGCAATA	480

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55

1343UP

	GATCGATTAA	AGGAAGCATC	TGCTTCCCGT	CATATCATAT	AACATTGTAC	CCGGGGCTGA	60
5	GCGGGACCAG	TAGCGAATTT	GATAGCAGTG	TTCTCCACGT	CCCCGCTCCA	CTGTGAGCTC	120
	CTTAAAGTAT	ACCGGCTTCA	TACACCAAGT	CCCACAATGA	TGCGTACTTG	ACTTGTAATC	180
	GAGAGCATTG	GGCTTATACT	GTGATTACGA	TGAATGTAGC	CAAGAGAGAA	AAGGTTTCATT	240
	CACGATATAC	AGTACTCACA	TTCATGGCAT	GCCATCCCCA	AATTCCAATA	CAGCCATTAG	300
	CACCAATGTA	GCGCTACTAA	TCCGGCGAGC	TTAATTGGCG	TCAGTTCAGA	GTGAATCTCG	360
	AGCTTAAAG	TCAGATTGAT	TAAGTAAGAA	AATGACGATC	AACAGGGTGC	TCAAAATAGT	420
10	TGATTACCAG	ATTCCGGCGT	GTGGtCTAgT	GGtATGAtTC	TCGCTTTGGG	TAAGCGAAgT	480
	TGCGGtTCAC	TGcGGcTTAA	CTACTAAACA	TGTGAgAGGc	CCTGGGTTCA	ATTcCCAgCT	540
	cGCCCAAAT	TTTTtGCTCT	CGCCTCCCGC	GGGAAAGGTG	AATATCATT	TACAAGTAGT	600
	TAACTCCTCC	CACGTTACGT	CCTTCTGCAG	ACAAGTTGCA	GCGGTTTACA	ATGCTCAGGC	660
	TATTTTGCGG	CTTCAA					

1344RP

	GATCCTTGCG	TACTAAGAGT	TAGACTTTAA	TTAATAATAT	TATTTGTAGA	AGATAGAAAC	60
	CATACTGACT	CACGTCGTAT	TFAACCCAAC	TCACGTAACC	TTTTAATTGA	CGAACAGTCA	120
20	AACCTTACTT	AGCTGTTACA	ACCAAGAGGA	TAGGTTGAGT	CGACATCGAG	GTGGCAAACA	180
	TAACCTACAA	TAGCTACTCT	ATCGTTATAT	TACCCTGTTC	AATTTGTGTA	TCATAATAAC	240
	ATTTAATTAT	TATTTCAATA	ATTCTCATTA	TTGTTGAGAC	TATTTCATTA	TGTATTATTT	300
	ATTAATTAT	ACATATTGGG	CTTTCGTGGA	TATAATTAT	GTTAATCCTA	CTCATATATC	360
	TAGTCGTTGA	ACGTTCTTAT	AACTTTTATA	AAAGGATTGT	TATAAGCTTC	GCTGCAGATT	420
	GTCTTTTATT	ATTATAAAAT	AATATTAGGA	GTTCCTTGCA	ATTAACCCAA	TTTACTCAAT	480
	ATATTTAAAT	ATTGATAATT	AAATTTTACA	ATTTAATGGG	ACTATTAATT	AATCCCTAGC	540
25	GTAACCTTTA	TTCGTTTATC	AAATACCAT	ACAATATGTT	ATATTTGTTC	ATTATGCCAA	600
	ACTTACGTTA	TTGTNCTACT	TGTAGTATTA	CNATTATAGC	ACAGTTACCC	CATCATATTT	660
	ATTTAATANA	TACCCCAANT	AGNTTTTTTT	ANCATAAAAA	GGANCTAATT	TCCCTTTTTT	720
	CNCCAANTCC	NNCTCTCTCA	ATATTTNTAA	AAATTTTAAA	CNNAANTAAG	AAACCCCNNN	780
	TNAACCNCAN	CTTTTPTCAN	GGCTTTCNAN	CCTNTTNAAT	ANCCCN		

1344UP

	GATCCTTATA	AAATGGGCAA	TAGACGTGTT	ATAATATAAT	ATACAAAATT	ATAAATAAAT	60
35	ATTTAATAAA	ATATAAAATT	AATAAATTAAA	GTATTATAAT	AATTAATAAA	ATTATTATTT	120
	AATAAGTATG	GATTTTTAAC	TGAAATTTGT	TAAAATGAAA	TAAGAAATGC	TAGTAATCTA	180
	TTAATAAGAA	AGTAATGGTG	AATACTCTAA	CTGTTTCGCA	CTAATCACTC	ATCACGCGTT	240
	GAAACATATA	ATTAAATAAA	GAATATTAAT	TAATTTATTA	ATTATTAAAT	ATTATTAAAT	300
	TTATTTAATA	AATATAATAA	ATATTTTAAAT	TTAAATTTATG	AATTAATGCG	AAGTTGAAAT	360
	ACAGTTACTG	TAGGGGAACC	TGCAGTGGGC	TTATAAATAT	CTTTAATATT	CCATTTTTTAT	420
	ACAAATAAAT	ATATTTTFTA	ATATATTTTA	TAATAACTAT	AATTAATAAG	TTAAATTTTA	480
40	AATTATAAAT	TAATAATTTA	ATAACTTATT	AATTAGAGAG	TTAGGGTACA	TCCCCCTAA	540
	TGCTATGCAT	TATGGTTGGT	ACCACTCTAA	TTAATAAACT	ATAATAAATA	AATACTAATA	600
	TTTTATATCA	ATTAAATTAT	AATTATTTTT	TATTAATATT	TTAATATTAT	TTAATGAAAT	660
	ATATAAATAA	AGTATTATTA	TTTAATAAAT	AAATAAGAAA	TGAAGANAAC	GACTCTCANA	720
	ATTAAAATTGC	ATTNATAGTT	TACCATTAAA	CAACATTCCC	TTATTCATAT	TATTTNATCN	780
45	ANTAATTAAT	ATCTTATTAT	TNATTAGAAG	GANAGGNTNC	CNCCCCAAT	GCTNNGCATC	840
	TTGTGGTACC	NCNNATTAAA	AAGTTTACAT	NA			

1345RP

	GATCCCAACG	TCTGATTATG	TGTGTGAATG	CTGTTCTCCT	GCTCCTCCTG	AGTCTCCTTA	60
50	GCCTTGCCCT	TGTACACTTT	GCCGTATGTT	CCTGCTGCAA	TATAGCCGAT	GATTTTCGTAC	120
	TTCTCCAGCA	CTGACACCCCT	ACCGGCGTCT	TTCCGCTGCC	GATATGGCCC	TATCGAGAAC	180
	ACATTGTTAT	TCGCCATTAG	CATCGGCAGT	TTGGACGTGC	TGGCGCTGCC	TTTGGTATCG	240
	AGAAGCTGCT	GTTGCTGTTG	CTGCGACCAC	AGGCTCCGGG	TGGATGCCTG	GTTGGATACG	300
	TTGAAATACT	TATTCGTGTTG	TGTTTGATGC	TGATTATTCA	TACTATCGGA	GGACTGTAAA	360
	CGTATCCCCA	TAAAATAGAG	AGCTCGAGCT	ACCACCTGAC	GACTTGTGTT	ATTTGTAGTG	420
55	TTAAATGGAT	ATCGGCATG	TTCTAAGCTC	GTTTTTAAGT	GTAACACATT	GCAAATCCAT	480

ATGCACACAG CTCATCCGGT TCTACCGACA ACCCTCTTGC GACCGGAGCG GTGGAGCTGG 540
 GGTGGATAGT TCCCGAGCCC CTATGTAGTA TATACAGCGT GCCACGGCTG CGCCTGCGCG 600
 GCTGCAGGGC CTCAGCACGA NTGCCCTTC CNCCACTGCT TTATCCTCCT GAAAGCCGTA 660
 CAACCNCCGG NNAATAACGG GGCACCCAAA GCNGCCCGAN GCCCCCCGAT AANAACNTGA 720
 CCAGCCNTAG NGAGGCCCCG AAANAACANT GCCCTTTTTC AGCGGGCCGT CGCACAAACC 780
 CCAAGNGNGN TCCCCNTTGG GNNTTTTAAT NGCCNNGGGG ANGCCCCNTT NCTCT

1345UP

GATCCGGCGT CAGCGCAAGC CAGTCTACTG GGGGACGGAG ACGCGCACAG CATTGGCGGA 60
 GGGAGAGCTG GAATATCGCG ATGACCACAT TTCGAAGGCA GCTTACGTTT ACTTTCCGCT 120
 AACGGAGGGC GCGAGCGCCA CGCTACGCGA GCGCCTGGGC ACGTCCCTCC CAGAACAGCC 180
 CATCGTGTGT CTCATCTGGA CGAGTACACC GTGGACTCTG CTGTCAAACA GAGCCATCTG 240
 TTTCCACGAT GACCACGCGT ACCTGCTTCT GCAATGGAAG GGTATGCTGG TGGTAGCCGA 300
 GAGAACTGAA CTAGCTGACT TTAAATGGAG TGGTGACACG CCGGTGGTGG TCACCTCATT 360
 CCGCGTCTCT GACCTCCGCG GGCTCTATTA TACCAATCCA CTCTTGGGG ACGCCGTTAG 420
 TAGGCCGCTG CTGCATGGAG ACCATGTCAC CGCCGACACA GGTACTGGTC TGGTACATAC 480
 TGCGCCAGGG CACGGCCAGG AAGACTACCT AGTAGGTCAG GCGCACGGCA TTGAAGTCTA 540
 CTCGCCAGTC GACCATGAGG GGAGGTATAT TCTGGATGAT ATTCTCCAC ACCTCCGTGA 600
 TATGCTAAGA GAAGAGAGCG GTAAGCCGCT GAAGGTTACA GACCACAAAG ANTGCNNGNT 660
 CTTTCATCAGT TTGCTANAAA AACCCTAAGT GCTCCTGCAT TCCCTGAATA CCACNCTCNT 720
 NTCCCTNCAA TGAGTCNAA NAACNTGTTT TCNAGANCTA CCCNNCCGTN GTTCNAACT 780
 GATGGACTGA ACTTCCCCCN GGAAACCTGA ACACTTTATT TTCCCTNCC AGGGGAAAAA 840
 NCGNTCAAGG TTCTCNAAAN CGA

1347RP

GATCATCATG CCAGCGCCCA TGCCGCCGGC GGCACACCTT CACACCCACC CGTAACTGAC 60
 AATACTCGAG CACCTTCGCTG CGCTGGCCCG CTGGCGGCTG CCTGGCCCAT TATGCAACCA 120
 CCCACACGTT TTATTCCACT TAAAAATTAC TTAAGCTGAC GTTACGCCTG TTGAAAAATT 180
 TTCGCTTCAC GGAATTTTTC TGGGTGAGAT ATAAAAGGGG CTAAGTTGCA CAGTGAAAAG 240
 GTGAAGTTTT TTGTGTTTAG ACTTCMTTA TGACCTCATA GAAGGAATTT GGGAAATCTG 300
 ACTTTCTAGC AGCCTCTCTC CAGTTGGAAG TGTTTACATA CTACTGCTAA ACGTGCGCTA 360
 AGTTAAGATT TTCTTTTCTT TAGTTTFAAA CTCAGTACCT TATTCCATAA AGCGACACTA 420
 CGATGTCTTC TAGATTCTCC CTCGTCTCGA ACCTAAGCCT ATCCTTGAGC TCTGTGGGGC 480
 GGATGCAACA GATGCGGTTT GCATCGTCGA AGTCGATGAC TGTGCGGGAT GCGTTGAACA 540
 GTGCGATGGC CGAAGAGATG GACCCGTGAT GACGATGTGT TCATCATCGG AGAGAAGTTG 600
 GCGCCAGTAC AACGGTGCCG TTACAAGTCA CCCAAGGCTT GTTTGACCGT TCCGGNAACG 660
 CGGTTNGTNG ANACCCATCA CCGAAANGTT TTTGCCGTCT TGCGTGGGTN CNCCTGAAGG 720
 CNTGACCTA TGTCATTGAN TNGTTCACTC TCCAGCAGCA NGACANTTCT GAATCCGCGC 780
 CAAATACANN TTCGTGTGTG CNACNNTCAN TGTTTCCAGC NAAGNGCGNC NCGNNC

1347UP

GATCCTACAG AACTCAACTC TTATATCCAG GACTCAGTCA CGGCGTCTGC AATCCGCAGC 60
 AGCCACGCGT GCTCCAGGCT GGGTGGCCAT TGGATGGGTG GGCACGACCC GAGTGGGCAT 120
 GTATTCTGA TAACGTTAAT GTGTATGTTT ATGCTGGGCG AGCTGCAGGT ATTTGGCCGC 180
 CGCGCAATCG GGAAGCTTTC TGCTGATTGT CAACAGCTGC AGGGCGCTCC TGGTAAATTT 240
 GTGGCAGCGA TTTTGCAAGC AAGTCCGATT AGAGAGCTAA TTAACCTCTGA AGCCCCCAA 300
 CATATTTTAA GACGCCFTTT CGTTCAACTG CCACTAGAGA GTCTTGCGAT TCTGGTGAGC 360
 GCGGTTGTTT TTGGCTTTCG GTTCATTGTG CTGGAAAACC CGATTCTATT GCTTGTCTGGT 420
 CTTATTCTGA CATGGACCTG GTCACCTCTG GTAACATATC TCTCTTTCCA TTCGTTTGGC 480
 GAGCATTTGA CCGGTTTGCT CTTGCGATAC CTTCTAGTTT TGGCGTTATA CTGGTACATA 540
 TAATGATCTA AGTAAAACTT GCAATATTAC ACACGAACGT TAAACTCGCC AGCTGATAT 600
 AGGCAAGAT TGCAGATGCT GTGCTTTCCG CCTAATATGC GGAAGATGA GCAGGCCAAA 660
 CCCAATGCAG AGTAGGTTTC TCATATAGTA ACCATCGCGC AGAATGACAA CTTCGCCCCG 720
 CTTTCGAAGC ACTCCCCCTC GGAAGGAACA TCCNATGGGC GAATTTTGGC CACCTTANAA 780
 TTNAANAAAC ATATCATCGC CGANACAATT ACCCCANAA TATCAAGTAT 840
 CNGAAATTTT CNTTANTTCN CCAATACGN

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1349RP

	GATCGTTATA	TATCAGTCTC	TTGCTATAGA	TTACTATAGA	GCCCACCACT	AATGTACAAG	60
5	TTATAACTAC	TGGTAACACG	TTATATAACA	GGTAGGAAAC	GGGGCCGCCG	GGGATTTTGT	120
	CCTATGGCTT	GGCCAGGTAG	CAACTGCTAT	AAAGGCGGAC	GTTTCTCCCG	GAGCTTTTTC	180
	ATCTTGCGCA	GTTTCACTTG	CTAGTTAGTT	TAGGGCTAGG	TCGACAAACA	TATTCCACAT	240
	CGTTTTAATG	GCTGGTGTAC	CTGATAACGT	CAAGGGCGTG	GTTGAGCTGG	ACCCCTGGTT	300
	AGCTCCTTAC	GGGGACATCC	TCTCTGCGAG	ACGGTTCCCT	GCCGACAAGT	GGAGGCACGA	360
	TATCGAACAT	GCGGTGCCCG	GCGGGCGGCG	CAGTCTAGTT	GAGTTTGCGC	GCGACGCATA	420
10	CAAGAGCTAC	GGGCTGCACG	CGGACGCGCA	GAGCAAAAGC	ATAACGTACA	GGGAGTGGGC	480
	GCCCAATGCA	ACCCGGGCGT	TTCTAGTCGG	CGACTTCAAC	GGGTGGATGA	GACCTCGCAC	540
	GAGCTCCAGA	ACAAGGACGA	GTTCGGGTGT	TCACGGTGTG	TTCGGACCTG	GGCGGACGGC	600
	GAATTCATAA	TCCGCNTACT	CACCCTTTAA	GTTGTGTTCN	AACTTGCCAC	CGGANCCCCGA	660
	TACCCGGTTG	CCACNTTGAT	TCAAAGGNAC	CCACCCACC	AGAANCCCAA	GATTTGGGCC	720
	NCCTTACAAG	CCGTCTGCAC	CCNCCCCCT	ACATTCCACA	CAAAGCCCCC	NGACCAACTG	780
15	ATNCCTNAAA	NNACAGNCNC	TTGCTCTCAC	CCGACCCGTT	TGT		

1349UP

	GATCGCGAAA	ACTAACGCAC	CAAACCCGAC	GGAAGCCAGA	GCTCTCTTGT	AAAGTGGCAA	60
20	GATAGTGAT	GTCTGGCCGG	ATGGCTCAGA	GGATTTCTTG	CGAGCATAGT	GGCAGCGATT	120
	GACATATGGA	GTTATCATTG	CAAAAGCAGT	GGCAATAGCA	AGACCGGTTT	TGTTCCAACC	180
	GCCGTTCTCT	TCTTTCATTA	TTGGCCACAA	GGGATTGTTT	GAGTAGAAGG	CCATCTTCAA	240
	CACAACGCTC	GCAACAGGC	CTAGAGACCA	AGTAATGGCA	AACTGCGCGA	CACGCGGTT	300
	GTCTTTCACA	ATGCTCTTCA	AGGTCACTGC	AAAGTTCATC	GTGCTGAGAC	CCGTGGCAAC	360
	CGCAACCGTC	ATCAACCTCC	ACTCCGGTTT	CTCAACTATG	TACGCTCCGA	TACCGATTAC	420
25	ATTAGCAAGT	AAAGGGCCGT	ACTGTTGAAT	CAACGTTGGG	AAAAATGGAA	CATAAAGCAG	480
	AACTGGGCTC	AATACCGCCG	CTATACCCCG	CCTCATAGCC	GGAGATACCC	ATGTACCAGA	540
	GCGGGAAAAA	CCATATCATA	CACAATAGGG	CAGTCAAGTT	CGTCCAGAAC	ATAAACGAGT	600
	CAAAGGTACT	GACAACAATG	TAAAACAGAC	TTGCCTGATT	GGTGATGGGC	TCGTCCGGCA	660
	GGTAAACGAG	TTCTCGTGCT	CCTGCGTGAT	AATCACCTCC	TCCCAGCATT	TCCTCCATTG	720
	CGCCGCCGCC	GAGTCCCTTG	CCGGCTGTAG	NAGCNNGGTG	CTTGCTTTTG	ANTGCACAAC	780
30	CCCCNCGAAG	GCCTGTGCCC	TGGGTTGCCN	AACTTTNCCT	NAGTCCTCCC	AGTTTGCTNT	840
	ACTTACCCTC	CNAAAAATTC	CAAATATCCN	GGACNCCCN			

1350RP

35	GATCTCTTGC	AATTCCCTGCT	CGGTCTCTCT	GTGATCTCTA	TTGATCACCT	TTTCGAGTTT	60
	GGTCGCCCTGA	GAAAGCGTCG	CAAAGTTGTT	CATAAGTTTC	TTATACCGTG	CCAGTTTCGC	120
	AGCCAGCACA	TCGTGCTGTA	TCGTGTGGAG	CGCAATTGGA	TCCCATCGG	CGGCCATGTT	180
	ATCCTTGACC	GCGATATTGC	GTGTTGATGA	AGTCTGAACG	GCCTCGTGCC	CTGGACGTAA	240
	GGCGAAAAAG	TAAAATTATA	TAGAACAGGC	ATGAGATTGG	CTGGAAGTTC	AGGGAGCCAG	300
	GCCTCGTGCG	AAGCAGCTTA	GAGAGCCATA	GGAAGCCACA	TGCGCAGGAA	CTAGAGATGA	360
40	GACCCACCCA	AGGTGAACTC	GCCCCACGGC	CAGGGGCAGT	CCTAGCAACG	TGGTAAACAT	420
	TAAAAATAAT	ACATACGTTA	CAAGCAGCCG	GCATAGCAAC	TGCCTGGAGT	CATGTTTTAG	480
	AGAAAAATAG	AAAAATTATT	ATAATATTCC	TTGTGTATGA	AATAAAGCTG	CTTTGCAACA	540
	CGCGGCAGAG	ATTGAGACCT	GCCTGAAGCC	GTAAAAGGAC	GAAAAACCGA	ACGAATAGAA	600
	TTAAGATAGA	AAAGCAGCAC	TCGGCCAAGG	CGAAGCGGGG	CGCGCAAGCC	GCCCGCGCTT	660
	TCCCTCNCNC	TCAGCTGCAA	ATGCTCCTCA	GTGGATCCTG	CTCCCCCTGT	CCCCGTCTCA	720
45	CCTCCTCCAC	TCCTCGTCNT	ATCCTTTTGA	TGAAACNAGG	CTGACGCGCG	TGTTCACTCC	780
	ATCTTCNCNC	GCNCCGCTCG	ATAAATTGCT	CAGCNCTACC	TCTTGNNNG		

1350UP

50	GATCCGCATT	AAGCGCGACG	ACGAAATCAA	TACCAAGAAG	CTCGACGAGG	AGAAGGAGCG	60
	GCGCCTCAAC	GCCATCATCA	ACGGGGGAGC	TAGTCATATA	AGCGTGCATA	TAGCGCAATT	120
	AAAGGTTTAG	CGTCATCGAT	AGTTACATAA	AGTTAGAATG	CATGCTCCGC	CACGCGCGCG	180
	TTCGACTCGG	CGAGCCAGCG	CGAAAGCGCG	TCTTGCGCCG	CGGGTACGAA	GAACCGCCGC	240
	AAGAAGTGGA	GTTCTCTCCG	CCACCGGTCG	TAGAGGTCCT	GGCTGAGTAC	GTTGTACTTG	300
55	ATCGGGTCGC	CCTTGAGAGAT	GGCATTTCATG	AGCCACTGTG	TCTCGTGCAA	CGAATGCGTC	360

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	GGCGCGCTGC	TGTGCGACTT	CATCATCGAC	AATTCGCGGA	ACGGCTCGAA	CCGCGTGATA	420
	AGCGCAAGCA	AGCAGAGCCC	CGCAGCGTAC	ACGTCCGTGC	TGTGCGTCGG	CTGGCCGCCG	480
	CCGATCAAGC	CCGGCGCGCA	GTACTCAAGC	GTCGTCGTGA	GCGGCTCCGG	CGCCGCGTCG	540
	CACACTGCCG	CCGACGTGAA	GTCCGCCAAG	AATGCTCCTG	CCCGCGCACG	AGCACGTTTCG	600
5	CGGTCTTGAT	GTCCCGGTGC	ACCACGCAGC	TCTCGCGAAG	GAACTGGAGC	GCCCCAACAA	660
	GGTCACGTGC	GTACCGCCAC	CACTGGCCCT	TGTCNCGGGC	GCGCGCCGGT	GCNCCGCTTC	720
	CANGTGGGGT	TCAACCGCTC	TACACAACGC	CGGGACCNC	TCGCCACCGC	GAANCGGCGG	780
	GTATCCCNAC	GTTTNCGCC	GCNCCCCGN	GGAANGGACC	ACTTNCGGTC	NCGANCCNCC	840
	CCCGCCNGGT	GGCAAGNGGG	AATTNTTTAC	CNTCT			

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1351RP

	GATCATAATG	ATTTGTCTTA	ATTCCTTTCT	TAATTATTCA	TTAAATAATT	AATTAATATT	60
	TTATTAATAA	AAAAATTTTA	GAGTTATGTT	CGTTTATGAT	AAATTCTAAA	ACTTTGCAGC	120
5	ACGAACTGAA	GACAACTATG	TAACGCCTGT	AATTAATTAT	AAATTATTAT	AATTAATATT	180
	TCAAAAAATG	GTAAGATTTA	TCGAGGATTA	TCGAATTAAA	TAACATGTTT	CACCTGCTTA	240
	GTCTGTAAAC	GTCTATTGTT	TTGATTTTAA	TTATTGCTAA	CGTAGTCATC	AGGCGGAATA	300
	CTTTAATTTT	CATTTAATTT	ATTCCTTTAA	TAATAAAAAA	TAAATAGGTA	TTCAATTGTTT	360
	ACTGCTAAAA	CTACTCGGGT	ATCGAATCCG	ATTTGCTACT	TTAGCCTTCG	TTCCCTCAATG	420
	TCAATTAATA	TATAATTTAA	ATTTTCACTT	TATAAGTCTT	ATTTCATATA	TTATTATTTT	480
10	ATCTTTACTT	GAATAATTCCT	TAAATTTATTT	TTATTAATTC	TAATTATTAT	TTTAAATAAT	540
	CATCTACGAA	CCCTTTAAGC	CATTACGAAT	AACGCTAACC	CCTTTGTCTT	ACCGCAGCTG	600
	CTGGCACAAT	TTTGGTTGGA	NGGANTTAAT	TATATATCTC	TTTTTAAAAA	ANAATCTCCC	660
	TCATATTAAAT	AATTTTATAT	TGANANTAAT	TATCNNTATT	TAATAATTAT	TGAATTTATT	720
	GTTACCCANA	NTAANAANAN	ATTATTTATTT	ACATCCCCNA	GTACNGANCA	CTTCACATTG	780
	CCAAATCCCN	CGCGTTCCNA	NAAATGATAT	ATTCNANCAC	GGATNTCTTC	TT	

1351UP

	GATCATTATA	TTATAAAATA	TAATAAGAA	TATATTTAAA	TAATAATAAT	AATATGAAAT	60
	ATTATATTAA	TTCTCCATTG	GAGCAATTTG	AGATTAGAGA	TTTATTAGGT	TTAACATCAC	120
20	CAATAATAGA	TTTTAGTTTT	ATTAATATTA	CTAATTTTGG	TTTATATCTT	ATAATCTTTT	180
	TATTAGTAAT	TTTACTAATG	AATTTAATAA	CTAATAATTA	TAATAAATTA	GTAGGTTCTA	240
	ATTGATATTT	AAGTCAAGAA	ATAATTTATG	ATACTATTAT	AAATATAGTT	AAGACACAGA	300
	TTGGTGGTAA	AGTATGAGGT	TATTATTTTC	CATTAGTTTA	TACATTTTTT	ATTCTTATTT	360
	TTACTATAAA	TTTAATTAGT	ATAATTCCTT	ATTCATTTGC	TATAACTTCA	CATGTAGTAT	420
	TTGTAGTATC	AATAAGTATA	ATTATTTGAT	TAGGTCTAAC	TATTATTGGT	TTTTTACTCT	480
25	ATGGTTTAAA	ATTCTTTGGT	TTATTTTTC	CACTAGGTAC	ACCATTAATT	TTAGTACCAT	540
	TATTAGTATC	AATTGAATTA	TTATCATATT	TTGCTAGACT	TATTTTCATTA	GGTTTAAGAT	600
	TATCAGCTAA	TATTATAGCT	GGTCATTTAT	TAATGTTATT	TAGGTGGTTT	AATATTTAAT	660
	TTAATAGCTA	TAAATATTTT	AACATTTTAT	TAGTTTCTTA	CCCATGAATG	CNAATTTAGT	720
	ATGGTTGTTT	ANAATTGGCC	ACCCTANTAT	CCACCTAANT	TGAGGTTTTT	TAAATCCCN	780
30	ATTTTAAAAA	TCCATTTTAT	TACATNNATT	AANAATAANA	TATTTAATAA	TATCCANNAT	840
	TNAANATTTT	ATAANTTTAA	AAN				

1352RP

	GATCCTGCAT	CGTTTCGTCG	GCCTGCAGGT	TGATTTTGTG	GCTCTCAATT	TTATCCTTTA	60
35	TCAAATTCAC	AACCTGGCAA	TCCACCTCAT	GCCTTTATCT	CAACGAATGC	CTCATCGTAT	120
	TGCTAACCTT	GAGGACCATC	TCCACCTTCC	GTTTAAACAAG	CTCGACGGTA	TCCTGTGTCA	180
	ACAGGTTTAT	GGCTGGGTCG	TCCAGCCCCA	ATTGGGCATC	CCAGGCAGTT	ACGTGATCTA	240
	TGTTGTCTCT	GGTGTTCGGA	GAGAAGCGAT	ATGTAACCGA	CTGCATGTTA	AGAAGGCCGT	300
	AGGGCGAGTC	CTGCTCCCGC	ACGTCCGCGT	CGAGCAACTC	GCTGGTGTG	ATGTTGATGG	360
	CGTCCTCACA	CAAATCGCTC	AACAGCGAAA	GCTGCTTGAA	GGGGAAGCGC	ACGTGGTGGA	420
40	ACAGCGACCG	TGCGTCCCTG	CCCGAGCGGC	TCGCGCGGCG	GAACGGGTTG	TGCTCGTCTG	480
	CGGACAAAGT	CGGGCAGCTC	AGGGACGGAT	GGAGCATCAC	GGGCGCCTGC	TTCCGAGGGC	540
	CCAGGTGCGT	AGGGTCCGGC	TGCGGCAACG	CGAGACCTTG	TACTCCGCGG	CCGCGCCGGG	600
	CTGGCCGAGC	GCCCCNGTCA	GTCTTCTACA	CCNCTTGACT	CCCCCACTC	CTCCGTNGAT	660
	GACTGNCCGC	GCTCTNCATC	CGGTGCTCGC	ACACNCACAT	CTCCGAATGN	TTTCCACCAC	720
45	CACCCNGNAC	AACCTTCCAC	ACCCGGAAAC	TCNNTNGNNT	TTNGGACCCCT	GTCTTTACNC	780
	TCCAATCCCN	TCTGCTGCAT	TTTTGNAAAA	CTCCCCCAA	CCCACCCCTC	N	

1353RP

	GATCTAACTA	TTAATGTGTT	CCTTGAAATT	GTGCTGAAAT	ATAACGAGCT	CTTAAATGAT	60
50	GTCTATCTTG	ATGACGATGT	CGTCAAGTTG	AGCCAATGGG	TACTTCAAAC	GTGTAATGAA	120
	TAAAAATATA	CAAGCGCAAA	GCCCAATAAC	CTTTACCCTA	TATATCTTGT	AATATATTAA	180
	GTTAATTGAA	CCATTTACGT	GCCATATTCT	GCGCTGGCAT	GGTATCCGTG	ATTTTATAAT	240
	ATATATTTCT	CGCAGGGGAA	GCAGAAACAC	TCAAGATCGG	CGATTGCCGA	TAAAAGAATT	300
	GCTCCCTGAT	TGATTGTTGT	TCGAAGGAGA	TGCAGATGGA	TTGTCCAGAA	AAACCGGTTT	360

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	TAAGACTCGT	TCATCAAAC	TGTTAAACCA	TTGCCCATCG	GCTTGCACTA	TATTGCCCAA	420
	GGTTTCGCGG	ATATTTCTTC	TGTCTAATGA	TAATCGTCCC	ACAGGCTGGT	CAGCGCCTGA	480
	TGCAGAGCGC	GAAGAGGGTC	GGTCTATCAT	AGGAGGAAAG	CTTTCTTGAT	CCGGGGAGCC	540
	GGTCGGGCTG	TCGGCTAAAA	ATGGAGGTGC	GTCTAATGAA	GACATTAGCT	GGACAGGTCT	600
5	AGGGGCTTCC	ATATCAAATT	CATCATCCGT	ATCCTCCTGT	TCTTCTACGC	ACCTGTCTCT	660
	TATGTTTAGA	TCTCCAGCAT	ACCGCAGTAT	ACCTCCCAAT	ATGATACGGT	GAGAACCCCA	720
	CTACCACCCA	GTGGCCNAAA	AGAACTTGAC	CCCCTGTNAC	CCTNCATGCA	TCCACNACCC	780
	CACCCCCCA	ATCNCNCTGT	ATGGTATGAC	CCTCAGANAN	CCNCCTCNGA	TC	
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1353UP

	GATCGGCGCA	CTCTGTGGTT	CATGTCCTGC	ACAAGTTGAC	CACTGTATAC	CAGTTTGACA	60
	TCAGAGGGCG	AAATCATCAG	TGTGTGGCCG	TACACAGAGC	AAATAAACTC	CTTTACTTCC	120
5	TGCACGGTGG	TGTCGACTGT	CACTTTCATA	GTCTTCATCG	CCAACACGGA	GTCCGAAACG	180
	AACTCGATAG	TTACACCATC	CCCGTCCTGG	CCGTGGTTGG	TACGGAAACAT	AATTAAGCAA	240
	TGCGAGAAATG	GGGTGGGGCG	AAAGTCAAAG	CCCAATACCT	CCTGTAGGCT	CAACCCCGCG	300
	TGTTCTGCCG	CGTCTTCGGC	GCCCAGGTAC	ACAGGGGTAC	GATCGCCCTG	CAACTTGGA	360
	TGCAAGCATG	TCGTGGGGCA	CATGGTTCTT	GTTCGAACAC	AGGTTCTTGC	AGCTGCTGCG	420
10	CTCGTACTCG	TTCACTATAT	CACATGCCAT	CGTCCGCAGC	GCCAGCACAG	ACGTCTTCAG	480
	AGGCACACGT	TGCCCTTATCA	CCGCCACCAC	TTTATCCATG	GAAAGCGTGT	TGACCTGGAA	540
	CTTGACGTTT	ACATACGCAA	ACTCACTGTC	GCCATCGTAA	GCCAGGTCTA	CAGTGCCGCC	600
	TCCGACCTGC	TCCGCACATC	CAGCTCCAGA	TGGACCAACC	CCGCGCCGCA	GCCTGCAATC	660
	TCCTCGCACA	ACATGGTCAG	ATTTCGAGCGG	ACGCTGTTGG	TATTCAGACA	GTATTGCTCA	720
	GGCGGCCAAG	CGCCATGTTT	TCCCCTGATG	CATGATAACC	AATGCCNTAC	TGCNATACCT	780
	NGCNACTGAT	AANTTGGGGG	ANGCCCGCCC	NTTCACGAAG	AAGATCCANG	CTCCNTTCA	840
15	AATAGNAANN	CNGANTGAAC	TGGCGNATNC	CNAATCT			

1354UP

	GATCGAACAC	GCCTGTGCCA	GGGAGCTTAG	GGTCGTGTGC	ATCCAATTGA	GATCGAAGCA	60
	AAAACCGACC	ATGCTTGTTG	AACCGAAAGG	CGGATGTAGC	ATGGCCCTTT	CCCAACGGTT	120
20	GAGATCCTGG	TTGCGCCCTC	TTACCCCTGT	CGTAAATTCT	CGCAAAGTCA	GCCTGGTCCG	180
	TCGTCAAGAG	CGCCTCAAGG	GCATGGCCCA	AATGATCTCG	GCTGCGACAG	CGGTCTGCAG	240
	AAGAGTCTGA	GCTCAAGCTG	AAAATTGGGG	GGGCTGCGA	CCGGCGCTGC	AGCAGCATTG	300
	ACGACGTCAT	CTTGCAAGAC	TTCTGTCACCT	GGGCGTCTTT	CCGCAGCAGC	GTGCGAGACA	360
	GGTGCCGACC	ATTTCAGAGG	CGGAAGTTGG	ATAGCAGATA	ATGCAGGTGC	GACAGCACAC	420
25	CAGACATCGC	ACTGGTTGAC	GATACATACC	GTGCTTGCCC	TTCTTGCGCG	CGTCCAGCA	480
	GTGCGAGGTC	CCGCGAGGGC	GGCACGAAGT	CTGCGATGGC	CTCAAATCGA	AGTCCTGCAC	540
	CTTGATCACC	CGCTCGATGA	AGGGCTCGAA	GTGTGTACACC	CCCGACCGCC	GGTCCCGGAG	600
	CGGCACCACC	GACAGCGGGC	TGGAACAGGC	AGCGTTCCAG	CCCGTGCGCC	AGCCGCGGCG	660
	CGAGCTCTGT	TGCACTGCTC	NTNCCACCCC	ATTGCTGAAC	GCCCCNTGAT	TACAAATTGT	720
	TCNCTCCCG	GCCCCGCTTG	CCCCGGTTGC	CCCTCCCNCG	CGCGGCACCC	CCGCNCCNNT	780
30	GGATGANNGT	TCNCTGATTN	NCCAAACCCG	TTCANNTTGT	CCGGTTTTNT	CANGNCANT	840
	NCCCNNTCNT	TGTNCCNNTT	NAATGCCCN	N			

1355RP

35	GATCATGGCC	AAAAAATTGG	GAATAGGAAA	CTGTTTCCAG	TACTCATCAA	GGTCAGTAAA	60
	AATGTTTGCC	AGCAGTGAAG	ATTGCATCCT	TATCTTGCCA	TTTGCGGATA	GGACATTTGT	120
	TTGCATATAC	CTGTGGTGAG	AGGAAAAGAG	TGTTGCCAGT	TGGGTAAAGT	CTCGTAAAAA	180
	CAAAATAAAT	TCTCTTCTGG	AAGTCTTACC	GTACGCGATT	CTATTCAAAA	TCCTCTCCAA	240
	GTCTTGCCCA	TCACGCAACA	TATTATTAA	CGACTCAATG	AAGATATTAC	CAACTTCGGT	300
	TGAAATGCAC	TGAACTGCGT	CCAATCTCTG	TTGTATCTGA	TCAATATTTA	TTAAAGGCTT	360
40	TGCAATCCAG	TTCTTCAAGT	TCCTTAACCC	GTAAGTTGTT	CTAGTATGAT	CTAATACCCA	420
	TAACAGGGAG	CCTTTACTGC	TCCTATCTGT	ACTGTTCTCA	AAAATATCTA	AGCTTTCAAT	480
	AGCGCTAAGA	AGGAAGAATC	ATGTGCGTCT	tCGAgCAGAA	TGGTTTAAAG	TTTTCCCTGA	540
	AGAAGAGTAA	ACnnncATTT	TTGAAGTTTG	TTAGGTAGCC	ATGCACCAGC	ATGAGCGCTG	600
	TTTGACAGAG	AACGTTGCCC	TTAAAGGCTG	GGTGCGGCTC	ACTGAAGATT	TCTTCATACA	660
	ACCCGACGAG	CTCGATCCTA	TTTAGAGTGA	TATCGGAATC	TGAAGTATGA	AACACCTTTT	720
45	CGATTTCTGA	GCCAAGGCCA	TCTCCGACCA	CAACTTCACT	CGGGTTTGTG	TATTTTATTC	780
	GCGTCTCCAA	AGCCTCCGTC	AGAAAACGCT	CCTCTTTGAA	GTCATCGAAG	ATAACTTCAC	840
	CGCTGTTGAG	ATTAACACTA	ACCAGGAAGT	ATCGCGTGTA	TGAAGGTTGT	CGCTTGACCA	900
	CAAGACCCCA	CACAGAAGCG	CTATCACCCA	GGACCCGACG	ATCTTTGGTT	CGAACGCTCT	960
	ATTGATGCCA	TAGGTAGCCC	TCGTGAATAT	ATTGGGTACT	TCCCTCGAGA	AAACAGAGCT	1020
	TGAgGTCCTA	CTGtTCTTTT	TCACTGCGGA	TGTCTCTGtC	TGcTcCACGa	CCCCACTTTT	1080
50	CAGATTGtGG	tGCATcAAGC	GCTGCAAGtG	GACTTcGAGA	CgGGTGTCTg	GGaATGGTGC	1140
	AgTACGCAAA	CTTcTTGtGC	tTGtGA				

	GATCATGCTA	TCAAGTGCAG	AGAACACGGA	TAGAGCCTAC	TCTGCAGGTT	CGGCCTCGCT	60
	GAGCGCGGCG	CAGAAGTCGA	AGAAGCCGCC	AAATACCGCC	TTCCGGCAGC	AGAGGCTGAA	120
	GGCCTGGCAG	CCCATCCTGT	CGCCGCAGAG	CATCCTCCCA	CTGCTAATAT	TGCTGAGCGG	180
5	GGCGTTTGCG	CCAATCGGGA	TTGCGCTGAT	CATCAGTGCA	AACAACGTGC	AGAACCCTGGT	240
	GATCGACTAC	AGCCAGTGCG	GCAAGCACGC	CACGTCCGAA	TACACGCCCA	TCCCCGAGAA	300
	CCTGGTGAGC	TACCACTTCC	GGACGTCCAT	GTCCGAACAG	CCTAAGTGGC	GGCTGCATTG	360
	CAAGAATGAG	TGCGAGCTAG	AATTTGAGAT	CCCCAACGAC	ATATCGAGCT	CGGTGTACAT	420
	ATACTACAAG	CTGACGAACT	TCTACCAGAA	CCACCGCAAG	TACGTGCAGT	CCTTCGACCT	480
	CGACCACTT	AAGGGCAAGG	CTGTTGCACC	AGACAAGCTG	TCCGACACGT	GCCACCCGCT	540
10	CTCGACTAAG	GACGGCAAGG	CTGTCTATCC	CTGCGGCCTG	ATCGCCAACT	CAATGTTCAA	600
	CGACACCTTC	ACGCCGGTCC	TCCGGGGTGT	CCAACGGCGT	CCCCCGACTA	CAACTCAGCC	660
	AACAAGGAAC	ATCGCCTGGC	ACACNGACCG	CAACAGGTNN	CAAGAAGAAC	AAGCTACAAC	720
	CCGCCAGANA	TNGTGCCGCC	CCCCGCCTTG	GCACGAACGT	TTCCCCCNAA	TGGNTANNAC	780
	AANCCAACCT	GCCTGACTNN	CTACTTGGGA	GAATTTCCCG	TNTTGGANTG	NNCCCTGCAG	840
	NCTGCCNCCT	NNTAAANCTN	CNTNCAAAAA	AAAAGCAACN	CCCTCCC		

pAG1355up

1 GATCATGCTA TCAAGTGCAG AGAACACGGA TAGAGCCTAC TCTGCAGGTT
51 CGGCCTCGCT GAGCGCGGCG CAGAAGTCGA AGAAGCCGCC AAATACCGCC
101 TTCCGGCAGC AGAGGCTGAA GGCCTGGCAG CCCATCCTGT CGCCGCAGAG
151 CATCCTCCCA CTGCTAATAT TGCTGAGCGG GGCGTTTGCG CCAATCGGGA
201 TTGCGCTGAT CATCAGTGCA AACAACGTGC AGAACCTGGT GATCGACTAC
25 251 AGCCAGTGCG GCAAGCACGC CACGTCCGAA TACACGCCCA TCCCCGAGAA
301 CCTGGTGAGC TACCACTTCC GGACGTCCAT GTCCGAACAG CCTAAGTGGC
351 GGCTGCATTG CAAGAATGAG TGCGAGCTAG AATTTGAGAT CCCCCAACGAC
401 ATATCGAGCT CGGTGTACAT ATACTACAAG CTGACGAACT TCTACCAGAA
30 451 CCACCGCAAG TACGTGCAGT CCTTCGACCT CGACCACTT AAGGGCAAGG
501 CTGTTGCACC AGACAAGCTG TCCGACACGT GCCACCCGCT CTCGACTAAG
551 GACGGCAAGG CTGTCTATCC CTGCGGCCTG ATCGCCAACT CAATGTTCAA
601 CGACACCTTC ACGCCGGTCC TCCGGGGTGT CCAACGGCGT CCCCCGACTA
35 651 CAACTCAGCC AACAAGGAAC ATCGCCTGGC ACACNGACCG CAACAGGTNN
701 CAAGAAGAAC AAGCTACAAC CCGCCAGANA TNGTGCCGCC CCCCCGCCTTG
751 GCACGAACGT TTCCCCCNAA TGGNTANNAC AANCCAACCT GCCTGACTNN
801 CTACTTGGGA GAATTTCCCG TTTTGGANTG NNCCCTGCAG NCTGCCNCCT
40 851 NNTAAANCTN CNTNCAAAAA AAAAGCAACN CCCTCCCN

1356RP

	GATCTACATA	TGCATCAAAA	CATGTGCCTT	CATGCCGATC	AGTAGTTATG	TTTGCGCTGA	60
	GAGGCGAGCC	ATTTCCAGCT	TGTCTGCACA	ACTCCATATC	ATTTGCATCA	TCAACCTCAT	120
5	TATCGCTATC	ACCATCCTTA	GTCGAGTATG	GAAAGGAGGG	TGACACAGCA	AGGCCAGAGG	180
	TATCAGTTGA	AGACATATCT	GTGCTCATGC	GGTGGGCCGC	ATCATAGTCC	GATGACTTCG	240
	TGGAGGATTT	AAAGTCATTG	TGCGGAGGAT	TCTGTGGCTC	TACTGACCTT	GCAGATTTCGT	300
	TTTCACTTTC	GTACAGAATG	GACTCATCTT	CGAACCTGAG	ATCTATCCGT	TTGTGATCAT	360
	ACGCGACTCT	TTTTTCAACC	TTCTTTGTCTG	TCATTGGCAC	GGAGTTTATC	AAGCTAGAGC	420
	CCAAGGAATG	CTGCTTATCA	AAGTTCTTCT	TAGCCATGGG	CATTTTCGTAT	CTATCATCTA	480
10	TCCCTTCGTT	CGAACCATAC	TTACCTGGT	AGCCATACTT	TGTATTATAA	TAAGAGTTGC	540
	GATAATGCTT	CGTACCAGAA	CTACCGGCAC	TGCTAGACTC	CAATATGGCT	TGGATGAGGA	600
	CTGCGCACGC	GAAGTTTACT	GCCATCCATA	TCAATTTGGG	CNTGGCTGCC	ACATTTCGAAA	660
	ANANTAAGAA	GAAGTACGAC	TAATCCTCCA	CTNGCTACCC	CGTCCNTAGC	AGCGAACC GG	720
	CTGCTGTCTN	NCNCATCCAC	CCCCGTGCTT	GCTTAGCTCC	TACNCCCNTG	TGGTTCCATA	780
	ACCCACCCCG	TGTCACCCCA	TCCCCTGANC	ATTNTGAGAG	ANN		
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1356UP

	GATCTGAACC	ATATTACCAA	AACCAAACAA	AGAATTTCGGG	CCCAAGCGAC	CCGTCCGCGC	60
	GTAAAGCCCT	ATAACCAGCT	TACGCGTCTG	TGGGCGCCAT	AGAAATTTGC	ATTTTCAACG	120
20	GAACCAACAC	GTCAATCCCA	AAC TACACTT	ATCATGCCCTT	AAAAGGGATT	ATCTTTTCTA	180
	ACGAGGAGGC	CCGCTTGGC	AGTAGGAAGC	GGATCTTAGC	GGCGTCCGGC	CGGCACATTC	240
	GGCCGTTGGA	CTGCAATATC	CTACTTCTGC	AGCGGAAGAT	AGCGCACGAA	AATCTGCGGC	300
	GGAGCAAGCT	CAGAATTATA	TGTAGGACCA	AACATTGTCA	GCAACGCCCTG	CGCCGAGTTC	360
	TGTTATCGAG	TAGGGGGATT	TCCTGCGAAT	GCCGTTCCCTT	TTTATCGTTT	CTTTTTTTGAG	420
	GGGCATCTGC	AGAAGCGATG	AGGTCCAAG	CATCTTGTG	CATCGATCAC	CGAGCCCACA	480
25	GGGCAGTTAG	AGTAAAGCCT	AGTCACCATG	TGTTAGTTG	ATAATAGCCG	CGGAGGCGCA	540
	TTCGCATACT	ACGCGGGTAA	GCTGCGAAAC	AAGGTAGCGA	CGCGGCGCGG	GC'TTTTAGGC	600
	GACTACGACT	ACAAGTACCT	GTTACGCGCG	CAGATATTCA	AGCGCCAGAG	AAGCTTCAGC	660
	CATTTTCTCG	ATCNATGCAA	AATCCCCGGT	GGTGC'TTGGG	TGGCNTTTGG	GGNTNCACNC	720
	CCCNNGCAAN	NCTGGCGGNT	TNNTTNCNCC	NCCAA'TNNTG	AATACCGGNG	GNGGGAANTT	780
30	TGAAAGNNAA	NCCNACATNC	TTATTGGGCT	TNCCNGNTGT	NGAACGGGGC	TTCNTNNAAG	840
	GNGNAATANN	CCCTTGNGAA	TCCTTAANAA	AAT			

1357RP

	GATCCCAGCG	AGGACATCGA	AGAGGGACTA	CTGTACCGCA	TGGACAAGCT	TCGCTGCCGA	60
	TTGATGAGCG	AAGACCGAGA	TGAAATGACA	GATGGCGGGA	CCGTCCGGGAG	CGTGATCTGG	120
	AAGGAAATGT	TTTCTGCCGT	CGGTATGGTG	TCCAGGCTCA	TGGTAGTACC	TGCATGATTC	180
	TGTCTTTCCG	TGATCGGCTT	CATGGTGGGC	GTTAGCGACT	TATAATAGTC	GGTGC CGGTT	240
	GCTGGCGCAA	GCAGCTGGCA	TGCAGTGTG	TCCGACAAAT	AGGAGTACCG	GTTGGTGTTC	300
	TTATTTCGTG	TGTTGTGAGA	AATGTTTGCA	AAGGAAATAGA	AACCA'TTTTC	CATGGTGGTC	360
40	GAGGGGACTT	GCGAGTTCTG	TGCGGGTGTC	TGCGCGACAT	GACATTTTCAT	TTCTTGTTC	420
	GCGCCCGCTT	CCGAGGAAA	ATGCGGGCGC	TGTGCCGCCA	TGTCCCTTTC	CTGCTTGTGT	480
	CCGTCTGTG	CCATCTCCCC	TAGGGGCTTG	CCCTGAAGAG	TTTCAAAGCT	TTTGAAC TTC	540
	AAGGAGGGCG	ACGCCGGGCC	CACGAAACGA	TATCGCTTTA	CTCCTCCTCA	GC'TTCCCGAT	600
	AGGCATCTCN	ATGCCATTTT	ATTAATATAT	TTCCCCCGTC	CGAACCCCAA	ATGTATGTCT	660
	CCCGGTTGGC	AAGGGATTCC	GACTTATATA	TTATTTGATG	TCCACCACAG	GTTTCCNAAA	720
45	TATTATACAT	CNATTGCCNA	ACCTCCCCNT	TATNCATCAT	CCGACCCNCN	CNCATTTGTA	780
	CNCACTAACN	TGCACATNNC	CCNATNTNNT	AACCCATCAA	CNCACCTTNC	CTGCCCATCT	840

1357UP

	GATCCTCGCG	TTCCCATGCA	ATTGTGTTGC	TTCCGTTGAC	CCGATATGAC	CTCAAAACCG	60
	GGTCCGAAGC	CACCAGCACC	TTGTCGCTAT	GTGACTTAGC	CGGCTCAGAG	AGAGCAGTGA	120
	CACAGATAGT	ACGCCGGAAG	GAGGGTGCCT	TCATCAACAA	GTCATTGCTA	GCGCTTGGAA	180
	CGGTCAATAGC	CAAACTTAGC	ATGTTGGGAA	GCCAGGCCAA	TGGCCTGCAG	CCGTCTCCCG	240
55	CAGCCGGCCA	CATACCGTAC	CGTGACTCAA	AGTTGACCCG	CATCCTTCAG	CCAGCATTGA	300

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	CAGGAGACAG	TATCATTACG	ACCATCTGCA	CCATCGATTC	GAAAGCCGAG	TCCTCAACCG	360
	AAACGACCAA	TACCGTCCGC	TTCGCGTCTC	GCGCCAAGAA	TATCGCCCTC	AACGTGCGCA	420
	AGAATGAAAT	GGACTCGCAC	GCCGAGAAAG	ACACCATCAT	CCAGAACTTG	CGCAAGCAGC	480
	TTGACGAGCA	GCACGAGACC	ATTGTGATGC	TCCGGCGCAG	TGCTGCAGCG	CCTAGCGGCA	540
5	ACGGCTCGAC	CAGCCCGCTG	GACAGCCCTG	GCGTCGGCGG	CACCCAGCTT	TGAGCGAGCG	600
	CACGCCACAA	CATTGGAAAA	AAGGNTTGCT	AAAGGTNGAA	AACAGCATCC	TCCAAGAAGA	660
	ANCTCCGAGC	CATTGCGAAA	AAGCNTCTCG	AANNAGGAAA	TGATGTCCTC	CGAAGAACCG	720
	CANTTTCNCA	NATTCTTNAA	ATCTCCCCCT	TGGAAATCCC	CCCGTCCCCC	CAAAACCAGG	780
	NTNCAGGGGT	TGATTTCCNC	NGCCCCATTA	CCGNNTTACT	TTCAAAANTA	AATNCACNCC	840
	CCCAGGNCCN	NGAAAAATNCN	TTCCCCCCCCN	TNTGGNGTTC	ACCGCCNA		
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1359RP

	GATCCATGTT	TATTCACCCC	GCTCACTCGC	GTAAACGATG	CTTTACGTTG	CTCACATCGC	60
	CGCCACCATT	AACAGCGTAT	CACATTTTAC	GTTTCCGTTG	AGCAAAAAGT	CGGTCCGAAC	120
5	ATAATGCTCC	AATACCACGA	TAGGTCCGCG	CAAGCGCCTA	ACACGTGCCA	TCCTGCTCGC	180
	CTCCCCACGG	GCCGCTCGCG	CTGTGCTGGA	TGAAACTCCC	CTCCAGCGTA	TGAGCGGACG	240
	GGCAATTCGCC	CTGCCATTAC	TGCACGCCCC	ACCGACAGGT	TTCCCATGTC	AGCATCGACG	300
	GCAAACCCGC	AGAAATCGAT	AAGTAGCAGG	ACACGCGTCA	GAAAGACCAG	TGTGGTATCA	360
	TGGCGCACGA	GGAGCTAGGC	AACCTCGCTT	TTCCGCAACC	ATGCCCGGCC	GCAGGTTCTGA	420
	ACGCGGGAGC	GCCTCACCAA	GCCGGGATTG	CTAATGTCCC	TTCCGGCCAA	AGGCCGTCAC	480
10	AGCTAAAAGA	GAGGCGCCCA	CGAAGGCATA	TAGCTGGCAG	GAAACGATAC	GATTCAGCGC	540
	ACTCGCAGCG	TAAGGAACAG	GAGCATCACA	TGGAACAGTC	GCCTGTGGTN	TCCATCCCCTG	600
	AAGGTNGACA	CTAACCTGAA	AAGCGGCGGT	TGGCACTAAN	TACAAACNTT	ACCACAGTAG	660
	ATGCCNAATA	CTGCTGACAA	ACGAACTGGG	ATTNCTNACC	GGTGTGNGG	ANANAAATCT	720
	NCCAAGAACN	TTNAACNCAA	TTGGCCACTA	CCCCCTCTGA	TCCCTCTTN	ATCNCACGGT	780
	TTGGGANCCG	GNGNGCAAAG	CCCTGATGGN	ATCCCTGACN	AANTTGACT	NNT	

1359UP

	GATCGGTGTA	GTACACGGTT	TCCGGCGCCG	CTTCTGGCAG	AGCAGCTCCG	ATCACCGCGG	60
	TACCCAGAA	CTGCCCGGGC	GCGTCGCAAC	ACTAGTGCC	GCTGTGATG	CCCGCCTTCT	120
20	AGTCGTTGCC	TATTTTATTC	CTGCCGCGCA	TGTTGCCGCT	GTCACGGCGT	ATCTCGATGT	180
	GCGCGAGCAG	GACGGCTATC	TTCCGCAGAC	CGTTCCCTGTG	CATCTGGTGG	CACCACCGCA	240
	ACCGCCGCAC	GAGCTGCGTG	ATGCGCTGGA	CGCCCTGCCC	TGTGATTCCG	TTTCTGGACT	300
	ACCCGTCTGA	CAATCCGTCA	TATACATCGG	CATCCCCGAT	GCCGCCACCT	TTGTTGGTCC	360
	AGAAGAATCG	CAGCGCACTG	CTGCCGTCAT	CGCGCACAAT	CACGGGCCCA	GTGGGCCCAA	420
25	CTACGAGTAT	CTGAAGCTGC	TCCACAGCGC	GCTGCACTCA	ATAGCCGAAA	CGTTTGGCGC	480
	CCGCTTGTGC	GAGCTGGAGG	ACCATTATCT	GGACGAGCTG	CTCGAAGCGG	TCCGACCGTCT	540
	ACGGGCCCCG	GCCTGTGCCG	CGGTAGGTGC	CTGATCTTCT	GCTAAACCCA	CGCCGAAACA	600
	AAGATAGCAC	CCGCGCTCC	GGGTAGCGGC	CGGCCGTCGT	GACCAGTTGC	TAGCGTTTAC	660
	TTGCATACCC	GTATCTGCTT	TAACCGTTTG	GAAGGTTTAN	CATCATTAGT	TNNTTTGTGC	720
	GCTTTGCTGC	CCCTGCNTTG	GCAAGGGGCN	CCTATTTTAA	NTTACCNCCC	GNTTAAACGNC	780
30	NCCTGAACAA	AAATGAATTC	NTTTNGANAN	TCCCCNATTT	TNAGGATATC	CCCNNGTTGA	840
	ATTTCANAAA	CTGATTTGCC	NTTTTTNTNT	A			

1360RP

35	GATCCTTCTC	CTCCGCATTC	ACAGAATATA	TCCTCGCGGT	CATATCCTTC	GCGGTGCAAA	60
	TAATGAACCG	TGAGTCCCGC	GACCATGTGA	GCGATGTGAT	GTCGGCGAAA	TGCCCCGCGT	120
	GGACCCGGTA	GCGCACAAAA	GGCGCAAAC	GCCGCTCAGC	ACTGACCCCT	GGAGTCCGCC	180
	AAATCTGAAG	AAACCTCCCA	CATGCCAGAG	CAAAGAGCTT	ACCGTCTGTC	GAAAACTTCA	240
	CGTCGTTTAC	TTTGTCCTTA	AAGTTGAAAT	GATGTATCAC	ATTCTCTGTC	TTTATATTCA	300
	CAAGGATTGC	CCGACCGTCC	ACGTCAACCG	AAAGAAGCAG	TGTACCCTGG	GCATTGACGT	360
40	CGATCCTCCG	CTATATTCTT	TCTATGCTCA	TATTCAAAGG	TAAACGACTT	GTTACCAATC	420
	AGGTCAAACA	CCGATACCTT	GTGCGCAACG	GGCGAGAATA	GCAGCGTTCC	ATCCTCCGAA	480
	AACACCACAT	TTCCCTGTCT	GTATACAGTG	CCTAGCAGAT	TGGAAAACTT	GAAATCAGAC	540
	TTCATCGTAG	TCCAATGCCT	TGCCCTTGCTT	GATCTTTTCT	TGGTGTAGCT	CATCTCATCT	600
	CGAATTAAAT	TTTCCGTACC	ACCCAAAAAA	ACANATCCTC	CANCTGCATC	TCAAGATTAT	660
	ATATATATGT	TCGAAAAATTG	AANATCCACT	CNTCTAAATG	GTACACNGTC	ATATGAATGT	720
45	GTTTNTTTGC	TCCANTATCC	CNACCATTAC	CCACTCCAGA	ATGGGAATAT	ATGCCAGGAT	780
	NTCCGCCACT	TCACCCTGTT	TTGACANATT	TCTTGAGNTG	CTGACAGCCG	AGAAAAAAGG	840
	TCAAGGTTAT						

1360UP

50	GATCGATGCA	AACCAGGACA	ACTACTTAGA	AGAGTGCTTG	AAAATTAAAA	GTGTATTGAG	60
	TGAATTTGAA	AATGACGTAC	CGGATAAGAC	AGATATCAGA	GGAGTTCTCA	ATCCGGTTGC	120
	AATTGTGGT	TCCCGTGAAC	ATGTGTTCTC	TGAAAAAACC	GGTGTATTGG	GAGATCTCGC	180
	GGCTGAAAG	GAGCAAGTAT	TCGGAACATT	CTTTGCACGT	ACCTTTTCGT	ATATGGGTGC	240
55	AAAGTTACAC	TATGGCCATC	CTGATTTTGT	TAA TGCTATA	TTTGTCACTA	CCAGAGGTGG	300

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	TGTATCGAAA	GCTCAAAAGG	GCTTACACTT	AAGCGAAGAC	CTTTTGTGTG	GGATGAGTTC	360
	CATATTACGT	GGGGGTAGGA	TTAAGCATTG	CGAGTACACT	CAATGCGGGA	AAGGCCGTGA	420
	TTTAGGATTT	GGGTCCATTT	TGAACTTCGC	TACTAAGATT	AGTGCGGGTA	TGGGGGAGCA	480
5	AATACTCTCA	AGGGAATACT	TTTACTTGTG	TTCAAATCTC	CCACTCGACC	GTTTCTAGTT	540
	TCTACTATGC	ACATCCGGGA	TACTACTTGA	ATATGTTTCC	AATATCCCTT	CTAACCCCTT	600
	AATTANGNAA	TTTANTCCCG	NATTAATGGC	GGTCCTGGTC	AANCCNACCA	AAAATNTNNA	660
	NATTCTNTTA	ACCCCCAAAN	CTGCAAAATT	TATTGTTGCC	ATTNAACCCN	TAACCAAGGT	720
	NCCCCNTCNC	GNTTNANCNA	TCCNTNTCCC	NCCGGTNCCC	TTCCCAGTTT	TGNAAGAAAA	780
	ATTTAAAAAC	CNACNCCGGG	TTNCCCCGAA	AATGAAACTN	NTANAAGNGC	CCCCTTTCAA	840
10	ATTTTTTTTTT	C					
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1362RP

	GATCATAAGC	TATTGGGTAC	CCGTTGTAGC	CTAGCCTTAA	AATAATCGAC	ATTTTGGGAAT	60
	TTAGTTATTG	CGTGGAATA	AGGTATATAT	ATTGCTTCCA	AGTTTAAATGT	CGCTTTTAAAC	120
5	TCACTAAAT	ATGGATGTAA	ATTGTCTCAA	TTGGACTTTC	ATGTTCTATC	TATACACTAA	180
	CTGCGATGCG	ACTCATTGTG	CTTCAGTATT	CAAAACATGT	TTTATATATG	TAATATGCGG	240
	ACGTAGAAGG	CAACTAAATA	TGAGAGGCAA	CTTAGTCGCT	GTCGCTGTG	CTGTTTGAAT	300
	CGCTGGAATC	TTTTTCATAC	ATGATCTCGT	CGCCATTATC	TTCTTTTAGA	ACGCTAAGTT	360
	CCAAGTCCTT	ATGAGATTCC	TTGTTCTCTT	GAGAGACCTC	GTCATCAAAG	ATGATCTTGG	420
	TGTTGGAAC	GACAGGCAGG	TTTTCTGCTT	GCGACCTGTG	ATAGCCTTCA	CTTAGCAGTG	480
10	ACCCCTCGAG	GGACACCATT	CTGCCCGCAG	CTGTAGACATT	TTTAAACAGTA	AATTTGAGTT	540
	TTCCGTCCAG	CTGCTTACCG	TTGCCGTCAC	CCAGTGCCCT	AGAGACCGGG	CCTTGCGCAT	600
	CCCTGTGGAG	AATCGTTTCG	CTGCTCCCGT	TGGTACTCTC	TTCGTTATGA	ATAAAGTCCA	660
	ACCATCCGGA	ATGTTATTTT	CTAATGAAGC	GTTTGAACCT	CGTGATCCAN	CAACCATNTT	720
	GTTGAGGTGA	CNNTTGAAAT	CCNCCNCGA	CNATCCCNAT	TTTNGNGACA	NCCNCAATTT	780
	CCCNGCCCN	NTTAANCCAG	GNTATCTGNT	CCANTGANTA	CATCTCNCTT	T	
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1362UP

	GATCATAGCT	GCAGGCTGCC	AAGCAGACAT	GCTGACATCA	TACAGCCAAG	AGAGCAGCTA	60
20	CGCTGTCACC	GAGCTGGAAC	AGAGGCTAAA	CGAGTTTCGC	ACTAAATGTA	GAAAAAATGC	120
	AAGCCACTTT	CAGGCACTAC	TTTCACTGGT	AACTGAGATA	GACCATCCCG	ACAGCAGCCG	180
	GCTAAGTCAC	CGTACAGTAG	TCTTGACATA	CATGGAATAT	CGCTAAGGAA	GGAGGTGTAA	240
	TAGGACACAA	AATCATGAGA	AGAGTATTGG	CTTGTGCACG	ATGCCGTGGG	CACAAGATCA	300
	AATGCGTGCA	CAACAACGAG	CCACCCTGCT	CTTACTGCCA	GCACAAAGGC	ATAGCGGAGA	360
	AATGCGTGTT	ATCATTTCCG	CCCAAGAAGA	GGCGCAAGAA	GCCGGAACCTA	TACTTAGAAG	420
25	GGGTTGGCAT	GGCGCTGGGC	GGGTATCCGG	TGCAGCAGTT	GGAAACTGCA	GATCTGCACG	480
	AGCATAAAGC	CAGAGCGGAC	GGCTCTGATG	AAAGCCAAGC	TCCTGTGCAT	GCGCAGGACT	540
	ATACGATCGG	GAGCAAGCTG	CGCAGATGTA	CGAGCTGGCC	AGCAGATGTA	CTACGGCTGC	600
	CCAGGCGTAC	TCGACGGTTA	TGTCGAGTAG	TGCGAAGGTT	CCCAGGCGGG	TTGATTCTCC	660
	CGCCAATTGC	CACCCGGATT	CTAAACCGAA	ANAATGCAAC	NCATGGAACC	NGCCNTACTT	720
	TNTTGGACTG	CCCCCAGTGC	CCNATGCATN	GTGCACTTGC	ATNGAGANNT	TGTCATCCTT	780
30	CCCCACTGCG	NTGTTTANAT	GANACCNCCC	AAGAATACCC	CCTGACCGTC	TTTGGTTCTT	840
	TTTGCCCCCC	NCCT					

1363RP

35	GATCATTATC	AGCATTAATC	TTCAACTCCG	CATTGCCTCT	TAAACCAATA	ACAAAACCGG	60
	CAGATTTGCC	TCCAATTGCG	TAAGGATCCT	TTAACCCCTT	GAGGGATACT	TCAAAAGGCC	120
	CTTCACTAGG	CCAGCGAATA	TTAATCTTGG	CATGGAACAT	ATTCTTAATT	TTATCCCAGA	180
	AGCCTATTTT	CTTGGATGGA	TCAACTGGAG	GTTTCGAAAA	ATTGTCFAAA	CAATTCATGG	240
	CCTGTTGTAT	AGCAGCTTCA	TAAGAGCCAC	CCCATGTCAC	CATCGTGATG	TCTTTCGAGT	300
	GTATATCCAT	TGTTACCTGA	CTGTAAATTT	TAATAGGCGT	TAAAGACCGG	CGGAAGCGCA	360
40	ACGAATAATA	TAGGCTCTAT	TCAGAAGAAG	TAACGGAAGG	AACAAGCGGC	ACAAATATCG	420
	TTCGTAGCTC	CTTGGTTGAT	TGAATCATAT	CCTCCAGTAA	TAAAGAGGTC	ACCATACAAA	480
	TGTATAGCCG	GAAAAGAACC	TTGTTGGGAA	GGCATAGCTT	CGGCATATGG	ACTAACGGTA	540
	GTNGGGTTAA	CCTTNAAANA	GCCCCCTTAA	TTCACCCAN	TTGGCTTCCA	ATNTAAAAGG	600
	GAAGCCNCCA	NTTATTTCTG	GTTANTTTTG	GAACCCCNNT	TNCCCNCAAN	TTTAATNAAT	660
45	TCNCNNTTTT	ACCCCTTCCA	CATNANGGCT	TAAANTNNCA	TGTTTTTACCC	CCCCNGCCAA	720
	GANNNTCCNCC	ATTTTGGA	TGTTANANTC	CANACCCCTT	TTNCATNTTN	NAGGANCTTC	780
	AACGTGCNT	TTNCCCCAAA	AANTTAATCC	CCCNAAAAAT	TCTTTCCTCC	TGGGGNTTTT	840
	CCCCCTTAC	CNT					

1363UP

50	GATCGAGGAT	ATTTCCGTAC	GCTGGATGTC	GCTCGATGTC	AAGTACATGG	GTGATCGGTT	60
	GGCCTTTTCA	GTGTCGCTTC	AAAAATC	GCACAATAAG	GTCTGTCTGC	TGAAGTCTGG	120
	TGCGCTCGAG	GTTCTCGGCT	GTTTCACAAA	AGACAGTCCC	TTTGGACTAA	CATGTGTTGA	180
	ACTGAGTGTC	AAGTTTCTTC	AATCACAGT	GCTGTGAGT	AACCTACTAG	CACTATTTAC	240
55	CTTGGGCAAA	GAAGAAGATG	AGGACGTCGA	AGGCTTTGCT	CGTAATATTT	TCGATGGCAT	300

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	GACCGAAGAT	CCACAACCTGA	ATGCACAGAA	TTGTGTGGAG	ATGATGAGAT	CAAGAGTTAC	360
	CACGTTGCAT	AGCTACTTTT	CCCATCTAAC	TAAGGTTGAT	TTTTTTGTTG	ATAAGGTTAA	420
	CCTGGCAGAT	ATACCACCCA	GCTTATTGCC	TGAGTTGTCA	TCTGCCTGTG	AGCCTTTGAA	480
5	ATACGAAGTT	GCGCTTTCTA	GTTTTACTTT	TCAAGTCACC	CGTTTTAGCA	CCCGAACAGC	540
	CAGGTATAGT	ATCCTTTTCA	AAAGTCTGAT	AGACCGTAGG	GTCCGTATCA	CATTGTCATC	600
	GTTGCAGTGC	GCTCTCAGTT	AATGCCCTA	AAATCCCCCT	GAAAAGGCTC	CTGAATACAT	660
	CCGGTTTTTG	AAGTTCCCAN	TTATATCCAT	ATGGTGANAC	TATACTTTTC	CTGAAAATTT	720
	GACTGGTCCA	CGCTGTTTCT	GANACAAAGT	CAATGGTGGG	CAGTTTCTCC	CCTACCNTAA	780
	NATTGAAATG	AAACCCCCAN	CTTGAACCCC	GTTNGCAATA	CTGTANGACT	ATTTNTTCCN	840
10	CANAACCCCN	CCACGNAN					
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1364RP

	GATCAGATCG	ACGTCACGTT	CCGTGCGCTG	GGCACACCTA	CGGACAAGGA	CTGGCCTGAG	60
	GTCTCGTCC	TCAGCGCGTA	CAACAAGATC	CAGGTATACC	CGCCTCCGTC	GCGCAGCGAG	120
5	CTGCGCAGCC	GCTTCATCGC	TGCAACTGAG	AATGCCCTCG	ACCTGATGTG	CGGTATGCTG	180
	ACGATGGACC	CGCACAAACG	GTGGGACACG	ACTCGTTGCC	TGCTCAGTCA	GTATTTTGTA	240
	GAGCTTCCGG	AGGCGACACC	TCCTACGGAA	CTTCCAAAAC	TAAATAAGTA	ATGACTATGA	300
	TAACCTAGAT	GGTATACTCG	GACGTTTTGT	GTTTGTGCTT	TGAGGCGATG	ACATTGGCTT	360
	TTATGGTATC	GCAGACGTTG	CCTGAAAAAG	ATTCAACGTC	TCGGTAACAG	ATTTGCGCAG	420
	ACTACTTGTT	GAAAGAACAA	AGACCAGAGC	GCTGGGATGC	TCACCCCAAT	GACGAACCCA	480
10	CTCCGCTTTA	TTGGCGCTGG	CTGCAGGTTT	CTTAGCACCA	ACAAAGGCC	GCCACTGCAC	540
	AAGACTTTTC	CCTCCAAGAA	GCTGGTGAAC	AGGATGCTGT	TCCGACCTTG	ATAGCCGACT	600
	GACCTTCCGG	AAATTACTTG	CCTTGTATAC	GAGCAGTTGT	ACACCCAATT	AGACAGTTAT	660
	TACGGGCAAT	TTGTTATACC	CCNCGNCTTG	ANGGCNCCGA	CNTTNTATCC	TGAAAAGNTG	720
	CTNGAAAAAA	TCCCCGCNAA	NGAAAAANNCT	ATCGCCATCT	ANTTGNCTNG	AAACAACCTGC	780
	TTTACTGCTG	CCCAATNGAN	ACCAAAATCN	CGGCCGTACC	TTGACCCNT	CACCCGCTNC	840
15	CT						

1364UP

	GATCTAGTGC	TTCAACAAGCT	AGAAGCTCCA	ACCATGAAAG	AGCGATCGAT	CCTGAGAACA	60
20	CTTTTTCTGT	GGAGGCTTAT	CAATGCTCTT	TCTATCCGCA	GCTTCTTCCA	GGCAGATGAA	120
	TACTGGCAGT	CGCTGGAGCC	TGCGCATGTT	AAGGCGTTTG	GATATGGTGG	GCTGACTTGG	180
	GAGTGGCAGC	ATGGGCTGCG	CAGCTATGCA	TTCCCCGATGC	TCCTTGAAAT	GTCGTACTAT	240
	GTGGCGTGGA	TACTGGGTGT	GGCCACCCGG	ATGGCGCTGC	AGGGGTGGC	ACATGCGACG	300
	GCGCTGTGTG	GGGCGGTGGT	GCCGAGCGGC	GCGGCGGGCG	TGGCCGCGAT	GAAGGCCGTC	360
	TGGGAGCTGC	CGGAGGCAGC	GCAGGAAGTG	GTGGAGTACT	ACGGGGTATT	GTACGGGCCG	420
25	CGAGTGGTGA	TGGCGCGCGT	AGCAGCGTGC	GGGGAGTTCT	ACAGCGTGCT	GCTGGTGCAG	480
	AAGCTGTATC	TGCGAGTCGC	GGATAAGGGG	GACGACCCAG	AAGGGCGACG	CGGCGCCGGT	540
	CAGCCGGTTG	GCGCTGAATG	CTGACCATGA	CAAACCTCTT	CAACTGTTTC	TTCCGGAACG	600
	CAACGTTTAT	CACTCCTNCA	AAATAACCCC	CACNGCGNTC	CCCTCTAACC	NATTTGGATT	660
	GGANCCGGGG	CCCANCTTTG	GTTCTCNTGG	GCTTCCACCN	CAACTTTNGC	GGTGGCTGCN	720
	TTTGCTTGCC	CTGCACGGCC	NATACTTTTT	ATCTTGGCCT	CCCTGCCTGT	TCTTGTGCCA	780
30	ACCTGTTGCC	CACCAAAGGT	GCACTCNNTT	ANCCTGTCCC	TAGGTTGCCC	CGNGCCCCGC	840
	GGGTTTTTCN	ATACCANTNA	NACNCTCCT				

1365RP

35	GATCTGCGGC	CGGCGGAAGA	CGCAGAGGAA	AGCGAATCGA	GCGCGGGAGA	GCGCTACTCG	60
	ACGGACAAAA	GCAGTTACGC	GTCTTCCGTG	CAGGCGGTGC	TCAGAGCGAG	GACAGCGTCG	120
	GCAGCCAGCG	CAGATACAGC	AATGAGCAGT	TCAACGGCAG	CCAGCGATAG	CGCGGGCGGC	180
	GCTAAGATGG	ATGCAGCCGA	CGCAGATGAC	GCGACGCGCA	GCTTGGAGCT	GCGGCTTGCA	240
	GCCCTCGCCA	CGCAGGACCC	GGCTGTGGAC	AGCGCAGACA	CGGCGAGCGG	CGCGTCGCCG	300
	GCGTCCGCCG	CCGCGCCGCC	CAGCCCGGCC	CCCANCGCGG	CGACGGAGGG	GTCGGACGAG	360
40	GCGGCCGCGC	CGCTGGAGGT	GCCCAAGCAG	CGCGGCGACG	CGGGCACGGC	GGCCGGCGGC	420
	GAGCCGGTGC	GGCGGCGGCC	CACCAACCCC	TTCCGCGTGA	TTTCGGTCCG	CGGCTCCAGC	480
	ACGTTCAAGC	GCGCGGCGGG	CGCGGACGGG	CAGGCGTCGC	GCACGTCTGC	CGCGGGCGAC	540
	AAGGCCGCAC	CCGTGTCCGC	GAACGAGCAG	AGCATGCTCA	AGTTGCCGCG	CNAGCNCANC	600
	TACCTTGACC	ATGAATTCNT	CNACTGTICA	AAGANATTAA	TTTCCTGANA	ACNTGAANAA	660
	ANCGGTCCCT	GTNCTTGAAG	AAANCCCCNN	ANTAACNACC	CCCTNGACAG	CTCNGATTTC	720
45	CTCCNCCTTA	TTNTAAAAAA	TTTCAAATNC	GGGTGGTNCT	TCCCCCNCTN	CCCAACNTTT	780
	TAAAANGTTC	CCACGGCNTN	NTGNCCCN	NATTTGGCCC	CCCGTTCCNT	TNCCCNNGT	

1365UP

50	GATCACGTGA	CGTTTATGGA	GCGTGCAGCA	CTGCACGACA	GCGAAGCGGT	GGTGCAGCGC	60
	ACGCGGCGGG	CGGCCGTGCA	GCTGTATGTG	GGGCGCGGGG	GCGGGCTGCG	GGGGCGCCTG	120
	GCGGAGGCGC	TGGACGAGTT	GCTGGGCGGA	CCCTTAGCGG	CGAGCCCACT	GCGGCGGGCG	180
	TGGGATGTGT	ACTTTATGCA	GCTGGCGCGG	CTCGCGGCCT	CCCGTTCCAA	CTGCATGAAG	240
	CGGCGTGTCT	GGTGCCTGAT	TGTGCGCGCC	TGCCCGCTCA	TTGCCACCGG	GTATAATGGG	300

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	ACGCCGCGCC	ACTTGCGCAA	TTGCCACGAC	GGCGGGTGCG	CGCGCTGCAA	CGGCGGCGGC	360
	AGTGCGCTGC	ACACCTGTCT	CTGCTTACAC	GCGGAGGAGA	ATGCGTTACT	GGAGGCCGGG	420
	CGGGAGCGCG	TGGGCGAGGG	CGCGGTGCTG	TACTGCGACA	CCTGTCCGTG	TTTGACATGT	480
5	TCGGTGAAGA	TCGTTCAGAC	GGGGATCACG	GAGGTGGTTT	ACTCGCAGAC	CTACCGGATG	540
	GACAGCGACA	GCTTCAAGGT	ACTGCGGGCG	GGCGGCGTCA	GGTCCCCGGCA	GCTACAGGAC	600
	GCGTTCCCCC	GCACTTTTTA	TTATATNNGC	NGGCNGCTTT	CCCNGCAACN	GCTAAACTTG	660
	CTGTTTTTNC	ATATAAGGNC	CCGGCGGTNC	CGACTNCAAA	GNAATNCCNC	AACCNITCTT	720
	TNTTCCGAG	GCNGGGGAAT	TTTCCCCGGA	TNTNNGGCC	CCCCCGTNN	TGCCGTTACC	780
	CANTTCCCCT	GCCCAATCCT	CCCCGCGAAN	CCNCCNCCAA	CCGTCTCGNN	TTNCTCCACC	840
10	CGNCCTGNCC	T					
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1366RP

	GATCCAACGG	TCAACCAATG	CCTCCGAGAT	TGCCGGCATA	GCGGATGAGA	TTGCCAAAGC	60
	GGAGAAGCAG	GACAGCTCCG	CGGCGGTGTC	TGCCATGGGT	GCCGTCTTAG	GGCATGCAGC	120
5	GAGTCCTTTC	GGTGCTTTGA	ACGTGCTTAA	CAGTTCTGCC	GAGCTCTTGA	ACCAGCCGGG	180
	AGCAAAGCCT	GCTGCCGGTG	CTCTCAAGGG	CATGATGGAG	GCTGCGTCTA	ACACGACTAA	240
	GGCAATTGAC	TTCATCATGG	AGCGTGCAAG	TCATCCAAAG	GCTGGCGCGG	CAGAGCAGGT	300
	GATGGGTCTA	GATATGGTAC	TCCAGAATGC	CGTGAACCTCA	AGCGAAACCT	TTGCAAAATAT	360
	CATAAAAATG	CAGATGGCAT	CGACCGAGGA	GTCGCAGAAAG	GCCCTCCCAA	GTTTGTGTGGG	420
	CTTGTTGTCTG	TACTCGACTG	ACAAGATCGA	GAGCATGAAA	TCCGTGATTA	AGCTGATAGA	480
10	GTTCCGGTGAA	AAGAGCCCTG	ATGTATTGAA	TCCTGTCCTA	GAAGTGCTGC	AAGCTTCCGT	540
	GAAGGTCAAC	AGATTGATAC	CCTCCGAAAG	AATTTTNGAC	TTACACCCAC	ATCCTGGAAA	600
	CTTCATNTTT	GCTGCGAGTT	ACAAACTGGC	ATTTCCCAAT	CTGCCATTTG	TTCCCTTAAC	660
	GGNCCCCAAA	GGTTTGACA	CCNCNNTCCT	NCAGGNTTCA	ATNCCTACTC	CTNTNNCCNA	720
	CCNANGAATC	CNNTTGGCCC	TTNTTTAANN	CAAATCNGNC	CANATNTACC	CCCAGGTTTT	780
	TTTGTGGAAN	CCCTTTTANA	CCTTTCCCCC	CCTCCCTTTN	NAT		

1366UP

	GATCTTATCA	GGATAAATGA	TTTGCTCCCC	GAAAGTCGAT	AAATTGCTCA	TATATGCCCT	60
	CTGGGGGAGA	TAATATATCG	GACTTTTCGCC	ATTTTCAGCA	TTTCTACGCG	GCATGATTAG	120
20	CTTCGTAGGC	TTCTTAGGGT	TAGTAAACGA	TTGCAAAACA	GGCCACAACC	CCCCAAGGAC	180
	CCTGAAAAGA	GAAGACTTGC	CGCAGCCATT	AGGACCTATA	ATCAATAGAT	GGTTACCATG	240
	CTTCAACTCG	AAGTTAAGTT	CGGGGATAAG	GACCTGATTA	GCAGGTGTCA	CTAGTGGAAC	300
	ATGAACGAAT	TGAATCTTAG	AATCGTCGTA	TTCTATAATG	ACCTTTTPTCC	CATCAGTCTT	360
	CGAACTACTT	CCAGCGTCTA	GCCTGTCAAT	GAAATTTGTT	AACCGTAGGG	CCTCTCCCTT	420
	TAGCTGCTGG	ATACTACGGC	GCAGTTTCGAC	ATAGCGGCCA	ATAGATGCGG	ACGCAGTTAG	480
25	CAGTAAACGT	CTGTTGGTGA	TAAAATCAGC	GGTGACATCC	TCAGCCATAT	TAGAACGAAA	540
	GAAGACGGGG	ATAGAGCATA	ATATCAAGCC	CAGCAGCGCC	CCAGACGTAC	TTCAACCAAA	600
	AGCTAGTACA	ATTCTGTACAG	TGCTCTTAAA	TTTATCTCCC	CCGGCTNAGA	ATAAGTTACT	660
	GGTTANAAAN	AAAAACCCAA	TCCCATATTC	GGTNTTTGAC	CNTGAATAAA	CNNTNCCNCN	720
	TTGCTTGACC	NCACTTGAAT	TTATGACCGA	ATTACCNCCA	TTTTCCCCCTG	ACATACCGTT	780
30	CAATTGNNNG	TTTGACCTCC	CACTNATTAT	GATTNAAATC	AACCCATCCN	GTCCTTCNGC	840
	TTTCCCTGNN	GATC					

1367RP

	GGATCCGCCC	CCGTTGCCCC	CGTGTGGCCC	CGTGCCCGCC	GCCAGGGCCT	GCGCCGCGCG	60
35	CAGGCCCACC	GCGCCTCCGC	CGTGTGCCCC	TAGCGGATTG	TTCAATCCCT	GTGTTGCCCT	120
	CTGACTGTCC	ACTCGACCTC	TTGTATCCGC	ACCTTTCTGC	CAAGTGCGCC	CCAAACTCTG	180
	TTTTCTGTCT	TGTCCAGAGT	TTCCGTCTCT	GGCTGCGCTA	CTGCCTACCT	GCCGTTTGGT	240
	ATGGAGGAGA	AGTGTGTGTG	TATCTGATTT	GTTTATCTGC	TTTCCTTCTC	CTATAAGCTT	300
	TTTGTAATGA	AAAAAATTAT	GAAAACGGGA	AATCTGTGGA	ATTTGGAAAT	GCTGCTGGCG	360
	CTGCGTTGTT	CAACTTCCAG	CGCCGCCGTC	TCGTTCTACT	GCTCTGTTCT	TGGTCTAGCT	420
40	TTCCGTTATTT	TTTCTGCTCG	GTTTTCGCTTC	TTTTTTCTGC	AACGCAAGGG	CGCGCTGCGT	480
	GCCTGAGGTG	CCAGGTGGCT	GCACAAGTGC	GGGCGCCCGG	GAACCGAGCC	GGGTAGTTAC	540
	CGGGCAACTC	TGCCGCCGAT	CCCTTGCGGA	GGCTTACGGC	AGCGCTTATT	TAATTGTTAC	600
	GTAAGTCACG	TGGAGCTAGC	ACGTGCTTGG	CAGCTCAGCC	GCACGTCACG	TAGCGTGTGA	660
	CTAATCGCGG	CGACCTGGTG	GGTTAAANGA	CGGGTTACNC	CGTTAAGTTG	GAAACGCNCC	720
	AATAAATTAC	NTACCCNTTA	AACACACGGG	ANAAAAANAN	NCCCGGCNCA	NAAGNANCTT	780
45	TTGCCCTTGA	AGCCCGGTGC	CCCAAGCCCC	GNCNCCCCA	GAAN		

1367UP

	GATCTTATGG	GTGGTTCTCT	AGGGCTGAAA	GGCGGATATG	GACAGTCGAA	ATGGGCAGCA	60
50	GAATTTATTA	TAAAACGTGC	AGGTGAGCGT	GGGTTACGCG	GTTGTATATT	GAGGCCAGGC	120
	TATGTGACTG	GTTCCCTTTC	TACAGGAGCT	TCTAACGCGG	ATGACTTTCT	GCTCCGGTTC	180
	CTACGGGGAT	GTGTTCAATT	AGGCAAAATT	CCTGATATTG	AAGGAACTGT	TAATATGGTA	240
	CCAGTTGATT	ATTGCAACG	GTTAGCAACA	GCGGCTTCCT	TCTCGTCATC	AGGCAATACA	300
	CATATGATGG	TTGTAAATGT	CAATGCGAAA	CCAAGAATAT	CATTCAGGGA	CTATCTACTA	360

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	GCACTGAAGG	AATACGGGTA	CCAGGTAACA	TCAGTTCCTT	ATGACGAGTG	GAGTAAGGCG	420
	CTTGAATCGT	CGAGTGATGA	AGAAAATCCT	TTGTATCCGC	TATTGTACCT	TGTCCTAGAT	480
	GACTTGCCCTA	AAAAC TGCGC	AGTCCTGAAC	TCGATACTAC	TAATGCGAAA	TTTGTTTTAG	540
	AAGAAGATTT	TGCGCGGACG	AATATTGAGC	CAATTATCAT	TACTTCGGTG	TCATTAGAGT	600
5	TGTGGGTCCC	CATATCTCAT	TTTTGCATAA	TTTAGCTCCC	NANAANAACC	ACCTAAAGTT	660
	CCCAGCCCCT	GCCNATATTC	NCTCTCCCGA	CGAACAAATT	CCTTAATANC	NCATACCNCT	720
	GCNCCGAACA	TACANCAACC	CNTAAATACC	NCAAATTGTN	GACAACATGA	NTGTTTATTT	780
	TTTTTATATT	ACAACCTATT	ATTAACCAAA	TTNTNATCAC	GATCNTCTNT	GACGCCCTCT	840
	CTGACAAATT						
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1368RP

	GATCATCTGA	AGTAATATAG	AATCTGCATG	GGCGCAAACC	GTTGCGGTCC	AATGTAGCGC	60
	CGGTGTAGCG	GCCATCGGTA	AAGGTGAGCA	ACGCAGGGCC	ATCCCATGGT	TCCATCAAAC	120
5	AGGCGGCCCA	GTCAAACCAA	GCCTTCAGGT	TAGAATCCAT	GTCTTGTGG	TAGGCTTCTG	180
	GAACCATCAA	GCACATCGCT	TCGGGTAATG	ACAGAACACC	ATTTATCACT	AGTAATTCTA	240
	GCACATTGTC	CAGCGCGGCA	GAGTCGGATC	CGCCTTCTTC	GATAATCGGA	TAAAGCTTCT	300
	CCAGTTGGTC	TTGGAAAACG	GCGGATGCCA	TGACACCTTC	CTTCGCACGC	ATCCAGTTTT	360
	TGTTGCCCTCT	TAGGGTATTA	ATTTACCGT	TGTGTGCAAG	CCAGCGCAGA	GGCTGGGCAC	420
	GGTCCCAAGA	TGGGAATGTA	TTGGTTGGAG	AAACGAGAGT	GTACCAGCGC	CAGGTGAGAC	480
10	TTGAAATGAG	CATTTGGTCAA	GTCGTGGTAA	TAATTATACA	CCTGGCAGGG	TCAATTGACC	540
	TTTGTACACA	ATTGTCCGGT	TATTTAGGAG	CACACAGTTA	ACAGTTCTGA	TACCGATGGC	600
	CGTTAAACCC	NNCTTTCTTT	AAATNTTAAA	CTGGCATCCN	GAAGTCTCTC	GTNATTANCC	660
	TGAATCTNCN	CCCGATACTC	CTGCCCATAT	TTCTTTTCNCN	CAACAACGTT	TTTGAAATGG	720
	TTTCCCAAAA	CCAAGGAACC	NAAAGAAATN	CTNTGGACNC	CTCCAACCCN	AACCCNNATT	780
	TAACAATCGG	TACTNGCCAA	TTTNTTCAAG	CNNAACCTGT	NNNCT		
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1368UP

	GATCGTGACG	ACTTTGTGTT	TTACTTCAAC	CGTATTGCAA	CGATCTTGGT	TTCGCGGGCT	60
	TTGGATGACA	TTGCTATCGT	GCGGGATGAA	CTGCCATTGG	TGACTGCATC	CGGATATCAA	120
20	CTGGAGAAGC	CTGTTTCATGT	GAATTTTGAC	AAGATTACGG	CTGTGAATAT	TGTGCGCTCT	180
	GGCGACTGTT	TCATGGCTTC	CCTACGCCAA	ACAGTGCCAA	ATATATCCAT	CGGTAAATTG	240
	CTCATTTCAGT	CTGACTCTCA	AACAGGTGAG	CCGCAGTTAC	ATTGCGAGTT	CTTACCAGTG	300
	AACATTGGCG	GCTCTTTTCGA	CCAGGTCCTA	TTGATGGATG	CACAAATAAT	CTCAGGCGCA	360
	GCAATTATCA	TGGCTATTCA	AGTGCTAGTT	GACCATGGTG	TTGAACTATC	AAAAATAAAG	420
	GTTATTGTCT	ACTTAGCCAC	TGAAATTGGA	ATAAGAAGGA	TAATAAATGC	CTTTAACAAC	480
25	AAAGTATCAT	ATATGCGGGC	GAAATTATAT	CAGACGAAAG	TATGACAGAT	GGCCAATGTA	540
	CTGGGCGAGG	GTGAGATTCA	TCGACTCAAG	ATACTTTGGC	TGTGACTGAT	TCAGAGCTTT	600
	TGCTGCCCCAN	GCAGGAATTA	ANAACTTTTG	GTGCTATTGC	ATGTTACAAT	ATTAGCATTT	660
	ATCATCCATA	CCATAGCTGC	TTTACNATAG	CATNTAATTT	TACTATCTTT	NAACCCACCC	720
	AGACTATTTT	TCCCCCNCNTA	CTTTACNAAN	ANTTTAANCA	ACTGACCCCC	CGNTATAAAT	780
	GCCCATCCAA	CACCCCCCNC	CTCNTAANAA	ANACCNACTT	GGAACGAGTG	GGAACCNCC	
30							

1369RP

	GATCGCCTAC	TTGTCTCAGG	AACTTGTATT	CATGAGAGAT	GATATGTGCA	ACAGGTTTAA	60
	GCGCAATAGC	ATTATTTTCC	CAACAGTGGA	AGAGGAACAG	AAACAGGAAT	ACATGCTGTT	120
35	ACAGCAGGAG	CTCCAGGATG	ATGAACGTAG	TTCCGATCTC	TCCATTAGTC	AACTGATTAA	180
	GTCCAGGGAC	CAATTGCCGTG	CCAGTGTTCA	GGAGTCCAGG	AAGATAGTCA	AAACCATCCT	240
	CGATCAGCAA	CACCTTTTCGC	CCTTTACCTC	GCAGGTGCGC	CCTATAACGT	GGGACTATGA	300
	CTACACGTTG	CACCTGTCCC	CAATACCCTC	CACTATGATC	ATTTGCGACC	CAACTGCACC	360
	GAAATATGAT	GTTACTTTACA	ACGGCTGCAA	GAGTATCAAT	CCAGGCTCAT	TTCTCCACAA	420
	GCGGAGCGTC	AACATATACTG	AGTACACTCC	TTCTGTTACGG	AAAGCAACAG	AGGAAGAAAT	480
40	TGTCGTGTAG	GACTTTAAAC	TTACATATAA	TGTCAAATAT	AAAGGTTTCA	GACGTCGTCA	540
	TGTTTCGTAT	GGATATTTCT	TGAACTTTTC	CCGTAATATC	GTATGGCATA	CAGTAGAGGG	600
	GGTCAATNGG	AACAACCCGN	CGTGCTTCTT	CAAACCTGGNC	CCCANNCAAT	CCCAAAAAAT	660
	TNTGGAAAAC	TTCCACCTAG	ATTTTCTGGC	CATCGCNGAT	GCCCNCCNCT	CTTTGATTCC	720
	TNCANCCCCA	GANNAATCNC	CCNCTTTCTT	GNTCATCCAT	NCCCNNTNGC	CCAATTCCNA	780
45	NCGTAAANG	CCCCCCCCNC	TTTTCAACTT	TNGGATTTTN	NTNGTTTCCG	TCGGCINNCC	840
	CCGTNCAGAC	C					

1369UP

	GATCAAGACG	AAGCAGAAGA	AGACGCGGTA	CGCATGTACG	TGCCACCTGG	TGCCGTCGGA	60
	GGCGGCCAAG	GCGATCGCTC	TGGAGCGCGA	CACGCGCCTG	GGGCTGGTAA	TATGCGTGGA	120
50	CCCGACGGTG	GACACACGGG	CGCCGCACAT	ACAGAGCATT	CTGGCGCAGC	AGCAGAGGAA	180
	GTACGGGCGC	ACGGTGCCAA	CCATCCGTGT	GGCGGTGATT	AATTCGATCG	AACATTGCGA	240
	GTGTTTTTTC	GGCAAAACGC	TCGACCGGAA	CACACGGGAC	TACCTGGTAA	ACGTGAGCGC	300
	TGCAATGGTG	GTGTTGCGCG	ATGTGGTGGG	GACCCTGCCG	CCCGACCTGA	GGCCAATATA	360
55							

EP 0 866 129 A2

	TTCGCAAAAC	CTGAGGTACC	TGATAGACTG	GTGGGATACC	CCTGAGAGGC	CATGGCCGTT	420
	GCCGGACTTC	TATCCGGTGA	AGGTATACAC	TGCAATGGAC	GTGGAGCGCT	CGCTGCTGAC	480
	CGAGGTGAAA	TACTCCCCAG	AATAATGACT	CCCTTGGAGG	ATGCGTTTTA	CCAACGGCAA	540
5	GAAACTTACC	ATAGTTCNT	GGACAAAGGA	ACCGTGGAAA	TGCGCCGATC	TCCCTACTAC	600
	CCAAATAAGC	GTTTGTGAAA	ATGACTACAT	TNGAATCCCN	CCNACCAAAA	TTGAACACTC	660
	CCCGGAANNA	NCATACNAAN	CCAAAAGTTT	GCTAAATATC	TCTTTCCNTN	GTACACTGAC	720
	CCCNACTNNT	GCAGGGAAAG	GNCTGTTTTT	AAACTTCCAC	TCNGACTTNA	TTTACCCCT	780
	CCCGCATCC	ACCNAANCAA	CACCTNTTCN	AACCATAGAA	CNNTTTTCCT	TTTAAACAC	840
	TNAGAAGCAT	TTNAAAAT					

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EP 0 866 129 A2

1370RP

	GATCTTGTAC	AACTGAGCCT	AGGTCTTGTT	GTTGAACGGT	AACCTCCACA	TTCATTATTG	60
	GCTCCAATAT	GGAGAACGCC	GAAGTTGGTA	AACTCGTCAG	TGCTGATATG	ATTAAAGGAC	120
5	GCACAGTCAG	CAGAATGGAT	GCAGCTGCTG	CGCAGTCTAG	CGGTAGCCGC	CAGCGTTTAA	180
	CATGAATCAC	ACACGAGTGT	AGAGGAAAGC	CTGCGGTTTT	ACCACCTCTT	TGCAAGCCA	240
	CTATGCAACA	CGAGATGATA	GAGTTCACGA	ATGCCTCATA	TTTCAATGGA	AATGGCCAAT	300
	TGTCTTCGTT	AAAGCGTGGG	TTTGGATCTA	TGACAAGATA	GTTATTATCG	CTTCCCAAGG	360
	GGTACCATCC	GTTACTGAAT	AGTACTTTAT	CTTCTTCATT	GTATTGCCGA	ACTTCGAGTT	420
	CGAACGAATA	TCCATCATCT	GTTTCAGAGT	GCTTCCTCTC	TGTAGCAGTA	TTAATGGTTT	480
10	CCTTGTATGA	AACTGCTACC	TTGCCTACTC	TTACAGGCGC	CTTAAATTCA	TTGAGCAGCC	540
	GTCCGCTGCT	ATTTCCAGTG	CATTCCCCCC	ATCCCATTCA	TCACTGTCTG	ACCAGTCTCC	600
	TCATCCCTCA	CNAATACCAC	NACGGTTCCC	CNCTCGTTAG	CTGCNNCANG	ATCACCCNAT	660
	ANCCTTTTNT	TCCCCAANTT	CCCCGGTCCN	NCANCGNCCT	AAAANGGTGG	NGGTANTCAT	720
	GGGTNTTTCC	CANTTGNANT	TCNGCTTTTG	AAAAACAATC	CCCTTTAAGN	TNNAAGNCNA	780
15	AANGGGTTCC	CTTCTAANTG	TGTCCCTTGT	GGCCNCNNC	CCCAATNCCG	AGAT	

1370UP

	GATCGCAGAG	GAGGAGCCCA	TTCCGACGCT	TGCATGGAAG	GAGGACACCT	TTGAGAATTT	60
	TCTGGCGGAG	GTGACATCCG	ATGAGGCGCG	CGAGACGCTG	GTTTCCGAGG	AGGATGCCGC	120
20	CACCTACCTG	GCCAAGCTTT	TATGACGGCT	GTCCGTGCTT	TTAAATTGTT	ACATACTGTA	180
	CATATTGCT	TTAGTCGTAC	CACATTTTGA	TCAGCTCTTC	GGAAACCGCG	CTGGGCGTCA	240
	GCACGCCCAG	GTCTGTGATC	AGCGCGGTAA	TGTGCTCGTG	CGAGGTGTAG	TCGATGGACG	300
	GGCTTAGCAG	CTGCTCTGAC	TCGTGCTGTC	GCGAGAAGTC	CAGCGGGTCA	CGCTCCATGG	360
	GCAAGTCGTC	GGGGGAAAGC	GGGAACATCC	TTACAAACTT	GTGCGATTTC	CTTACCACGT	420
25	AGAATGGCTT	GCGTGCGTTC	TTGGCGAGGA	CCCCTACCGT	GTACGTCCCC	ACGAGATTTA	480
	TGATGCCGCC	GGACTCGGCC	ACGCCCTCCG	CGCCAACCAG	CACCTGTCTGA	TTTGTGTAT	540
	GATGGACCCA	CCGCGCTGTC	CACGATCATC	GTCACCGGAT	GCCCTTTGCT	TGCAGCAGGT	600
	CATACAGCTG	CTTGCCCTGC	CCCGAAGGCC	CGTGCTCCGT	CACGANACAC	CGGAAGCAAT	660
	CACTCTCACC	TGTTACTCAC	ACGAAANNCG	CCCGCAAACC	AGTTCCCAAA	AAGTCTCCTC	720
	TGTTAGATCC	NCCCCATCTT	GTNCTTTTTN	TNGACGCTTG	CCCGAANCAA	AACGTCCNTT	780
30	CCNCNGTTGC	TGCTGNACCC	CCCTCCCANA	TNTTTTTTCC	CCCCCNCCC	NATTTCNTCT	840

1371RP

35	GATCGAGAAC	AACTACGACA	ACAGCCACGC	AGACGGCGCG	GAAGCGCTCA	AGCCGAGCTA	60
	TATTTTGTAG	TACCTTGCCCT	CGCTCATGTA	CCAGCGCCGC	TCAAAGCTGA	ACCCGCTCTG	120
	GAACGCCATC	ATCGTCGCCG	GCGTCGAGGA	CGGCCAGGCC	TTCTGCGTTC	ATGTGGACCT	180
	CAAGGGCGTC	AAGTACTCCG	CCCCAAGCTT	GGCTACTGGC	TTTGGCGCCC	ATATGGCCAT	240
	TCCTCTCATG	CGTAAAGTCG	CAGATGCCGA	AAAAGACGTC	GCCGGCGTCG	ACCTCTCAAT	300
	TGCGCGAGCG	ACTATCCTGG	AGTCCATGAA	GGTGTATTTC	TACCGCGATG	CGCGTAGTTC	360
40	CCGTGCGTTC	TCGCTTGCCA	TCATCGACAA	TGATGCCGGT	GTCAGCATGG	AGCAACTGGA	420
	AGTGGAAC	ATGACCTGGG	GGTTCGCCAA	GGATATTCCG	GGCTATGGCA	CCCAGAATGT	480
	CTGAGTACCG	GCGCGCAAGC	GCCGCACCTG	TATACTATCT	TGTCGCGGCT	GCTCGCCAAC	540
	CGCTGGCTAC	TCACATACAT	ATCAAGATGC	ATAATCAATC	TGCTCATGAA	CGCACCTCTG	600
	TTTTGTGGAT	ACTCTTCTCG	CGCGTATCCT	GAGTACGCTG	GAGTGCAAAA	AGAGCCACTT	660
	TGAAACAACA	CGAGTCGCAG	CTAAGGNGAN	ATCCGANTAA	NCAACNCACA	CTTCAATTGA	720
45	CTTATGAAAT	GCCCAAGGTT	GATTGAACTG	ACGTCTTTGG	AACNNTGGGN	CGTGGAACG	780
	CCCTCTTCAN	TTGAACCAAA	GTCCACAANN	AGGTATTTNT	TTNAACCGTT	CCGCC	

1371UP

50	GATCCATTGT	GCGTTTGGAG	GTCACGCCAC	GGACGTGGAC	ATGTACGTGA	TGAGCTTCGA	60
	CGGGCAGCTC	TTCAATTCGTG	CGGCACGCAA	GAAGCTTGAG	TTCCCGACGT	CTCCGCGGGA	120
	GAGTTGGGCG	TACCTTGCGT	ATTACAGCGG	ATACAAATTC	GAGCGCATGG	CGCTCCTGGA	180
	CCGTCCGGTG	GCCGAAACTC	CGCGCGAGGT	TCTGGAGAGC	CGCGGCAAAAC	AGGTGCTCCG	240
	CAACGGTCCG	CAATACAGGA	CTGTGATGAG	AACCGGCGTC	GGGGAGCACA	AGCTGGTGCT	300
55	CGGAGCTGAG	ATCGACGGCA	TCATTGACTT	CCGCGAGCCT	ACGGGCGACA	ACCTGAAGCA	360

5 CTACGTGGAG CTGAAGGTGT GTCAGAAGAA CCGGAAC TTCAGAGAAAC TTTTCTCTTC 420
 TTGGCTGCAA TGCTTTCTGG TGGGCATAAA CAGGGTTATT ATTGGATTCC GGGATGAGAA 480
 ATTCGTCTCG AAGAGCGTCG AGGAGTTCGN TACGTCAGAG ATCCCACACC TGTAAAGGG 540
 CACGGAATAT TCCAATGTAT GTGTGGACGC AATAGAGTGG TATGGTGCTC TTACGAAGTG 600
 GCTATGTGAG CTCCGCGGGG CCTGAANACA CTTCAACTGT ACAGCTCTCC NGCTCCCNTG 660
 GTGCTTACGT NTGCNCCCCT GCCCNACAAT ACTCCCNAN NGGGACNATT NTCCTGTTTG 720
 TTCCCAATT GGCGCGGGCC CNATATAANN CANATTCCNN CNTTNTTTC CTTNTGNTTT 780
 TAAAAACCN TTNTTCCAC CNATTNCCC AGANNACANA GGNNTTCCCC ACCANNCTTN 840
 CCCANCCNCA

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1372RP

15 GATCTTAAAA TAAGATAGAA TGGTAATAAA TATCATTCAG GTACAATAGA TGCTGGTGTT 60
 ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT 120
 ACAAAATATG AAAAGAAAAAT TATAAATACA AATACTGTTA CTAAATCTTT AAAAATAAAA 180
 TAACCATGCA TTGGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA 240
 TGTACATGTA ATAGCATTAAT ATGCATAATT ACTATTGCTG CAATAATAAA TGGTACTAAA 300
 TAATGAAATA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TCCTCATAAT 360
 CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA 420
 GCACCTCAAT GTGACATTTG TCCATATACT AAACAATAAC CTAAGAAAGC TGCTGCTATA 480
 GTTAAAAATA AGATAATAAC ACCAACTGTT CATACAATA CTCTAGGTGA TTTATAAGAA 540
 CCATAATATA AACCTTTACC AATATGAATA TACATACAAA TAAAGAAGAA TGAAGCACCA 600
 TTAAGATGCA TATATCTAAT TAATCAACCT AGTTGTACTC TCTCATAATA TGTTCTACTG 660
 ATGANAAAGC TAATCCATAT TANATGAATA AGCATNNCTA AAAAATACCN GTNAGAATTG 720
 AATACTAACN TAACCTATAA AACCNAATTC NTCCATATAA TGAGAAGGTG AGGGAATCAT 780
 ACNACTATAA CNATTTAATA TATTGATTCT ATTNCCATT TNTNTNAAT TTTTC

25

1372UP

30 GATCTAGAAT TATTAAGTCA ACTATTAAC TATATCTATA ATAATAATGG TTTATCATT 60
 AAATCATTA AGATAATTAT TAATAAATTA CCATTTAATA ATGATATATT ATTATCAAAA 120
 AATTATGTTA ATAAATAAAA TAAATATAAT TTACTAATTA ATAATAATTT AAATAATAAT 180
 AAAAAAGATT TAATTAATTT ATATACTTTA GATAATAAAT TATTAGATTT AAGTATTCCT 240
 AATAATATAT TATTAGGTAA ATATTTAGTA GGTAGTAATA TCCAATTAAA GGGTAGACTA 300
 TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAAGGTAC ATTTAATAAT 360
 TATATATATC AATGAAGTAA ATTAATAAAT TTATATAAAT TAAATTATAT ATCATTTAAT 420
 ATTAATAAAC TTAATAATCT ATTTATTAAT AAAAATGGTA TATTTAATAT TAAATTTAA 480
 TTAATACTA TTTAATAAAT ATTCTAAAGT AATTTCTTAT TTATTTTATA ACATTTTAAA 540
 ATGTTTATG TTAAATAGAT AATAATCAAT TAAATAATAA AAATTAAGAT GCCACAAATA 600
 ATTCCATTTT CTTTATGAAT CAATTAACCT ATGGTTTCTA TTTATTTTAC NATTTATCNC 660
 ACTACTNATG TTTTTTTACC NNTGAATTTN ANAATATATA CTCNCNANTA NATATTCNCA 720
 AATTATAATA TTAATTAAT TTAATTAATC TATTATGATC CTNNTTNTAA ANATATCAGA 780
 ANAATTTAAT ATATATATNG AAATATNTTT ATCCCCNGG NCACCTGAAN AAAANTATAG 840
 TTTCNTCCCC ACAT

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1373RP

45 GATCTTAATT TAAAATTTTA ATTAAC TATT TATAATTTAG AAATATATAA TCTAGAGATA 60
 TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAATA 120
 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA 180
 ATTTTTATTA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240
 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTAATATT 300
 AAATATACCA TTTTTATTAA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA 360
 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420
 TTTTATAATA TTTATTTTAA TTAGTCTAGT AATATCTAT TTAATAGTCT ACCCTTTAAT 480
 TGGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAAT ACTTAAATCT 540
 AATAATTTAT TATCTAAAGT ATATAAATTA ATTAATCTTT TTAATTTATA TTTAAATCAT 600
 TATAATAAGT AAATATATTA TTATTTTATT AACATAATTT TTGATAATAA TATACCATTA 660
 TTAATGGNNN TTATAANAAT TATCTTNAAG GATTTNNTGG AAANCCTTNN TTTTAGAAAT 720
 TNGGTAAANG TGNNCTAAAN NCCAATCCCN AATTATTAAA TTAATTTAAN AANAANNANC 780
 CTTTNTTNA ATTTAGTTTN AATTTAACCC NCTCCCTNT TTAANAT

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1374RP

	GATCAATGAT	AAATCGAAAT	AAACTGATAC	TATTGTAGCC	ATTTTCTGA	ATTAGCACCT	60
	GGAAACACTT	TTTAACCTGT	TCCGGAGTGG	TCTCTGACTG	ATTGGAGTTG	AGCGTCTCGC	120
5	GCGTAACTGC	CTCTGCTGTC	GTCTTAGCTC	CGACGTTTTC	CACTGCCCCG	CGCTGGGTCCG	180
	CCACACGCGT	CTTCTTCTGA	ACTGCGAGTG	GCCCCAACAT	GTGGTCCACT	AGCGTTGGTG	240
	CGCCGCCAAG	TTGCTGGAAT	AACGCACCCA	TCCTAAACCA	GTTGAACTGT	GCAAAATCTC	300
	CATACGCTTC	GAATTGCCTG	AGATAGGAGT	TGCGCTGCAT	GCTCTGGCGA	AGAGCAGCAT	360
	CCGCATGCTG	ATTGGTGCTC	TCATCTAGAG	CGTCGCTGGT	AGCATCTCCA	TCATTTTCGA	420
	TGCTGTCTGT	CTGGGTATTG	CTAGCATCGT	CTGTTTCCGG	ATACATAGAG	CCAGGTACAC	480
10	TCAAGTGATT	CAACTCAAGG	TAGTCTTCCA	GCAGAAACCG	CTTCGCCCCG	TTGACAAACT	540
	CCTCAGGGCT	CAAAAGCTTC	CCCGCATTTG	TCAGTTTTAG	ATTGCGTATA	CTCAAGCTTG	600
	CAAGTCGCTG	ACGCTCATCA	CGGCATGCGA	ATCCTGGGCA	AAAGAGAATT	GACCTCAGTT	660
	CAATCGCCCC	CCCTGCTTTA	AAAACATATT	AACTCTCCCN	CCGCNCCNAG	GANAGAATNC	720
	TCCCGTACTT	CNANGNAGNC	ANCTNTGCC	NTCATCTCAA	ATTGCGNACC	TNGTNANTTG	780
	GANCCNTTCC	CGAGCCCCCT	TGCCCCCCTA	TTGANGNTCG	NCCCCGTTCC	A	
15							

1374UP

	GATCTTAAAG	GCGGATATAA	AAGCTGTACA	AAAGAAGATG	AACAAGCTTC	CAACGCTTCT	60
	AAACTTTGAT	ACTTCCGCCA	TTGCCTTGGA	AGATGAAGGC	GAAACAAAAG	AAAGTACCGA	120
20	ATTTAGGGCT	ATTATTAAAG	AGTTTGAAAC	ACAAAATAGT	TTCCAGAAGA	TTTTATATGG	180
	GAATTAATAG	ATAAGACTAG	CATCTTTTCGA	AAACTTTATA	TAAACCAGGC	AGATTAGCTA	240
	CCTCTACAA	GTCTTCAGA	AGTCTCGTCG	ACGCTAGGAG	TCGCCTCTTT	ATCGTTGGGA	300
	AAACCACTTG	TTCCAGAACT	GTCCCAATAT	GCTCTGCCCT	GGAAATATAA	TAAGCGCGAA	360
	CATCGCCATC	GATTGTGTCT	TCGTTTATAT	CTACGTGCTC	AATAATCTCA	GGAATATAGA	420
	ACAAGGCAAG	TTGTGCAAGG	ATTCTTTCTA	GGCACTCCTT	TTCCGACGAC	CAATCTACCT	480
25	TAGTTCCCAT	TCTGTAGAGG	AAAAATGGAA	GTTTAGAAAG	AGGCGGGACA	TAATCCTTTA	540
	AAAGTAAGGG	TACACTCTTA	ATGCCAACGT	TCGTCAAATC	GGTCTCGTCT	CCACATATTT	600
	CAATCGAGTA	ATAGTTCTCT	AGCATTCTCT	CATGTCCACA	CTGTTGAGTT	ATTCCAAATA	660
	TCGAATGCGA	CGCATATATC	ATCTTAGATA	NCGTTGGTAT	ATCGCTAACT	TCCGCAATCT	720
	CAACNCANC	CTNGATATNA	TTTCCCGAAN	TTTGNNAAATN	NNNATCCCAT	TGANAAAATT	780
30	CCTTCTTAG	GACCTATCAC	CCAAATANTT	AACGCGGNTT	NANGATCCCT	GNTTGGTCAC	840
	AACNCNGGT	CTTNNN					

1375RP

35	GATCTTAATT	TAAAATTTTA	ATTAACATT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAATAAAAT	TAGTAAAATA	120
	AATAGAAAAC	CATAAGTTAA	TTGATTCATA	AAGAAAAATG	GAATTATTTG	TGGCATCTTA	180
	ATTTTTATTA	TTTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATAAA	240
	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAATTTAA	TTTTAATATT	300
	AAATATACCA	TTTTTATTAA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
40	ATTTAATTTA	TATAAATTAT	TTAATTTACT	TCATTGATAT	ATATAATTAT	TAAATGTACC	420
	TTTCATAATA	TTTATTTTTA	TTAGTCTAGT	AATATTTCTA	TTTAATAGTC	TACCTTTTAA	480
	TTGGATATTA	CTACCTACTA	AATATTTACC	TAATAATATA	TTATTAAGAA	TACTTAAATC	540
	TAATAATTTA	TTATCTAAAG	TATATAAATT	AATTAAATCT	TTTTTATTAT	TATTTAAATT	600
	ATTATTAATT	AGTAAATTAT	ATTTATTTAT	TTTATAACAT	AATTTTTTGA	TAATAATATA	660
	TCATTATTAA	ATGGTAATTT	ATTAATAATT	ATCTTTATGA	TTTATGACAA	CCATATATTA	720
45	TAGANATTGT	TAATAGTTGA	CTAATATCCN	ATCCAACCTN	TATTNATTTA	NAGATCATAN	780
	ACCTTTTATA	CAATTATTTT	NATATAACAT	NTACCTNATT	ANAATATN		
50							
55							

1378RP

	GATCCTTATA	AAATGGGCAA	TAGACGTGTT	ATAATATAAT	ATACAAAATT	ATAAATAAAT	60
	ATTTAATAAA	ATATAAAAT	AATAATTAAA	GTATTATAAT	AATTAATAAA	ATTATTTATT	120
5	AATAAGTATG	GATTTTTAAC	TGAAATTTGT	TAAAATGAAA	TAAGAATTGC	TAGTAATCTA	180
	TTAATAAGAA	AGTAATGGTG	AATACTCTAA	CTGTTTCGCA	CTAATCACTC	ATCACGCGTT	240
	GAAACATATA	ATTAAATAAA	GAATATTAAAT	TAATTTATTA	ATTATTAATT	ATTATTAATA	300
	TTATTTAATA	AATATAATAA	ATATTTTAAT	TTAAATTATG	AATTAATGCG	AAGTTGAAAT	360
	ACAGTTACTG	TAGGGGAACC	TGCAGTGGGC	TTATAAATAT	CTTTAATATT	CCATTTTTAT	420
	AAAATAAATA	TATTTTTTAA	TATATTTTAT	AATAACTATA	ATTAAATAGT	TAAAATTTAA	480
10	ATTATAATTT	AATAATTTAA	TAACCTATTA	ATTAGAGAGT	TAGGGTACAT	CCCCCCTAAT	540
	GCTATGCATT	ATGGTTGGTA	CACTCTAATT	AATAAACTAT	AATAAATAAA	TACTAATATT	600
	TTATACCATN	AATTATAATT	ATTTTAAANA	NATTTAATAT	TATTAATGAA	ATATATAATA	660
	AGTATTNTNA	TTTNATAATA	ATAAAAAATGA	NAAAAACGACC	CCTAATAATA	ATTTGCATTT	720
	ANANTTACCC	TTACACCTCC	CNTTAAATTT	TTACCCTNAT	ANCCNTNTTA	ATTAAGGANG	780
	GNGNNCCCCN	TGCTCCCCNN	TGTCCCCCCC	ATTNNANTTT	A		
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1378UP

	GATCCTTGCG	TACTAAGAGT	TAGACTTTAA	TTAATAATAT	TATTTGTAGA	AGATAGAAAC	60
	CATACTGACT	CACGTCGTAT	TTAACCCAAC	TCACGTAACC	TTTTAATTGA	CGAACAGTCA	120
20	AACCCCTACTT	AGCTGTTACA	ACCAAGAGGA	TAGGTTGAGT	CGACATCGAG	GTGGCAAACA	180
	TAACCTACAA	TAGCTACTCT	ATCGTTATAT	TACCCTGTTC	AATTTTGTTA	TCATAATAAC	240
	ATTTAATTAT	TATTTCAATA	ATTCTCATT	TTGTTTCAGAC	TATTTTCATTA	TGTATTATTT	300
	ATTAATTAAT	ACATATTGGG	CTTTCGTGGA	TATAATPAT	GTTAATCCTA	CTCATATATC	360
	TAGTCGTTGA	ACGTTCTTAT	AACTTTATAA	AAAGGATTGT	TATAAGCTTC	GCTGCAGATT	420
25	GTCCTTTTATT	ATTATAAAAT	AATATTAGGA	GTTCTTTGCA	ATTAACCCAA	TTTACTCAAT	480
	ATATTTAAAT	ATTGATAATT	AAATTTACCA	ATTTAATGGG	ACTATTAATT	AACCCCTAGCG	540
	TAACCTTTAT	TCGTTATCAA	ATACCATTAC	AATATGTATA	TTTGTTCAT	TATGCCAAAC	600
	TTACGTTTATT	GTTCTACTTG	TAGGTATTAC	AATTATAGCA	CAGTTATACC	ATTATATTTA	660
	TTTATATATA	TCCCATATAA	GTTTTTATTA	ACATATAAAC	TGTNCATTAT	TTATCTNTTT	720
	TATATAAAAT	ATNATTATAT	TAATNATTTA	TTAANATTTA	NACCCNTATA	TTAAATATAA	780
30	TCNTTTTAA	TAATAAATTA	TTAAGGACTN	TCCAACCTTT	TTGAAAGACC	CCCCACTNCC	840
	ATTAATGTGC	NT					

1379RP

35	GATCCAATTC	TCTCGGTAGT	TTCTTCCAT	ATAGAGACTG	ATCAACTAGC	CACATTCCCA	60
	CAACAAAAGA	GTTTCTATCT	AACGTGCCAT	CGCGTCTTGT	ATCTACCATG	TCGTAGATTT	120
	GAGCCAAAGT	ATCTTGAGGT	AGATTGCTTC	GAGACCAGAT	ATCTGTAACA	ACTAAGTTCA	180
	ACATTAGACC	ATCCTCTGGC	ACCTCTCTTG	TCTCATCGTA	GTTACCGTTA	TTCCACCATG	240
	GGAGCAAGTC	AAGATAAGTG	TCTCTATTGC	TGACCCACAT	TCCCTCGTAA	CGCTTTCTTT	300
	CCCTTTCACT	TACGTACCCA	ACATCAAGGT	GCGACTTCCA	AGGTTTGTCT	TCGTTGAAGG	360
40	AATTACGGTA	TCGAAGATTT	TGACGTATCT	TCTCGCGCTT	TTTGCCGGAT	CTTCTTCTG	420
	GACTTCGACT	ACGGGAGTTG	CGGTCGCTTC	CGTAATCCTC	TTCAGAGTCT	TCGCTGTCAT	480
	CGCTTAGTTG	ATGGGGCTCT	GAGCTGGAAC	TGTCATTAAAG	TATACCCCGC	ATAGTGTTTT	540
45	TTAGCCGCAC	ATGCAATTTA	CTCTGCACGA	GAGCGTTATC	GTTCTGCGTA	TATATATGTG	600
	ACGTTGGCGG	GTGATTCTTG	CTGGGGCCTA	GCCCACTTTG	CCCATGGCGC	TTGAAAGCTT	660
	CATCCACTTG	GANTGCTGCG	TTGANANTTT	GGTATTAAATN	CAGGAANATT	CCTCCGTAGT	720
	CCAGTTCATA	GGAATTTGTT	CATGTCAATT	ACAANCTTTC	NACGGGAATC	TTTTGCGACT	780
	CNTGTACAGT	CGANGNATNT	GTCNTCCGTA	CANCTCCCGA	TNCNCCAAAN	TNNCCNCATT	840
	CNCNN						
50							
55							

1379UP

	GATCCGGAAG	TTAACACTGC	CTGGGATTCA	TAAC TTGGCA	ACAGCGTATG	TGCGTGTGAA	60
	CATAGTCGAT	GGAGCACATG	AATTGGGGTA	TCAATAC TGA	TTTCATAATG	CTTTCTGGAG	120
5	CCATTGACCT	TGCGTGACAA	CCTCAAACAT	ATTTGGAGCC	AATGGTTGGA	CTTTATGTGG	180
	GGAGATGCAG	TATTCCGGATG	TATGCACTGT	TGGTAGTTCA	ATCTTTCCGGG	GACAAAAACC	240
	TGGTAAGTGA	ATTGTCTCTT	TGAAGCGCCA	CCCGCTCCAT	CATCCAGCAG	GTTTCCTAAG	300
	TTTTTAGCAC	GCGAAAGGCT	CGCGCCTTCG	TGTATACCCT	TAAGTGGTGG	TGCTTTGTGC	360
	TCGACCAGCA	AGAACTTCTT	TGTAGGCTCC	ACTCGGTGTA	CTTTCCGACC	TTTACAATAA	420
	TACTCTAAAG	TTTCCGTCAG	GAATATTCTA	ACCCTGTGGA	GCACGAGATT	AGCCCGTGGG	480
10	TTTAGCGAGA	GCGATATTGG	TAGAAATGCG	TCCAAAACTA	TATCTTTCGA	TGCAATTACG	540
	ATTTCATAAC	TCAATTCTTT	TTCCCAGTCA	CGTGATATGA	CTATCGGTTC	GGTATCTTCT	600
	ACAGAGTTCC	GAGATAGTGT	GCGGATAAGT	TAATCGGAAC	ACGACGTGGA	CATTGGACTT	660
	AAGGTCCTAT	GCCCTCAATG	TCACTCAAGC	AGGTATTTAC	GTTCCCNATG	TTACTAGAAT	720
	CTTCTTGCTC	GACNCCGGAN	TNGANCCCCA	AGAAAAATA	TCCCCGCCNG	AAAANAATTT	780
	CCCTGGNGTG	ACGTGTGNAT	NACCCNACGA	AAACNTCCTC	CTTCGAANGT	NCCTTATATT	840
15	CNNTNAAANA	ATANA					

1380RP

	GATCGCATCG	ACCTCGCCAA	AGTAAGGCAG	GCTCTCGACG	GAGATCCAGT	CGACAAGGTG	60
20	AGGAAGCGTG	GTGTTCTTAC	CCTCGAACAC	AATTGGCTCC	TTCTCGCCCG	GCAAGTGGAC	120
	CGCCAAGGTC	GGCTTCTTAG	TTGGGTACTG	CACAAATACA	AAGTCGTTCC	GGAGCAGGTT	180
	GGCCAGTTCC	TAAAAGGACT	CGTTTCAGGCC	CTTCACGCCA	CCGTCAACCA	CCACTGCGGT	240
	CTTGGACTCC	GCAAGCAGGT	CCTCCAGGTC	CTGGGCGGCC	TCCTTGCCCT	CCAGCACCGT	300
	CACGGCCGGC	TCGGCCTGGC	GCAGCATGTA	CGCCACAATT	TCCTCGGCCT	TGCGTGCGCC	360
	CGTGATAGGC	ATGCCCTCCT	CTGACGCCCC	ACTGTGGAAC	ACCTTCAGCG	TCGGGTACCC	420
25	GCGCACGTTT	TGGCCCCGCG	ATAGATCCAG	CTCCTGCTCG	CAGTCCACCT	GCGCCAGCTT	480
	GATGCCCTTC	TCGGCCAGCT	CCCCAGCCGC	CTTCACGTAC	TCCGGTGCCA	GGTGCTTACA	540
	GTGGCCACAC	CATGGCGCAT	AAAAC TCCG	CATCACAAGC	GGGTTCCTCT	CTAAGAACTT	600
	CCCGAACGTC	TCTCCGGTCA	ACTTGACACT	GCAGAGTCCT	CTGGTGCACT	GGCATCTTGG	660
	GCCTGTGCAA	CTGTGCCAGC	AACCGGCGAT	GGACAACACA	AACCGCTTGT	CCAAAANCNT	720
	TCTCGTTCGG	TCTATCCTAC	CCGTGGTTTN	GTGNACTCTG	TGGCGATCAA	ANCCGGNTNG	780
30	CNATTTTGT	TTTATACTGA	TCCAGAATTC	ACCCTNTCNC	AAAACNNTTN	CCNGAAAAGA	840
	NCNGNTN						

1380UP

	GATCTCGCCT	GTTGTGAGTG	ACGCCGAGTT	GCGCGAATTG	TAGCAGTGCG	AGAGGAACGT	60
35	GCCGACGGTA	TCGTTTGCCA	GCGCGACAAC	GCGCACGCTG	CCCAACCCGA	CCGCGTCCAA	120
	CTGCTCCTGG	TACATCTTGA	CCACGTCCTT	GCCGATCGCA	TCCTTGATGT	TGAAGCCCTT	180
	CGTCCAGCGG	ATCAAAGTGC	CGCTCGATAG	CGATGTCTGC	GCCACGGGAT	ACGAGAACGT	240
	AAACCCGAGC	TTCAGTTGGC	CGCCCTCGCT	CTGGAGCACT	TCAGAGTGGT	AGCGCTTGAC	300
	AAACGCCATT	GTGCGCTTCG	CGATGAAGCC	GAACAAC TCG	TCTGATGTTA	CGTCGTCGTC	360
40	AAGGAGCTCC	TCGGGGATCT	TCGACTTCAA	CTGCTCCAGC	TTGAACGTGT	GATCACC GTT	420
	GAGACGCACC	GAGCACACCC	GGAAATTCGT	GCCGCCAAGG	TCCGCCGCCA	AGAACGTGCC	480
	CTCCTCAGTG	CCATTGGGCC	TGCCCATCAC	GTACGACGGG	ATCATCGGAA	GCCCACGGTA	540
	CTCCCGTCCG	TCTCTCCGTT	CTTGAGACCT	GTTCCATACA	TTCGATGAAG	TACGCGGTCA	600
	ACTCGCGGAG	TTTGTCTCTC	GTCACCTCGA	AATCCTTACA	TATTTCTGTC	ACTGCTCCTC	660
	GACTTTCCCG	CGTTGCGCTT	GTGCAAATCT	TCNAAAANAT	CCTGGTACTG	TAAANATTAG	720
45	ACTTCGANAC	GTTGGTTCGAG	TCTTTCNNGC	TTNCCTACTC	NCCNGCCNTG	TCNTANTATT	780
	TTGANGGCGN	TCCAATAAAA	AACCC TTTNG	GGGGTCNCAA	GNGACCTCCC	ACCCTCTTTT	840
	GTTTCCCCNT	CCCNNAATGA					

1381RP

	GATCATTATA	TTATAAAATA	TAATAAAGAA	TATATTTAAA	TAATAATAAT	AATATGAAAT	60
	ATTATATTAA	TTCTCCATTG	GAGCAATTTG	AGATTAGAGA	TTTATTAGGT	TTAACATCAC	120
	CAATAATAGA	TTTATATTTT	ATTAATATTA	CTAATTTTGG	TTTATATCTT	ATAATTCCTT	180
55	TATTAGTAAT	TTTACTAATG	AATTTAATAA	CTAATAATTA	TAATAAATTA	GTAGGTTCTA	240

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	ATTGATATTT	AAGTCAAGAA	ATAATTTATG	ATACTATTAT	AAATATAGTT	AAGACACAGA	300
	TTGGTGGTAA	AGTATGAGGT	TATTATTTTC	CATTAGTTTA	TACATTTTTC	ATTCTTATTT	360
	TTACTATAAA	TTTAATTAGT	ATAATTCCTT	ATTCAATTTGC	TATAACTTCA	CATGTAGTAT	420
5	TTGTAGTATC	AATAAGTATA	ATTATTTGAT	TAGGTCTAAC	TATTATTGGT	TTTTATACTC	480
	ATGGTTTAAA	ATTCTTTGGT	TTATTTTAC	CACTAGGTAC	ACCATTAATT	TTAGTCACCA	540
	TTATTAGTAT	CAATTGAATT	ATTATCATAT	TTTGCTAGAC	TTATTTCAAT	AGGTTTAAGA	600
	TTATCAGCTA	ATATTATAGC	TGGTCATTTA	TTAATTGTTA	TTTTAGGTGG	TTTATTACTT	660
	AATCTAAANC	CACAAATATT	TAACNTTTTN	TTAAGTTCNN	CCNATGAATG	CTATTINAGT	720
	ATGTNTGTTA	GAATTTNTAT	CTTATACCNG	CTTANINTGA	AGTNTNAATA	CNCCNTATNA	780
10	AAC TATTTAT	TCCTTATTAA	ATTAACANTT	NAACNCCCNA	TTANTTTNTA	TNCTT	
15							
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1381UP

	GATCATTGTC	CAATATTCCC	CACTGCTGTA	TCATATAGAT	ATTGATTATA	ATTTCTAAAT	60
5	CAACGTGATT	GTTCTAACTT	TAATTAACAA	TTATGAATTT	TTGGCTAGTT	ATTATTTTTT	120
	AATTAACATA	TACCTAAATC	ATTATAAGCT	TGACTTAAAA	CAAATAATTA	TTACATTATT	180
	CTTTATTTAT	TATTTAATAT	TTAGTTAAAT	TTTAAGTTCA	TTATTCTTAA	TTTTTACTCA	240
	CGAGTACACC	ACTTATTAAT	ACTATTAATT	AATAATATTA	ACGTTTGATT	CGCATGTGTA	300
	ATGTCCTTAG	TTAGCGCTTA	ATCTGAACCA	ACATCATGTT	CTCATTATTA	TTAACTATTT	360
	TTAATTATTT	TAAATAATTA	TTTAATACGA	AAGTTATAGG	ATTCGAACCT	ATGAAATCAT	420
	AAAGATTTAT	AATAGCTCAA	ATATTACACT	TTAAACCAC	CAGTCAAAC	TTCTTAATAT	480
10	ATATACCTTA	TATATGGTTT	GATAATTTAC	TTATAATATA	TAGTATATAA	TTTAATGATA	540
	AACCTCTTATC	ATTTAGGTGC	GTAGGGTTCA	CCCCCCTATT	GCTAGTCAGC	AATATGATGT	600
	ACCTCCTAAA	TGATAAAGAA	GTATAATATA	TAAATATTAA	TATTAAGTA	TTTAATGAAT	660
	ATTATTTATTA	TTTATTTTAT	TATTATTTTT	ATTTAGTAAA	TAAATAAATA	TTTCCACTTA	720
	TTGAAATATA	GGTCTTNGA	TTAGAAATAA	GCNATNATAA	TGTNCCATTG	ACTATTAAAT	780
15	ANTGTGCTCN	CNNGACTTCC	CTATTTNCCN	NNGANAANTC	NGAANATCAG	AANANAGATT	840
	CCNANATNNT	TAATNNNCCC	CCA				

1382RP

	GATCTCACAC	GTGACTAAAA	TCACTAACAC	CACGTGACTT	CGTGCACGTG	GCATCGTCCC	60
20	ATTCTGTGCG	TCGCTAGCAT	TCTGCCC GCG	CATCTGTGTC	AGGCCACTGC	GCAGCTGACC	120
	ACGCCGTACC	ACGGCAGGCT	TCACGACAGA	CGGCAAGCTC	AATCGCTATC	TACGGTTTCA	180
	GGTGGAATTT	CTTACCGGCA	TCCGATTAAT	TGCTTTTTTG	GCCTCTTTT	GCCCTCTTT	240
	TTCCAGTGGG	TTGCTTCTCG	AAAACAGGGA	GCTAGCTTCC	CGTAGTACGT	AACAGTCTGA	300
	GAGGGTTAGG	CATCGCTGAG	CTCGAGACCC	GGTGATGCAA	TGTGCACAAC	CCTCGTCTGC	360
	GCAAAACGGG	CACGAAGATT	GAAAGTATCC	AGGAGTGCAG	CCCAGGGTCA	TGCGAGACAG	420
25	AATGGGGCCAG	AAAAAGCGAA	AAAATGGACG	ACGCTTTTAT	ATATATATGT	AGCGAGGCCG	480
	GGCGTTCCCA	GAACGGGACC	CGACACAAC	TGTTGTAGAA	TTTCTATCTG	CAAGGAATCA	540
	AATACAAAAT	GGAATCTAGA	TTGGGATGGC	TAACCTGTTT	GAACCTACGAC	ACTGGTTCTG	600
	CATTGAGAAG	AACCTCATCA	TCCGGACAAT	GGTCTTAAGA	CCAACCAACC	AGANACTTNG	660
	TGGANCTTAA	AAAGGNGGGT	TGAACATCCT	GAGAATGAAC	TTCTCGCNCG	GTCCCTACAA	720
	TNCCACCATC	GGTGNTCNAA	NACCCNNAAT	TCGAGATTNT	NCCNGTTAAC	NTTGGCCTTG	780
30	CTTTGAANCC	AAGTNCCTGA	ATNAAATGTN	CCTNTCGAAA	NTTANTACCN	TCCCCTACCC	840
	AAANC						

1382UP

35	GATCTATAAC	AGGTGCCAAG	TTGGCAGATT	TGTTTCAGGG	GCTCGACGAT	GTAGAGTCCA	60
	GTAGAATGCT	CTGTAAACCC	AGAGCATACT	TTGCGCGAAA	GTCTTTATCT	GTTGAAATCA	120
	ACTGGGGTAT	CCGTCTTGAT	GCTGTCCCGG	AGGTTGATGC	CTTTCTTGAT	CGCCTTGTC	180
	AGTATCTGGT	TGGTAAGCTC	AATGAGCTCC	GCATGACCAC	GTCCCATATT	GTTTTGAAAA	240
	TAGCACGCAG	AAGCAGGGAT	GCCCCCATCG	AACCCCCCAA	ATACCTGGGC	ATGGGTGACT	300
	GTGACAGTTA	TAGTAAATCG	TGCAGATTAG	GTCTTGCTAC	CAATATTCCT	GGGGTTATAT	360
40	CTGCAGAGAT	AAAGGCAGCT	TTTTCGATGC	TATGCTGCCC	CGCAAAGGAA	CTGCGTGGTA	420
	TAGCCGTTCA	GTTTCTTAAA	CTGAAGGAGG	CATCCATTTT	TCAAATGCCC	CGTCAGCTCA	480
	GGTTTCCATT	TGGTACAATC	AGACCTTTAA	CAACTCCAAA	GAATCGTATC	ACAGCGTCGG	540
	TTACAGAATT	GCCACCTGTA	GTTTATAAAA	GGGCCACTCC	TATTAAGGAT	TTTTTTGACC	600
	GGCACAAGAG	GACTCAGATT	CACCATCACC	TGATTCACTC	ACATGATGTC	TGCGTCAGCC	660
	TTGTGCGAGT	CATTCTGGT	GGATTACCTA	CGATCTTGCG	GAATAATCCN	AAAAAACATT	720
45	GACNATCTNA	AACCAGACTT	CTTTNTTGCN	ATTCCCAAAA	AAATTGGGNN	GNGCCNNGT	780
	TNNATCCCAN	CATGCCCTTA	AAATTTAGAT	CCTTGACCCT	ACTCCNANTT	GNTNCCCNAA	840
	AAAAAACTA	TCAATGTNTN	CT				

1384RP

50	GATCTGCATC	GCGTCCACCG	TGGACTGGGC	GGTCTGTTGGC	GGTCACGGAA	AACTCGGCGG	60
	ACTCGGTGAT	GGTGCCGGCA	AGCGTCTCGT	AGCGGATGGG	CACGACCTTC	GCAAAGTAGG	120
	AAAAGAAGTG	GCTATGGCCG	TTCCGGAACCT	CCATGGCGCG	GCCATTGAGC	GGCCCGGGGT	180
	TGCCGGCAAT	TTCCGGGCCA	AAGGAGAGAC	TATGGATCAC	GTGGTTGAAG	GAGAGATGGG	240

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	GGTGTTCCTT	GTAGAAGGAA	TCGTGCTGGG	CGTGGCCCTT	GCCAACGTGC	GCAGAGCCCG	300
	GGCCGAAGTG	AATGTTCCCG	TGAACGCGGT	TGAGCTGCGC	GGTGCCAGCG	ACGCGGCATC	360
	CCTCGTTGAT	CTGCTCCTGC	AGGCGCTCCG	TGTAGCCCTC	GCGCTTGAC	TGCTCAAAGC	420
	CTTTGCCATC	GAAAGTGGCC	CAGTTCATCT	CTGCGTACGC	CGCGCGCACC	TCCCCGCACG	480
5	TCTGACAGCA	CACGCGCTCG	CTGCGCGGCA	GGTTCTCGTT	CTGGTCCTGG	TCGCGTGCGC	540
	CATACACGGC	CACAGTAGTC	TTGGTCGTCT	GTAGACGGCA	ACGTCTCGCC	ACTCGGAATT	600
	CCTCCTTCCC	CACGTCCGTC	CNTGTTTGTC	CACCNITTTT	CCTTGATCCT	CCTCCAACNA	660
	ATTCACTGTG	CTCCCTGTTC	TCTNTANNTC	CATTTCATAC	TCCCCCGGAT	CTTGCAAAC	720
	TATATCNAAC	CCCACTCCNC	TCTGCTGCCG	TCCTTCAANC	ACTGNGCGTC	TCCCTCCCCA	780
	NTTCCCTCCT	ANCAANACN	CGTTCACAAC	ACCNCNTATN	CCT		

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1384UP

	GATCACTTTG	TTTGTGTCTG	CACGATAAAT	GGCCTCGGTA	CAGAGTTTTA	CGAGTGTTC	60
5	TTGGCTGAGA	CCGGACAGGT	CAATCTCAGA	GTTTTTACTA	TTCATTAGTG	AGTAGATTGA	120
	CGCGTAGTTA	TTATCAAAGG	CCACCGGGGA	ATTGTTAAAG	AAGTTGGAAA	CAGATGATTT	180
	CGACATGGTA	TAGTTCTGTA	GCTTAATTAG	AACGGGCAGG	TCTGAGCTCT	CCGCGACGGG	240
	AGTACTGTTT	TGAATGGGTG	GCACAGCCAG	TGGCGGTTGG	GGCGTGACCA	TGCCAAGCTG	300
	TGCGCCCCGCT	GTCAGGCCCCG	CTGGTACTGG	AGCCGGCACG	CTTATCGGCG	GGTCTGCTGG	360
	TGTCGGCGAT	TTGGAATAC	GGTTGTTGCA	CGCTGCTAGG	TATTTTTTCG	GCTCCGCTGG	420
10	GCTCATCTTC	TTCTCGGTCA	AAGCAGGGTC	GAAGTTTACA	ATACCCTTAC	TCTTCGTCTC	480
	CTCTGCAATC	ATGTGCAACG	TTTGCGCGAT	CTTCCCCAGC	TTGTGGTGAT	AGGGCGCCAG	540
	GTCGCCCCGAG	TTCCGGATCA	GCTGCGCTTT	CATGCCAAAG	TTAACGAAAT	TCTTGTAACA	600
	CGGTTTCGACG	CAGCGCTTCC	CAAGCGGTAC	CGCAGCGCAA	ATCGTTTTTC	TGCTGGTACT	660
	TGTTGTGAT	ATTGAATCNA	ACAGGCCCCC	CAATAANCCT	GTCCACCGGG	CCCCGTTCC	720
	GANNAAACCA	GCATCACACC	GCNAAAAAAC	GGGCCCCACN	CGTCGTATC	NAACTTACCC	780
15	CTCCAGACTG	NNTATCCANN	GCATNCNCCT	TTTTTNTCCC	GTGTNTCTGA	AANTNCNAAG	840
	CCCCCACCT						

1385RP

	GATCGACCTC	GTCATCATGG	GCAAGCAGGC	CACCGACAGC	GACAACAACA	ACACCGGGCA	60
20	GATGCTGGCG	GGCCTTCTCA	ACTGGCCGCA	GGCCACCAAC	GCCGCGCGTG	TTGAGCTGGA	120
	CCGCACTGGC	ACGCGTGCGA	CCGTACGCG	CGAGGTTCGAG	GGCGGCGAGG	AGGTCTGTAG	180
	TGCCGCGCTG	CCACTCGTGG	TCACCACGGA	CCTGCGGCTC	AACACGCCGC	GCTACGTAC	240
	GCTGCCCAAC	AAGATGAAGG	CGAAGAAGAA	GCCGATGGCG	AAGCTCAACC	TGCGCGCGTT	300
	CCCCGCGCTC	GACTCCGCG	CCCGCTCAA	TCTGCTGCGC	TTGAGGAGC	CGCCGCGCG	360
25	CGCGCCGGGC	ACCGTCGTCG	CGTCCGTGGA	CGAGCTGCTC	GCCAAACTCA	GGGAGGCCAA	420
	GGCGGTTTAA	CACCTATATA	AACTAACAGC	CCCTATTTCC	TCCGCGGACG	CAGCGTCCCG	480
	TCTTCCAGCA	GCCCCGGCGG	CTGCTTGCGC	AGGTACGTCT	GCTCGTACCA	CGCCTCCCAC	540
	TCCCCGCCCT	GCGCCCGCGC	CTGCTGTACG	CTCTTCCAGC	ACGCGCCGGC	ACTCCTCGTC	600
	CCACGCCGCG	AGGTTGCTCC	CCCGGTGCGT	GCCGCCCGCG	CTATCTTGCA	ACNCCGCCAG	660
	CTTGCACTTT	CGCCCCGCCC	CCCCGCATGT	NNCCCNCCAA	CNCNTTTTTA	CACNGGATNT	720
30	TNCCCNNTTG	TTNTCCNTNN	NTTCCNCCCC	GTGGAANTGN	TTTGCCNTTG	CTTGANAATG	780
	CTANCCAAAC	CCCCAATTTG	ATNGNGCCCC	CCCCAAATNA	ACTTTTCCACT	TTGCCGAGAC	840
	CCCGCCCTGT	NCCCTTNTTT	AA				

1385UP

	GATCCTTGAG	GGCTGGTTCC	TGGGCTTCGA	GCCCGCGGCC	GAGGCCGAGC	TGCGCGCGCG	60
35	GGCCGGGACC	TACGGCGCGG	CCGCGCTGCG	CGAGGTCAAC	GCGGCGCTCG	AGGACTACTC	120
	TGCGTGTCTG	TGGCGCGCGG	CTGGCGTGCC	CTCGGTTCGG	ATCGTGTTCG	ACGCGCAGGT	180
	TCGCGAGTGC	GTGGCCCGCT	GGCGCATCCA	GCAGGAGCAC	GAGCTGCGCG	AGCGCTGCGG	240
40	CGCGGCATG	ACCGACGCGC	AGGTGCACGC	ATTTCTGGAG	CGCTACCTGG	TGTGCTACGA	300
	CGTCTACTAT	GCGCGTCTGG	TGCGCGAGGG	GCTCGGGAAC	CTGCACCGGC	TGACTGTGGG	360
	GCTGGACGGA	GACCGAAAAG	TTACGTATGT	TAGCCAGAAG	AATATGTAAT	GCCGAGTCTA	420
	TAGTTCTTGG	TCCGAGATGT	CCTCCCAGGG	GATGAGATAG	CGCGTCTGGT	GCGCCTTGTC	480
	GCGCGTGCGC	GCGGCGGGGC	CCGGCGGCGA	CGCGCGCTGG	CGCGGCGCCA	TGCTGGGCGG	540
	CGGCGTCGAC	GGCAGCACGC	TGCCGCCGAG	CTCGTCACGT	GGCGCGCCAG	GAAGGCCTCC	600
	GTCTGCGCCT	GGCGCGCGCT	CAACGCTTGC	AGTCGCGCGA	ACGCTGCCCA	NCACGTTTCT	660
45	CGCGCNGTCC	ACTGCNCGGG	ACTTNTTAAA	CATCCTGCT	TTCTTGGAAAT	CCTTGAACNA	720
	NCGCNGTTGC	GCTTNTCNAC	TNTNATGANC	CCCCCAAACC	CCTNTTTTNG	GGCTGCGGGC	780
	NCCCCGCCCC	NNNNCTCTCG	CCNGGTTNNG	TGTCCTTNAC	CCTNCCCCCT	TNCNTTAACC	840
	GTNTANNNTN	N					

1386RP

	GATCGCACGT	CATTTTACCT	ACAGGCTGGG	CTTTTGAAGA	AGACGCCTGC	ATGGTACAAT	60
50	GTCTAGCCCA	GGATCCCACC	TGTGACCAAG	TTCCGCCAGAG	AACCGAAGCT	GCATGACCCA	120
	GTTACGGGCA	AGTACAAGGG	CGAGCTGGAT	ATAATGACGG	ATAGATTAAA	CAGAAACACA	180
55	GAGACGTACA	AGACACGCGC	TGGGAGTTCC	GACCGGCAGA	CGGCCGCGGT	GCACAAGCCT	240

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	TCTAAGCTGC	GGTTTATCGA	GGACAAGCTG	CGGTCGCTGT	TTTTCCAGCA	GCATCCCTGG	300
	GAGCTGTCGC	GGCCGAAGGT	GCTGGTGGAG	AACATGGGAA	ATGAGCAGTA	CGACTGGTCG	360
	CGGATGTTGC	AGCTAGGCAA	GCCGCTTGAC	GGTGAGTCTG	TGGTGCAGCG	GACGCTGTAT	420
5	CTGCTGAAGT	CGGGCGCGCA	CCGGGAGATG	CTGGCGGCAT	ACGACCAGGC	GCGGTTTGAG	480
	TTCTATCGTC	TGAGGATGCA	GCAGGAGCTG	GAGGAGCAAA	TAGCGTACGA	GGAGGCCACG	540
	ATGGTTGGCG	CTGTGTTCAA	GACAACCGCT	GTGGAGCACG	GTCTGCAGCA	AGAGCAGAAG	600
	GTCCTCGACA	GTGGAAAGAA	GACTTTGTTG	CCGGGTTTGC	CCTGATTTTT	GCNAAAAAAAA	660
	ACTCTACAAA	GCAGTCCNTG	GGCCNAACCC	ACCGAAGAAA	AAGAAGAACC	AGGACNNTGC	720
	CGAACCCNAA	GACNCCACCT	GTGNACTCCN	TTGCCAACTT	TGTTATAAAAT	TCTTACNNTT	780
10	TTATTCCTT	NGTACAATNC	NANNTACTGT	TNTGTGCCAT	CATGTGCCCC	AACAGGTTCC	840
	CCCCNTTGA	NAAANGC					

1386UP

	GATCCATGCC	TCGTTATAAC	TGAGCAGAAG	TGTGCATGCG	AACAGAGGCG	TTTCCTTGTT	60
5	CCTTGCCAGT	TCCCCCATTC	CCCAAGTTGC	ACTGCAAAAT	GTGAATCATT	GATGTCTTGT	120
	CGTCGCCATC	GGTGCCTGA	AAGATGCTGT	TCCGGTAGAC	CGCATTCGT	CAAGCGGAAC	180
	TCTAGGCGGC	GCCGTGAGAG	TCCAGATGAT	GAATCTGAAG	TTGAGGCCCA	GCACGTGTGC	240
	TTAAAAGATT	GTAATCGGGT	GCTGCTTTGT	GGTATCCACA	TGTGCAATTA	CAAATGCCAT	300
	GCAGGCAAAAT	GTCCTCCCTG	CTTAGAATCA	GATTCCAATG	ACCTTATCTG	TCCCTGTGGT	360
	AAGACAATCG	TACCAGCCCC	TGTCCGTTGT	GGAACAAAGC	TCCCTCGCTG	CACTCATCCA	420
	TGTCGAAACT	CGCTGCTGGA	TACTTGGCCC	TGCGGACACA	GTCCACCTTC	GCATAATTGT	480
10	CATCCCTTAG	ATGAACCTTG	CCCCCATGTA	CCATCACAGT	CAAGAAAAC	TGTCGCTGCG	540
	GTAAAAACGA	GATCAGGACA	TTCTGCTACA	ATGATGATGT	TCGTGTTTGA	GACCGTGTA	600
	GAAGCCATGT	CCTATTGCAA	TCACCTCTGC	CAATTNCCTG	TCATTCCGAT	GGCAATGCCA	660
	GCAAACTTGT	TAGCAAGCCT	GTGGTCNACC	ACCGAAAGCC	GCACNTGTTT	GTTAGGGAAA	720
	TGCNTGGCNT	NCGNATGCCT	GAATCCCTGT	NCNAAAAAAA	AANCNCCGTC	CGTTGTCCAT	780
15	CNCCACCAAT	NTGCNTGATT	TGCTGGAAGA	GAANGTTCCG	ACACCNCCCC	GTCCGTGNAAG	840
	AATGTGCAAT	CNNCGN					

1387RP

20	GATCAACCAC	TCGTGTGCCT	ATACATAGGA	ACCAAAAAGC	CTTCTGGCCT	GGTCCTCAAG	60
	TAGTATTGTA	TAAGTTTGGA	ATCCTTGTA	GCGGTTGCCT	TCCGCGCACC	TTTCATATTT	120
	TCGGTAAAG	CCTCCACAAG	GTTCCTATCT	TTATCCTTGA	AGTTGTCTCC	ACAGGACTCC	180
	CACAAGAACG	CCCCAGCAAG	CTTCTTATCT	TTACAGTATT	CCTTCTTTAT	TTTCATTGAA	240
	TCCACATTGT	CGTAGACGAC	AAGAGTTTTA	GTATTAGGAT	CGTAGCTATA	TGCAGAGACC	300
	CAAACATTGT	CAAACCTTCT	TGGGCGGTGA	GCTAGCGGCA	ATTGGTTGTA	TAGCCACATA	360
25	CCCGGTTCCC	CTTCTGATCC	TCCGCCTACA	CCAGAATATT	TCGGGCCAAT	TAGTTGTTCA	420
	CCATCGCCCC	GAACGTTGGT	GAAGCCACGG	CCATACCGTG	CCATGCGGAG	TGCAATTTTT	480
	CTTGGGCTGA	CCTTAAATTG	TTCCGTCATC	ATGAGTATCG	CATCATGTGC	ATTCAACTCA	540
	TCAAAGTTGT	CAATACCCAT	ATCTTCATAC	CGACGCTTAT	CTAGGTGCGA	TTGTACGGCG	600
	AATTCGTAGC	ATTGTACAAG	TTGCTATGGT	AGCCTGTTTC	CTCTGACCAT	GCACCGTGGT	660
	ATCGTATGTC	ATCATATCCN	CATGCTGAAA	ACTGTTCACT	CNCAACCGGA	AATGCAATNT	720
30	CTGAAGAAGC	NGGCTGCCAG	CTTNATTGAA	CCGTCTGTIN	TCCCGGGGCC	CNANATNTTT	780
	CCATCTCNNT	GTTNGCAGCG	GTNCTTTTNA	AAACTGGNTC	GNNCNCACCA		

1387UP

35	GATCACCACA	ACACAGAAGC	ACGCAACGCT	ACAGGACTTC	CCTGTTCTTT	TGCTTGACACA	60
	CGTCCAGCCC	AGAGGACGAT	TACACCGCCG	TCAGGTTTCG	CTAGTCTCCG	GCAGCACAGG	120
	CTCCTTATCA	CATTTTGCAT	TTTTCAGCTC	GCACATGTCA	CAAATAACCA	AATACATCCC	180
	CAAAAGCACG	CTTTTTCTCT	GCCCGTTCTT	TCTCATCGCG	TCAGACTTCG	TACTCGCTAT	240
	GAGCGGCAAG	GGCACGCGCG	CAGGGAGCTC	ATCTACAGGC	ATCGGGTCGC	GGCCACCGCG	300
	TCTGCAGCGG	CTGCGGCAGC	TCGTAGCGCA	TCGAGATCCG	GCAAGAGGCC	CGTCAGGTGC	360
40	ACTTACGAGC	ATCGAAGAGT	TTACTAGGAG	ATGACAGCGC	CTGCACGTCC	CTGAGGCTAG	420
	CCTCCCGAGG	CGGGCGGGCC	GCTTGGTATA	GGGTTTACAT	AGCAGAATGG	CACGAATATT	480
	TGCTCTAGGC	AACTGCAGGG	ACGGAAGGGG	CCTCATGCGA	AATCCTTGCA	CCGCCGGGTG	540
	CCGTATATAA	GGTGACGCAG	CTGCGCAGCT	GGGGCGGGCA	TGCTAACCAC	GACAGGATGT	600
	GGAGTGGTGC	GCGATTATAT	ACGACAAGCC	GGCGTGGACG	GTCGGTGCAC	AGGCAGGACA	660
	CCTGGCGGAA	ATCCCAANTC	GTTGAACAAG	GGAACGGGTG	CAGCNGGCGC	AATCTACAAG	720
45	AGTTGTTGAN	GGCGGCCGTC	ACATTTGCCG	TTNCACTGAC	CCTGTCTCGA	TCCANGAAGA	780
	GGNCTGGCAT	NTCCCANAAAC	CTCCCCACAG	CTGTNGACTT	GAACCTCNGC	CTACCTTGAT	840
	TTGCANNCCA	GAAAAAN					

1388RP

50	GATCACCCA	AATTCGTCTG	TGCTGGACCA	GCTTTCCCAA	CAGTCTCCGA	GGTAATCAGG	60
	CTACTGCGTT	CCTATTTTAT	GGCCTTCAAT	AATCTTTTAT	ACTTAATTTA	GACGTTAACT	120
	TCCACATCCG	GTATTTTCA	CATCTGAGAT	ACTGGCAAGC	ACGGCTAGCT	TTAGGAGAAC	180
	TGTATCCCAT	GACTTGTGGA	CAGGGGCTTT	ATGAAAAAAC	GCCTGTCCGT	GTAAGGATAT	240
55	AGAAAACATA	CTGAGATGGC	TTTTGTTGCT	GAATCAGACA	TTCTTAGGTT	ACATTTTGGG	300

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	CCTGGCTGTA	CAAGGCACTA	ATATGAAGAT	AGAGTTATAG	CGCGTGAGAA	GGAAAGGCTC	360
	CACTGGGTGT	TGCATGGGAT	TTCAGGGTCG	TGATAATAAT	GCCAGGCAAT	CATATAGATT	420
	ACCACGAGGG	AAACATCAAC	GCTATTTAAG	GTCATCCTTT	TTGACATCTG	TCGAGGAAGT	480
5	GCGAATAGCT	GTAAGCGCAA	CTCTACAAGA	TGCCGCCGTC	TCCAAGACCA	ATGCTAAGCA	540
	CCACAACCTCC	AATGACCTGA	TTACTGGGGA	GCAATTCCGT	CCTCGAAAGT	TGGCACGTCG	600
	ACTGACTGGT	TTTCTGCCCC	GAGATCAATC	NATTGATCCN	TNATCCCTTA	CATCNCCGGA	660
	CTTTNGAAAA	CCCAAATTAA	AATTCCGNAN	NCCAAAATCC	NGGGATTTCNC	CACCCTTGAA	720
	CTACCCACNC	GGCCCTATTA	TTTTATAATT	GCNNACAANN	CCCGATCCCC	CGNNAACCGN	780
	GTAAANCGAA	AACCCCCCGG	NNTTCGGACC	NNCNTTTTNC	T		
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1388UP

	GATCCAGCGG	CTTGGTAGCA	TGCTGGCCGA	GGAGTTCGGC	TGTTCTGGTT	TTGCGCGCTG	60
5	AGGCTCACTT	ATAGGTGCCG	ACTTCGATTG	CCACTTGTGG	CCAAGACTTG	CTTCTTTACA	120
	TAGCTAAATG	CCACTGATCA	TATAGACTGC	TTATTCTCTG	TTAACTGCCT	CAACGTTCCA	180
	TACCATCTCC	GCGTACTCCT	CTATGCAGCG	GTCACTGCTG	AAGAAGCCAA	CGTTGGCGAC	240
	GGACAGGATC	GACTTCTGGA	GCCAGGCCCG	GCGGTCGCCG	TGGTAGACGC	GGTCAACGAG	300
	AGCCTGGCAG	GCTATGTAGG	AGTCGAAATC	GTCGCTCACC	AGGTAGTAGT	CCCCGTGCTG	360
	GGCGACGGAG	TCCACCAGAG	GTTGGAATTC	ACGCAGGTCC	TGAGGGGAAA	ATGCGCCCGA	420
10	GGAGAGCGTC	TCCAGTACGC	GAGCAATGGG	GGCTGGCAAC	TCTTGGCGGT	GATACCGGTG	480
	CCGGTAGCGG	AGGTCTTTCGA	CATCTTCTGC	GAGATTACCA	AAGAGGAAGA	TGTTGTCTTC	540
	GCCGATCTCG	CGTGTGATCT	CGACGTTGGC	GCCATCGACG	GTGCCGATAA	TGAGACACCA	600
	TTTATAACGA	ACTTCATGTT	NGAATTCCCN	GAACCTCATT	ACCCGCTGTC	AAANGTGCTC	660
	ATAATCCGGA	ACNGGGANAA	TATTGCGCCG	GAANATGTAT	CCCGAATGAA	ACCCCTCAGA	720
	AATACNATCC	CTCTCTTANA	CACNGCCCN	TTATTACCTA	TATNGCTGCC	NTTTTACCCG	780
15	GCCCTTNC	CNAAAANACC	TTGAGAAGNC	CCCCNTNTNT	GGNNCCCGTN	CCNTTTTA	

1389RP

	GATCTTCTTT	TTGAAGCCCA	CAGACACAAA	CTGTGATGGA	GTGCTGGAGA	CGCCAGCTTT	60
20	GGACGACTTC	CTTTTCTTAG	ACCGGCGAGT	CTTTTCTCTA	GGTGATATGC	TTTCTTGGT	120
	GCCGTGTTTG	CTCACAATTG	CCTTTAGCTC	TTGACGACA	ATCTTTGTGG	ATAACCTTTG	180
	GCCATCTAAT	GAGCCCTTTT	CAATTGCACC	TTTGATCCAA	CATCTTCCAT	TCCAAACGAT	240
	ATTGGTCACC	ACCAACATAT	TAGTGAGGTT	ATCTTTCCCC	CATGATAAGT	AGAATCTGGT	300
	ATGTATTTC	AACGCACCTC	CCGAGGGTAC	ATCTGGCGTC	TTCGTTATCT	GCTCCACTAC	360
	TATGTAGAG	TTTCACATCG	AATGTAGGAT	TTTTTCTTGG	ATCAAGCATC	GCGTCTGCTT	420
25	AGGACCAACA	GGATTGTTTA	ATGGCTTGAT	ATATTATAT	TCCCTCACAT	TATCTGAGAA	480
	TTGACACGGT	ATAGCTGAAA	TATTATGATT	AGCCTGTTTT	TCTAATATCT	TTTGCAAGTA	540
	GGACGTGTCC	TCACCAAATA	ACAGCTTGTA	CACGACACCC	AATGGTGCTG	CGATGGAATC	600
	GAATCATCAA	CAATAACATC	TCTGTGTTGC	TCGTATAGGT	GTTCTTCGTC	GGAGGANGCT	660
	ACTAGGGCGA	TATTNGTAAA	TATTAAGANA	CANTTGTGTA	CTGTTNGAAC	TGCCNCGTAC	720
	TTGATTNTAT	AAAACCTCMN	AATGTTACCG	TTCNACNCTT	TNGAGANTTN	ANCCCTCNA	780
30	TCCNTTCCNC	GTGANTTTNC	ATCTCCCCCT	NTCTATACTG	ATACNT		

1389UP

	GATCCGTCGC	ACTTTCACAA	TTGTGAACGA	CTTCACACCG	GAAGAAGAGG	CTGCCATCCG	60
35	CCGTGAGAAC	GAGTGGGCGG	AGGACCGCTA	GCCACGGCCC	GCCTCTATGT	ACCATAAGTA	120
	GCCGATATCT	ACCGCTGCCG	GCGCGGGCCC	CGCCCGCGCC	ACCGTTGCGT	GCCAGGAGCT	180
	GGTCTGCCGA	CTATCCGTGC	CAACGTACGA	AACGATGCTG	GTTTATGTGG	TCCGCCCGCC	240
	GCTGGTTACA	ATTAACCGCC	CCAGGTTCATC	GGTAGACGGA	GCTAGCTACT	CGTTGTCCCTG	300
	TAAGTGAGTT	AACGCACAAG	GGGAACCTATT	CGTGTGGTCA	GGCAGCAGAG	ACGCTGCAGG	360
	ACATACTACG	AGTTATTTCT	CATAACTAAA	CATTTTGTGA	ACCTTTGTGT	CGGGGGCCAG	420
40	GTCGTTTCGC	AAAAGGCGGC	GGAATAAACA	GGGAGGAGAG	GTAGATGCTC	TTCTCAGGCA	480
	GAGGCTAGCA	AGGATGGCAG	AACAGCGGAA	GCGGTCGCGG	TCGCTCAGAG	AGAGCGCGCG	540
	GGCACTTTTC	AAGAAGCATA	CGGGGGAAGG	GGCGGCGGAA	GGGGCGCGCG	ACAGTGCCAA	600
	AGACGGTTAC	GACCCGAATG	GGGAACCGCG	GANC GGCC	GAGCGGTNAT	TTCAAGTTGG	660
	CGCNGGGGAG	GCCCCGANTTT	NAAACCGGTG	TNTAGACAAA	AACTTGTTCCA	GTTTNCACCC	720
	GTNGTTTACC	AANNNNNNAA	TCTCCNCCCC	NGGGTNGGTG	GCCNGAACCC	CCNCTGGCTT	780
45	ACGGGGNCCA	CATCTCTCCC	CCCCCTCCCA	TTAAANACCC	CGNCNCCTTT	TNTCTGNCC	

1390RP

	GATCAAGTAA	TCAATCAGTT	AATAATATTA	AGAATATAAT	ATGTAGACAT	TTAGTCTAGT	60
50	CTATTAATTA	TAAATTATTT	TGTAATTGTG	TGTTAATTTG	TTGATATTTT	ATTGATTTTG	120
	TTGACATTTT	GTTGACATGT	TGATATGTTA	TAAAATATAA	TTTAATATTA	TTTTATATAA	180
	TTATTATTAT	TATCTAGTCA	TAGACTCATA	TAAATATGAA	TATATTCCAT	TATTAATTGT	240
	TTAGGATAAA	CATAAATTAA	TATAATAACT	TATTTTAAAG	TTCAATAAAT	ATGTTTCATAT	300
	TTATATGATT	AATTTCATAAC	GTATTCGATA	TAAATATCTC	ATACCCTTTT	ATGAATTAAT	360
55	TAAGCGGTAT	TAAATTATTC	TGATTGGATT	AAGTTATTAT	TTAATTTATG	TTCTTAACAA	420

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5	TTAATTGATT	CCATAAATAT	CGATATTTAT	TATTATTTAT	TAAAATATTA	ATGATAATAT	480
	TGTAATACTT	CAATTATTTT	ATCAAAATGGC	AAGTAATCTA	TTAATCNTTT	AATACGATTG	540
	ATAAGAAAGA	AAAGAATATC	ATCTATCGTA	TAATATATTT	CAAGTATGAC	CTCTTCAATA	600
	TAATTAGAAG	TTTAAACTTG	TAGAGAATTA	AGAATTTAAT	ATGAGTCTTA	CATTAAACCT	660
	GATATGAACC	TTTAATCTAC	TTATTTGTTT	AACCGTTGAA	GAGAGAATAG	TTAATCTNAG	720
	TATNACTTAT	ATATTGATAC					

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1390UP

	GATCAAACCTA	AGAAACCTAA	TAAACTAATA	GAACCTATTA	GATAAATTAT	AGAAATTTCA	60
5	CCAAATACAG	GTTTTTTAGA	ATAAGTTGAT	ACAATATGTG	ATATTATACC	AAATAGTGGT	120
	ACAATTATAA	TATATACTTC	AGGATGACCA	AAGAATCAAA	ATAAATGTTG	ATATAAAATA	180
	GGATCACCAC	CACCTTGATC	TTCAAAGAAT	GATGTATTAA	AATTTCTATC	TATTAATAAT	240
	ATAGTAACAC	CAGCTGATAA	TACTGGTAAT	GATATTAATA	ATATAACAGC	AGTAATTTAA	300
	ATTGATCATA	GAAATAAAGG	TATTTTATGT	AAAGTTATAC	CATTAGTTCT	TATATTTAAA	360
	GCTGTAACAA	TAAAATTAAT	AAGTCCTAAT	AATGAAGAAA	TAGTAGTTAA	ATGTAAAGAG	420
10	AAAATAGCTA	AATCAACAGA	AGCACCAGAA	TGTGATTGAA	TAGAAGATAA	AGGAGGATAA	480
	ACAGTTCAAC	CAGTACCTAG	ACCAGATTCA	ACTATAGTAG	ATGTTAATAA	ACAAATTAAT	540
	AGTGGTGGTA	ATAGTCAAAA	TGAAATATTA	TTTAATCTAG	CAAATGATAT	ATCAGAAGCA	600
	CCAATTATTA	ATGGTAAATA	ATAATTACCA	AAACCACCAA	TTAATATAGG	TATTACTAAA	660
	AAGAATACTA	TTAAAAATAAG	ATGTCCAGTA	ACTAATACAT	TAAATAATTG	ATTTTGACCT	720
	TGTAAATATT	GTTGACAGGT	GCTGATAAAT	CTATTCTAAT	AATAAATGAT	ATA	

1391RP

	GATCTTTTTTG	CTCCAGGTTA	TTCCCTTCTTT	GGACACATTT	ACGAAGTGTA	TTTTCAAGAC	60
20	CTGACTCGCG	CATTTAGGTG	TTACGTTAAA	GCCTTTGAGC	TAGATGCCGG	CGACCTCGTC	120
	GCTGCTAAAT	ACATGGTGGA	ATACTATAGT	GACCTGTGCA	ATTGGCAGGC	GGCGGCCAAC	180
	ATCTGTGACC	GTGTAATCAA	GAATGATATG	CATCTCAATT	CCGTCAACTG	GCCGTACAGA	240
	GTTCTGGGTG	TTTATTATTT	GGAGCTTCAA	CAGGAGGCTG	AATCGATCGA	ATGGTTCCAA	300
	TCTGCTTTAC	GGATTGATTC	GTCTGATGTT	GAGGCATGGA	TAGGCCCTGG	ACAGGCGTAC	360
	GCCGCATGTG	GCAGAAATCGA	AGCCTCGATC	AAGGTTTTTG	AAAGGGCATT	AGAGCTGTCT	420
25	CCAGAACATA	AGTATGCAAG	GTTATTCTCT	GCTATATCAT	TATGCCAGCT	TTCAGAATTC	480
	GAAAAAAGTC	TCGAGGCCCT	GAGAAAACCT	GTGAATAAGT	ATCCACAAGA	AGCTATCTTC	540
	AAAGAAAGAC	TAAGTGCAAC	GTTGGTGGAG	CATGCTMTGC	AGTTCTTCGA	CCAAGGTTAC	600
	CTGATAAAAG	CGGCAACTTG	CGCTGCTGAG	GTGATATCGA	TCATAGAAGG	CATTGTATCT	660
	GAACAGGTAG	AATATACAAC	CAATATGTGG	ATTACTTTAT	CAAAGGCTTT	GAATATTTT	720
	ATTTCCACGC	GTTCTCAGTT	CGACAACCT				

1391UP

	GATCGCCGCG	CAGATTGTGC	AGAACGTGCT	TGCACTAGGG	TCTCTTACGA	CAAAGGACTA	60
35	CATGCAGTCG	TTGGCTTCCG	ATGTTTCTGT	GAATGATGTG	GCGTCCATGT	TTGTGAAGCT	120
	GGTTGAACCTA	GGCTTTCTGG	TCCCGCTTTC	CAACGTGCAC	TACATGCCAC	TGGCCGATCT	180
	ATGGGATGTG	CTCTACAAGA	AGGAATACAA	TGCTATTCCA	AAGAAATCGA	CGTTGTGAGA	240
	TGCCAAGAAA	CGTGCAGAAA	CAAAGGCGAA	GACGAAGGTT	CAGTTCAATA	CGTTGCTGAA	300
	GAATGTCGAA	ATGAGCAACG	TACTAATGAC	TGATATGCAG	ACTTCAATGA	GACGTGTCCA	360
	AGACAATCTT	CCTCTAACAT	TTAACTTCCG	CCGGTACATG	AAGCACCAGC	GTTCTCGGCA	420
	GCTTGATACG	TTTGACAGTT	CCCGTGTGGG	GAGCGTACCA	GCCATGATCT	ATAAGGTGGC	480
40	ACTGAAGATA	ACCGAACAA	GTGCCCCTGC	GCTTTTCAGAT	CCGCTATGTG	AGACAGGCCT	540
	AATGCAGGAA	CCTGAGGAGC	AACCTGGCTAT	TCAGGAAGAT	ATGGCGCTAG	ACGATGAGAA	600
	GCTACCGGGC	GTTACATTCA	ATGCGGTGGA	CATATCCAGA	AACCTTACCA	ATAACATGGA	660
	CCTACGTGGC	ACACTGACTT	CTATGCCAAG	AAGATCACCA	GAACGTTGCA	CGCACCAAGG	720
	TCAATCCCAT	AAGCGGNTGA	AGGCTGAAGA	TGGGATGGCT	GTAGCAG		

1392RP

	GATCCCCACC	ACCGTCACCC	GCGTGCCCCG	CACCACCCGG	TTCTGTAGGT	ACCGGTGCGCA	60
50	CGTCAGCAGC	AGGTTGCGCG	GCATCTCGCC	GATCGGTACG	GACTCCGGCA	CCTCCTGGAG	120
	CTTCAGGAAC	TGCTGGTCTA	CGAAGCGCGA	GCTCTCGTGA	ACGATCATGT	ACGGGTCTCTG	180
	GCCGCAAGGG	TTCCCCGCGG	CGCTGCCATC	GTCAATTCGAG	TGGTCTGCCA	GGCAGCCCCG	240
	CGGTAGCGCC	ACGTTGCTCC	CCGCAAGCGA	CTGGAAGTTG	TTGAGGTCCA	GCGCCGTCTGT	300
	GTGCCGGCAG	TTGCGGCACA	TCAGCGCAAC	GTGAGTCGCA	CGTGACGTCA	GCACCGCGCT	360
	TGACACCACG	ATCCCGCTCA	GCCGCACCAG	CCGCGAAACG	CTCTGTGAGT	CCAGCTGCCG	420
	CAGCGCCGTC	TCAGCCGCGG	CGCTCTGCGC	CTCCACCTGC	ACCGCCGGCA	GCGCGCCCCG	480
55	GTCCTCCGCC	CGGAGCGCG	CCATCCGCGG	CGCTATTTC	GTCACCGCCT	GCTCAAAGAG	540
	GGGCACCGTC	TCCACAGGCT	CGTCGCGCAC	AGTTTGTACA	GCGCCTCGTT	GTACCAATCA	600

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GATGCTCCGT GTTGACGCGC AGCGCGTACG CCGCACCAGC AGGTTGTTGC GCAACTGCTC
 GCGATATAAN NAACCGCGCG TCNAACGAAA CTCNGCACA AANCNCCNGA AGAGCGCACC
 NCCTCCGANC GGTGCTTTCG CGCCCGCCTC CTC

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1393RP

5	GATCACGGAT	TGCCCAAGT	ANTGCGCAAC	AGTCGTCAAN	TCTGACATAT	CTCTTGCAAA	60
	TGCTAGCCTC	TGGGGGCTTG	AACTAACCAT	TACTTCTAAT	ACCTGGCTAG	CTGCCCTCAA	120
	ATCCGGATCC	AAAAAAGCAA	TATTTATACA	TAACATATACA	CGAAATCTCA	GTTTCATCGCT	180
	AGCTAGCTCA	TCGTATCCGG	GACTGGGAGA	GGAACCAAT	GCTGTGGAAC	CCTTCGAATA	240
	TGGCAGCGTC	GGCGATGTTG	ACCAAGGACT	CGCCTGGGCC	AAACATGCGG	ATGCCACNTA	300
	GGTGGGTGTC	TTTGCCGTTT	TCGTGGTTAG	TCACGACCTC	GATGCGCAAA	AACTGGCACT	360
	TGAGCAGGCC	GTCGGAGGGT	CGGTGTCTCT	CGAAGGTGAA	CTTGACCCAC	CCATTGACTT	420
10	GCGGACTTCT	AGGGTCTTGT	AGTAGGTTGC	GTGCGAAGGG	CTGTGGCCAG	CGTATATGCG	480
	GAGCGTCTCC	NANGTGTAGG	ACTCATCGAC	GAAGAGCGAG	AAGTACATGG	CAAGCTGGAT	540
	GATGTCAACG	CGCTTGCTGA	AGAAGACGTC	TATGGTGTGT	GGCTGGGAGC	CGTCGCTTTG	600
	CCANAANGTG	GCGGGGTTAT	CATCCNAAGG	CGTTTTCCAT	GGGGTANCCG	GCCTTGAANG	660
	AAGAAGGCTT	CCANTAGGCC	AACNAAGTGA	TATCNACTTA	CCCTGGTTCT	CCAATGTTTG	720
	CAAGCCCNCC	TGTTATTTNG	NCCAGAAAAG	AC			

1393UP

20	GATCCAGGAT	ATCATGCCCA	AAATCCTTGA	AGCCGCTGCA	AAGCGCCTCG	TGCAAAATCAA	60
	GAATCTGCAC	ACGGCAGAGA	ACTTACTCTT	CGTATTTTGC	TACCTGACTT	CTATTGATGC	120
	GCGGCAGACA	GTGGACTTTC	TTTCATCAAC	GATCATCGAT	GAAGGCGGCC	GTACCGCCCT	180
	CCAGGCTATC	GTTCCGCGTT	GGCTAGAAGC	ATTTCGAGGT	CTCCGCGGAG	AACATAAAAT	240
	CAAAGAGAAC	ATTTTATCCC	TTTCCAAGCT	TTTCTTCCTT	GAGGATCCCC	GTATAGCGGG	300
	CATCACGGTC	AATGGGGATC	TGATTCCCCA	CGATGGCGAC	ATCATAATCA	CCCGCTCCAT	360
	GGCCAAGAAA	ATGCCTGATA	AGTACACGCA	GATCTCCGCG	GCCGAGAAGA	TAGTCAAGCT	420
	CTTTGTTGCA	GAAGTAGCCT	TCCAGCAAAA	CCAGCCTGAC	CCTGGCCGTT	ACCCTAAAGA	480
25	CGGGTCTGGC	CCTGCTGACC	CACATGAGTC	CGAGGGAGAC	TCAGCTGATG	AAGACTGGGA	540
	GGATGTCGAT	GACATCCTTG	ACTACGAAAA	ATTGCGGGAG	TACGCGGATG	ATAGTGACAT	600
	TGACGACACG	GTGACAGCCT	TTTATTACCA	AGTAACATCG	AAGAGGATGT	AACCACTCTG	660
	CTTACTCAAT	TCTTCAAGGA	AGCGGTTGCC	AGAAATGCCT	CTGGCTTCCA	GGAGATCTAT	720
	AGCAGGCTCA	CTGAACAAGA	GAAGAAGAGC	TATCTGCATG	CATGGTATAG	GAT	

1394RP

35	GATCTCGACG	ATTACCGCGT	ATGATTATAT	CCCAGCAACA	TGGGCACACG	CCGCACACAC	60
	AGACATGATA	CTGGTCGGTG	ATTCGCTGGC	AATGTCCACG	CTGGGTCATG	TGTCCACGGT	120
	GGACCTGGAT	CTGCAGGAGT	TCCAATACCA	CGTCCGGTCG	GTGTGTACAG	CACCAGGCTC	180
	GTCCCTTATA	ATTGCAGATA	TGCCATATGG	TAGCTTTGAG	CGAANCATTG	AGCAGGGAGT	240
	AGAGACGGCG	ATCTCGCTTA	TGAAGACATC	CAGCAGGGTG	GGTGCTGTTA	AGCTCGAGGT	300
	TGGCGCGGAA	GAAAACGACT	ACTGTCTTGA	GCTTGCCGCA	GAGCTCTGCA	GGCGCGGGAT	360
	CCCAGTAATG	GGCCATGTCT	GGCTGACCCC	GCAGCGCATG	CATGCATTGG	GCGGGTACAA	420
	GGTTCACGGC	GCAAAGGACT	TGGGCCAGGC	GCTGGCGGCG	TACCACCGGG	CTAAAGATCT	480
	GCAGGCTGCA	GGCTGTTTTT	CCATCGTCAT	CGAATGCATT	CCAACATAAC	TAGCCGGTAT	540
40	CATAACCGAG	AAACTCAGTA	TACCTACTAT	TGGCATTGGC	GCGGGCCCCC	AGACAAGCGG	600
	GCAGGTGCTC	GTACAGTCGG	ATCTGCTGGG	CATGTGCCA	NGGAAGGCC	CAAAATTTTG	660
	TGCNGAATTC	CCCGGACTTC	CNCNCGGACG	CCATANGTTC	CTGTGCCCC	CTATGTTGAA	720
	AANGTGCCCA	NGCNTCTTC	CCNAAAGTNG	GGGCA			

1394UP

50	GATCGAACTC	CATGAAGGAG	CGTAATGGCC	TCGTGGAGCT	GCACCGCACT	GGGTGCGTAC	60
	ATAGCGGGAT	GTAGGAATGC	GGGATAACG	ATTTCGAAAA	GCTGACTGGG	CTGCGCCTCT	120
	AGCTTCAGCT	CAAGCTGGCG	CAGCAGCGTT	GCTATAGGCT	GTGTGTGGCG	CAAGGTCGAC	180
	ACTTCAGTTG	CAGTAGGAGC	AGGTAGCATA	CGACTAGTTA	TATCGAACTG	GTGCCGGTAA	240
	TGAGGATGAG	GGTCAATTTC	TGGCTCCGAG	CGCTGGCTAG	CACCACAATT	ATCACCAGT	300
	CCATACCTCC	ATGCAATTCT	GAGATCTTGG	CTACGTGCGA	CCGGTTTTGC	ACCCCTCCG	360
	GCTAAGTTT	GCACCGTGAC	CTTCGATTCC	TCCTGGGAAA	TGCGAGATTT	CTTTACCTCT	420
	TTACGTGTGC	CCTGGAATAT	CCCCGGCAGC	TCCTTCGCAT	ACTGAGTGT	GAGCGTGATG	480
	ACCACCATAG	CGGTATTCCC	TCCCCGCTGT	GCGCCGCGAC	TTTCCGCGCG	GTTATGTGCT	540
55	GCTCCCTGCG	CTGCAAAGAG	CTTTCCAAGT	ACCGATGCAA	AGTCTGTACC	CCCTTGTCT	600

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TCCACCAGAA GCATCTGGCC CATTGGCAAG CCCATATGCC CTAGGAGCCG ATCCATATCT
 GCACAACCCG TGGATGTTGT GGGATGCGAA GTAACCGGCG ACGGACGCAA GCCCGGATGC
 GACTGCCTGC CNCCTCACTG TTGGATGCCA ACCTCTCCAC GCCTCTNGAA ANC

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1396RP

	GATCAATCAT	TCTAGAGCTG	GAGCAAAGGA	TACCTATAGG	CTTGCCCTCGT	CATTGGCCCC	60
5	TTTCATTATT	ACATACCCAT	CGTTCCACAG	CGTGTCACAT	TCTGCCATTTC	GAGAGCAGGA	120
	CACCCAAGTT	TTCAAACAGA	ACAGCCTCGT	TCTCTTGGA	AAAGTTGGAC	CTTCTAACGG	180
	TGTCCTCATC	GAAGCCGTCG	TCGCCACTGA	GGACCTTGAG	GGCGTTGGAG	GTGGCTTTGA	240
	TGTAGTCGTT	GAGCATAGGA	ACCGGGTCGT	CGGCAAGCTT	ATTGAAAAAT	TGGTACTTGT	300
	TGGCTGTGGA	GCTGANCTGC	AGGGGAGAGC	AGTTGGGTCT	TCTTTTCGAG	GGTTGCCAGC	360
	TGCGGCTCGA	GCTGGCTGGT	GACTGTGTTG	AATTCTGTGA	GCAGCAGCAT	CCCCTGTTGG	420
10	GCAAGGGAGT	TTTGGGCGGA	CGCCGGTTCCG	GGATCCCTTAA	CCGGGACACG	TGGCACGCGG	480
	ATGTCGAAGA	CCAGTTCGCC	GTAGGTGGAG	GTCTTGTCGA	CCTGGATGGT	GTAGTTGATG	540
	CGCACGGGGG	GGATGGGCTT	GATGTGGGCG	TTGACACCTG	GGGCAGCTCG	GTGAGCTTGA	600
	GGTACTTGCG	AGGCTCTGCG	GCGGGCCGCA	GGAACCTAAC	GATCATGGCG	TCCACCTTGA	660
	TGACAACTTG	TCGTCTGTTCT	GCGTGCTCTT	GGCGTTGCCG	CTNGGGTCTG	CGACNAAGAA	720
	CTCTTGAACA	GGATTTCTTG	TNAACC				

1396UP

	GATCGGTTAC	TTAGAGGGAG	TGCAAGACCT	GGCCTGACTT	ATCTTAGGGT	TATTAGCTAT	60
20	GACGGGTGTG	TTCCGATTTC	TGTCCAAGGG	TTTAGATGCC	ATCAACTCCC	TGAATTCGCA	120
	CTACTTTGCG	TTGTCCGGTG	ATGAACAGAA	GGCCATGACT	TTCGTTGAGC	GTATTAGATA	180
	CTACAATTGG	ACGTTTGAGG	GGATCTGTGT	GGTCTGCTC	GGGCTGATGT	ATGCCGTGTA	240
	CGTGGCGGGG	ACCAAACTAA	ACGAGCGGCG	CTCGGACCGT	CTGTTCTGAAC	AGCTGAACAA	300
	GTTCTTCTGG	GAGGAGCTGC	AGTTTGCGCG	CGTGGGTTTT	TCGTCCCGGG	ACAAGGGACG	360
	GCTGCCATAC	ATCAGCGATC	GGAATGGCAC	ATGGTGCACC	GCATTCTGCTA	CGGGGCGCAC	420
	GTGTGTGGAC	CATATTGTGG	TGAAGGCTCA	CTACCCGGCG	CGCTTCAACC	CTGTGGGGCT	480
25	TGTGGTGGAG	AAGCTGCTGG	GGATGTTCTT	CCCGCAGGTG	GTGGACCGCA	CGGCGATGAG	540
	TTTGTGCAGG	TGACGGTGAC	CCCCAACGGG	AAGTGGACGA	AGGACGAGAA	CAGCGCGGTT	600
	CAGGCGACGG	AGGACGGGCT	GAACCGGTTT	CGGTTTCATCG	CGTCGATCGT	CCACAAGAAC	660
	GGGATGAACG	ACTCGCGCGG	CAAGAACTAC	TTCTCTCTCT	TGACTCACNC	GTCCGANGGC	720
	GAAACTCTCC	CATGGAANTA	CTCTTCATGT	CCGANAACAA	CCACTGAACA	AC	

1397RP

	GATCCCATT	TTCTACAGCA	AATATTACAC	GGCCGGCGGA	CCCTCGACAA	TGCAGAATTC	60
35	GATGCATACA	CAAAACATAT	TACTACAAAG	CTTTCAAAAG	GTGTCTCTCC	CACAGACGCA	120
	TTTCTAGGCG	CACTCAAGGT	TTACATTCTC	AATTGCAGTT	TGAAACGTTT	ACGCTTGCAG	180
	AAAGCACACG	TTATACTTCT	TGATAAAATT	GCGATATTCA	TCAATACAAA	TGTGGTCCAT	240
	GTGTCTGTCTG	AATCGATACA	TACGATACTG	AAAAGTTTAG	CTGAATATTT	TATTGATGCC	300
	AAGGAATATA	AGCGACTCAA	CAACGTCGTC	AATATTTTCAT	TCAACGCATA	TGTGATGTAT	360
	AAGCATGAAA	GCCTTATACG	ACTTGCAGCA	GATCTCGAAT	TATTTCTCTT	TATGTCCGTC	420
	AAACAGGACT	GGTCAATGTT	TACCAAGTTC	GAGAAGTTTA	TTTCTGTCTG	TTCAGGAGAC	480
40	ATCTCAGTAT	CGCTCTTTGA	ACAGTGTTC	AATGTTTATG	TTATGTTCTG	GGATCCCTCA	540
	TTGGCCGGCC	TATGGGATGT	CTGCTTGAAC	AAGTCGTTGA	AGTGTTCATA	GAAATTGGGA	600
	CTAACTAGTT	ACACAGACTT	TAAGGCATCG	TCCGAGCCAA	TGCTAGTGTT	GGTATACAGT	660
	GGATTTGTTT	CTGATATTTT	TACAATACCT	TATAATGGCT	GGGCTCCGCT	ATCGAAAATG	720
	TTATTTCATGG	CATTAAATGG	GGTCTATAAA	TTG			

1397UP

	GATCTGAAAT	ATTGCTCACC	CCCACCGTGA	CCTATGTAGA	TGAACGTGCT	GGAGTTCGTG	60
50	ATCATTCTGA	CGAATTTCATC	CTCTTCTGGC	TTTGAGCCAG	TTACTATCCG	TGTTGAACCC	120
	AAGTCGCAAC	AAAGTCTGGT	AAAATGTTCT	TTAAAGCGCA	GTTCAGTCTT	GGTCAAGTCC	180
	CCATGCGGGT	TTAAAACAAT	TAAGTCTGCT	CTGTCTAGGT	TAATCTTTGG	AGAGATCTCT	240
	CCTCTGAATT	TAGTTAGTAG	CTCGTGAAGG	AAATTTATGG	ATGGTACGCG	GCTCACAGAA	300
	GCATCGGAAA	ATATACTGAG	AGATTCCCAT	GGAACCAAAC	TGCATTCTGGA	GCTTATTACC	360
	AGAAACGTGT	GTCCTAACCT	TGGCGCCTCT	GGTGCCTTGG	CATGATAGTC	GTGAATTAGT	420
	TCCTCAAGTT	GATATGTAT	GAGATGAACG	TCAATCTCAT	CATAGGCATT	TTCTTCGCCA	480
	TGAAAAAGCA	ATATGTCAAA	GATGAAGTAT	ATCAAGTCCT	CCATGAATTC	CACCTTCTTT	540
55	TCGTGAGGAA	GGGCATCCCA	ATCCACCTTT	AAAAATAACT	CTAATATGAA	ATCGTCCACC	600

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TGTTAGAACA TAGACGGGTT TCCATACTGT CTTCTTGTG GAAGATTGT TGTA AACCT
 TTGAAATCCT AATTGAATA NTGCAAATG GTTTTATCCA ACTGTTTTG GNTGAAGAAA
 CCGCNGAATC CCATATCCAG ATCTCATGCG GGCNTCNAT CTACATC

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1398UP

	GATCGCTCTT	CTTTGAAAGA	ATATGTAGGC	ACCTCTCTCT	ATCTTGCGCC	GGAATTGGTT	60
5	CGCTGCAAAG	ATATGAAGAC	GATGACACCT	GCAGAAGCAG	AAAGAATCCC	AGAGTACGGT	120
	GCAGCAGTCG	ACATATGGGC	TCTTGGTGTC	CTCTGCTACT	TCATGATGAG	TGGCTATATG	180
	CCGTTTCGATT	GCGAAGACGA	TGCCGAAACT	AGTGACTGCA	TCTTGAAGGG	TGACTATTAC	240
	GTTGACGAGG	AAGCTCGTGC	CAACGCCAAT	GAGAGCTATA	ACAGCTGCTG	GAACCTTCATG	300
	CAGCGCTGCT	TTACGATGGA	TGATAATATC	CGGCCGCGCG	CACACGAACT	CATGGGGCCAC	360
	GCATTTCATGC	GGGAATACTT	CCAATCGGCT	CGGGCCAATG	ACTTCGCATC	TATCCCGCTA	420
	CTCGAGAGAT	CAAGATCCTC	GAACCTCCCTG	CACCACTTAG	CGCCGCCATC	ACGCGCACCG	480
10	TTTATCTCGT	CTGGCGTGCC	GGTTATTAAC	GAGCGCCCTG	TGCCACGTGT	TGGCTCGCGT	540
	GAGCGCAATT	TGGATAAGTT	GCGGGATACT	TTGCGGAAGA	CCTTTCCCTC	ACTTCGCTTG	600
	AACCTATGCG	CTTTGTTGCT	CAAGCGAATA	CTCCTAATCC	TAATAAGAAG	AACTCTACTT	660
	TTGTTCTTGA	GCCAGCTCCT	CCCACGGGGA	GTCTAATGAA	TGGGTGTTTC	ACGTCACACC	720
	GGAAAGTAAT	CCAACCTCAA	TACGCCAGTC	CTTTCGCGCA	GAAGCTCCGG	CCAA	

1399RP

	GATCATTACT	CGCAGAAACT	GAGATGTTAG	GGGGACCAAA	CTCTTTTCTT	TGATGAGATA	60
20	CGGGAGGATG	CCCTCGGAGA	ACCAGAACAA	TGCAGCAAAA	GGCACGAAGA	ATGCCAACGA	120
	GAAAAGCACG	CATCGCTGCA	TATGCAGTCC	CACCCCATAG	TAGTTCCTTG	CGCCATATGC	180
	CTGGGGGCGAG	AGTGATATCTA	AGCTTGTTGA	AATACCCCTCN	AATATTGCGA	AAGTGATATT	240
	GGTGGTCAATG	GAAGCCAGGG	AAACCGCTGC	CAACTCATTC	TTTCCCAGGT	GAACCCACAAC	300
	TAATGTACAT	ACAACCGGAA	ACATCTGCTC	AAGCAGAAAT	GTAAATATGA	GCGGCACGGA	360
	GTAACACAGA	AGCACCAGAC	TCTCGGACTT	CACGGTGGCT	GGTTCGTCTG	CGAGATCCTC	420
	GGACCCTCGG	AACGCGCTGG	AGGGGCGGCC	CTTGCTGCCA	ATGGAGTAGT	AAGACAGCTT	480
25	TCGGGGCCGT	AGAACACGCA	CTTCTGCCCTT	GTCCGACGGC	AGTTGCTGCT	TAACCCGATG	540
	CATGAAGTGA	GTGTAGTGCA	CCATGTCTGG	CGCGGCGCCC	TCCACATCGA	CGGCCACGAT	600
	GTCTCTGGCG	CTGCCGTTAA	CAGTCGAGTA	CCGCCGTTCTG	TGCTCCTCCA	ATATCCAGTC	660
	TACATTCACT	GCAGAGGACG	GCCCCGCTCA	CTCGCAAGCG	TCGACGGCAG	CGAGACTGTC	720
	CGCGACAGCT	CTCCTCCGTC	AAGCACGCC	TCCTCC			

1399UP

	GATCTTGTAC	GACGGCCGCG	GAAGAATCGG	TGCCATCGTT	TCCAACAGAC	AGTTCCAGTT	60
	TGACGGCCCA	CCACCACAGG	CTGGCTCCAT	CTACGCCAAG	GGTTGGGCCC	TAACCGAGGA	120
	GGGCAACTTG	GCCCTAGGTG	ACAGCGACGT	CTTCTACCAN	TGCTGTGTCG	GCAACTTCTA	180
35	CAACCTATAT	GACCAGAACA	TGCGACCACA	ATGCTCTCCA	ATTAAGCTCC	AGGCAATCAA	240
	ATTGGTCGAT	AACCTGCTGAA	CAGCCACAAA	GGTATATAGT	GCATATATTG	TATTAGTTAA	300
	ACTAGGAATT	TTTGTGGCA	GCTAGACTGC	CCTACGTGGA	TTTCTCGTTG	CGGATCCTGG	360
	GCTGCCGCTG	GCGCTGACGC	ACAAGAGCAA	CTGCACAAC	ACTGGCGTAC	CGCATGCCTC	420
	CTTGTCATT	TTTGCCGCGG	TGGACGTGCG	TGACGTCAGC	GTGGCACGTG	ATCATAATAT	480
	GTCCCGGGCC	AGGCCCTAT	TGTGGCGGAC	AGGAATGCAT	GCGGAGGTGC	AAAATGGTGC	540
	AAAATGGTGC	CCGATGCAAC	TCTAGGCCCG	AGCTGAAACA	AGATTACCTG	GGCAGCCTAA	600
40	ATTGTCAGCG	GCTGCCTGGC	AGCCCACATG	TGTATTGTGC	TTTTACAGTT	CTTGCTGCGG	660
	CTGTCCAATA	CAGCCGATCG	CGACTTTGCT	GCGCACGGGC	CAC TAGGCCT	GCGCGACAAA	720
	AACTGCAGGC	GCGCCGGCGT	GAATGGCGCC	GGACGATGTG	CTGCCGCGGA	ATTCC	

1400RP

	GATCCTGTCA	AATATGGCCA	ATACCAAGCA	GCCGCGTGTT	GTAGAGCATG	TGGTTGAACT	60
	CAAACCCCTCA	AGCAGCCGGG	TTTTGGACTG	TGCACAGGAG	ATATTGTCTC	CATTTCACA	120
	GTCCAAGAAC	AAGCCCAGGC	CGGGGGACTG	GAATTGTCCC	TCTTGTGGTT	TTTCTAACTT	180
	CCAACGGCGC	ATTGCATGCT	TCCGGTGCTC	CTTCCCAGCC	ACTAGTGCAG	TGACGGTCAG	240
50	CAAGCTGTAC	AAGCCATGCT	AGCAACGCCA	TTATCAGAAC	CCACACCACG	TCCCATCGAA	300
	ACAACAGGTG	CAGCACCOCG	AGATTTCACGA	CCAAGACACA	CAGCAGCATT	CTCAACATTT	360
	CAACATCCAG	CAGATGCCGC	AGCAACTCCA	AATGCAACAG	CAAGCGCACG	GTACCGTTCA	420
	AGGGGGCAGT	AGCATGCAGC	AGTACAAGCA	CAGGCCTCAG	CACGGCTTAC	AGGCGTATCT	480
	TGGCTGCTAC	CAACAGCAGC	AGGCGAAGTC	ACAGCAGCAG	TACCAGATGA	ATCAGCAACA	540
55	GGTGCAGATG	ATCGCTGGCG	ACGCCAGAGA	CGGTATAACC	GGTACAACAA	AATGGTGACG	600

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GGCAACGGGC AGAACGGTAA TTCTTGACG GAAATGGCTC CCTGGGCAGT AGCAACGTGC
CCTTCAGAGC TGGCGACTGG AAGTGCTTGA ACTGTTCCTA CCATAATTTT GCCAAGAATA
TTGTTTGTCT GCGTTGTGGT AATCCAAAGA CGGCCAT

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1400UP

	GATCGGCGGG	TACTTCAGGT	CATTCTCCTC	CACCACCACC	ACCAGCTGCC	CGGGCCCCGG	60
5	CTCATACAGC	TGGTACGCCA	CGCGAACATG	TCGCTCCGCC	TGCGGCACAT	CCGCCTCGTA	120
	GAAGTATGCC	GCAGCCACCA	GCCGCGTCGC	GCACTCCCCG	CCGCGGCTT	GCGTCAGCGT	180
	CCCCACTAGC	TGCGCGACCG	GTGTGAGCTG	CACCATCTCA	GGGGGCATCA	GCCAGCTCAG	240
	CGTCGATGGC	ACCACCAGTG	CGGCCGAGTA	CCGCTCGCCG	AGCTTCCCGC	TGAACTCGAC	300
	CTGCGGCTCG	GCCCCCGCGA	GAAGCGAATG	CGGGTCCATA	GGGCCGAGGC	AGTCCAGTTG	360
	GTGTCTGGGA	AGACGCTCAG	ATTGCCATTG	TTTGAAGTGT	CCACAGTTAG	AACTTGCACT	420
10	ATGCTACCTC	CGCGGCGCCT	GCGCGACCCC	ATAGTCACAT	ACTATCATCC	TCACACAAC	480
	CAGTACTTGC	TGCGAGTCCC	AACTCAAGCT	AACGAGTACC	AGACTTGGTT	TTGGCTGTTG	540
	CTGTATGCAT	TCCAATGGTT	TGTATAATCG	AAAAATTGTT	CAGTTGCTCA	GCACATCTCA	600
	TACAAGCAGG	AACAAGAGCG	AGTCGCGAGC	CAAAGACCTC	TTAGGCATTA	GTATCGGTAG	660
	CTAGGATGTC	GGCAGAACAG	TTGCGACAAG	TACACGCAGT	TGCAGGGCGA	ATTGGAGGAG	720
	CTGGTGGTGA	CAGACAGAAG	CTGGAGACGC	AGCTGCAGGA	GAACAAGATC	GTGAA	

1401RP

	GATCTTGTG	TTGGCAATAC	CCTGTCTTAC	GTTGAAAAGA	AGTGTCTCTG	AGGTGTCCAT	60
20	CAACAAAAAT	ATTACCAAGT	ACAACACCCA	CCCGAACTCT	ATTGGCCAAA	ACATCCAACA	120
	ATGTCGTCTT	ACCTGCACCT	GAATAACCCA	TCAGAGCAGT	CAAAGTCCCA	GGCTTTACCC	180
	AACCATCCAC	GTTGGTTAGG	ATCCTCCTGG	TTTCATTCTT	AATCTGTATA	TCATAGCAGA	240
	CATCTCGCCA	GTGGAAAATG	CTATCAGAAC	CAATTCTCTG	AATAAGTTCG	CGGGATTGGT	300
	CACTTCCTAT	AGTACTAGAT	TCCTTTCTCT	GTGCATTACC	AAATTCTATG	TCGCAGTTGA	360
	TGGCCTTTTT	ATTTTGCTTT	TTTATTTTCT	TCAAAGTTGA	CCTTAGGAAT	ACAGCCATTT	420
	CACCTTTTTG	CATCCCACTT	TTATTATACT	CAATTAAGAT	CAGATAAACA	CCTAAGAAGA	480
25	AAAATGCATA	AGCAAGAACG	ATCCCCCAAT	TCATCCACTT	GTTTTTGGTG	TTGTAACCAT	540
	AAGCAAACCT	TATGTAACGG	GTCCCAATTA	CAAAGCTCTG	ACCAGGAACT	GCTCCCACCG	600
	ACAAGCAGAC	TTTATTTCGA	ATAGGGAATC	CCTCATAGAA	ACTACCATCG	GGTACCATT	660
	GAGAACATTC	GAATATGCGT	CCGTCAAATT	CATTCGCAAC	CATGGCTTCC	ATGATGCGTG	720
	CGA						

1401UP

	GATCTGCTGA	GATTAAAGCCT	TCGTTGTCTG	ATTTGTTTTT	TATTTGGAAG	TCTGCAGGAG	60
35	CAGGCTTTGA	AATAGAGTTC	TTATGTTATT	TAACGTCGGG	GTAACGAGTA	TACAAGCATA	120
	TGTTTATGCG	TATGCTAGTT	ATATGCTTTG	AAGAGGTGGT	CTGCAGCTGG	CGGTCTATTT	180
	TATTTTATTT	TTTCATTTCA	CTAAGACTTT	ACATTTTTTT	TTTAAATTAT	TTTTTTTTCG	240
	CTAAGACTGT	GAACAGCGAT	TTTAGAAAAA	AGCGAAAACG	TTCAGGAGGC	CTCAGCTACA	300
	TGATATCCCA	GGCCTTGAT	TTGTGAGACT	GCACTCCCGG	GCTAGGTTGT	GACCAAGAGT	360
	TGACGTGCGG	CGCGGTGCGG	ATTGCAGGGC	TTCACAGTGT	GGTTAATTTA	ACAATTTATA	420
	GAGAATAGAG	ATGCCCCGAG	TTAATCAACT	GTCGGGCGCG	CCAAATTCTGA	TTTTTTTGGAG	480
	TTTGTGATT	TTCACAGCAG	ACGAGAAAGC	AGGACAGGCG	GCGCGCGCCA	GGCAGTCCCC	540
40	CCTGCAGGCG	TGAGCGGACA	CAGAGAGAAA	ATACAGGAAG	ATGAATACTG	ATAATCTACA	600
	GATTTTCATT	ATATCTCATT	GATCCGCTGA	TTATCAATGA	AAGTACCCAA	TGATCCATGA	660
	AGCCAGTAGA	TGTTAGTATA	TTTTATTAAA	TATATGCACC	TTTGTATTAC	AATCTCTGTT	720

1402RP

	GATCAGGAGC	CCATCAAGGC	GCCTAAAAAT	CGCATCCCCG	CTGTCGGTTT	TCCCCACTAC	60
50	GCCGCTGTTG	CTTGAAATAC	AATTACTGCT	GTAGTTCCTC	CTGTGATGCT	GGTTGAAATG	120
	TTGCGGCGCG	AAAGGGTCTG	CCTGCTGAAA	GGAGCTGAAA	GGTGGTGACG	TGGTTCCGGG	180
	ACTACTAGCG	TCTGCAACCG	TCTTTGAGCC	CAAAACACGG	AGGCCGATTA	CATTCCCGTC	240
	AGCCGGCCGG	AGGGTAGAAG	ACCTCCCCCT	ATGGGAGTTC	ATGCTCTTAC	TGCGGGTGTG	300
	GTAATAGTAC	TCACCACCAC	TGCTCGACGA	AAGCGGAGCA	GGGGGTAGCG	CTGCCATCTG	360
	TTGTTCCCTC	CTGCGACGTG	CTCTAACTG	TGCCAAACGC	AGCTGTGCCT	GTTGCTCCTG	420
	GTGCGCGTCC	ACCTTGCCCA	AGAGCTCCGG	ATCATCATGC	AACATCTCCA	GCACCTCCAA	480
	TTTCCGCCCT	AAGCCACGTG	ACTCGGCTTC	CAGGTCGTCC	ATTTCTCGAT	GCTTGATCAT	540
55	GACCTGCAGA	TGGAGCTGCT	CCAGAATCTC	GCGCTTCGCT	ATCTCGTATT	TTATCCGCTC	600

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CGTCTCCTCG CTCTCAGCC CCAGCGGCCC CTCCTCCGCA CGCAGCCCGC TGTATTGTC
GTCGCCCAGG GAAAGCTCGT GCGGCGACTT CGGTGTCGCC ACCTGGTAAT ATGCCGGCC

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1402UP

	GATCAAGTTA	TCGTTGATCA	AAGCGTCAAT	ACCCCTTTTCT	CTAAGCATGT	GCCAGGTTTC	60
	CTTCGCGGCG	CGTAGGTATG	GTTTCCCGTA	CAACGCAATG	AAGCAGTAGG	CATAGTGGTT	120
5	GAAGTACTCT	GCCATCCATT	CAAAGACACC	AACAACGGCA	TCCAAGATTA	ACCACAAGCA	180
	CTGCATCCAC	CCACTGTCCG	ATATCCCGGA	AATAATCCCA	TTGCGAAGCA	GCTGAATAAT	240
	CTGCCGCGAGT	AGTTGAATCA	GAGACACAAAT	CAGCGAGCCA	AAGCAAATGG	ACCCAAAGGA	300
	AGTGGTCAAC	GCTCTCTTTA	ATGAGCCAAA	AGCTGGCCAA	CGTGGCATGC	CTTGGTCCGA	360
	CTTCGAAAAA	TAGTACCAGC	AGCCGTAGAT	GCCCGCGATG	GTGCAATGAA	TCACATTCCT	420
	GATGACCTCA	GAAATGTAGA	ATCCACAGAA	GAAAACGAGT	ACCAAAATAC	CAATTAACTT	480
10	TCCACGTGAG	CAAGAGCCAC	CAGATACATC	GCAGCCACCA	TTCTCGCTCT	TCGGGTCATA	540
	CTTTATGTAG	GTCGCAACCA	ACACTACAGA	GAATATGACA	GAGAACGCAG	CCGACACAAT	600
	GGTACCTAAT	AATGACACAA	GCCACGTCTG	TGGATGTTTC	TTCAATACTG	ACATGACCGT	660
	ACGCAAGACA	GCGACACTAA	ATGGAATCCT	TGAGCGCATT	AACCAGTAGC	ACACCGCCGT	720
	CAGAAT						

1403RP

	GATCCGTTCC	TTGAGAAGCA	CCTAAAGCCT	GAACCTCTGG	CAGAAGCGAT	CAAGGGAACC	60
	TCTTGGGAGG	GTAAAGTTAG	TATTAACCTG	GTAGACGGAT	TCGACCACTC	GTATTACTTC	120
20	GTCAGCACGT	TCGTGCCGGA	ACACGCAAAG	TACCATGCAG	AAAAGTTGGG	TCTAGTTTGA	180
	GATTTGACGT	TGCGCCTGTT	AATTGGTATA	TACTTACATA	TTTAGTCATA	TGACGGCTTC	240
	AAGTACTCTG	ATTCTGCATT	ATAAGTGCAG	CCGAATGCCA	GCCTCCGGCA	GTAAATGGCAA	300
	CGCAAACGTA	ATTTGCCGGT	AGTTCAACCT	TGGCCGGTTG	CAGCACGCGT	ATGCTCCGAG	360
	CAGACTCAAA	CGTCGCTATT	TGGCGGGTAT	CTACAGCCTC	GTCCGGGATCT	CCCTGCCCAA	420
	GACAGCCACA	GATATCACTC	TCCAGCCCCC	AGGAGTAGAG	TTCACCTTTG	TCGGTTAGAG	480
25	CTAGGTTGTG	GTAGTCTCCC	GCAGATACAG	CAATAAACTT	CTGGCCTTGT	TCCAAATTCA	540
	TCTTCATGAA	TGAGTCCTCG	ACGATATCAC	CATTATTTCAC	CTTCAGGGTG	TATGTGCTAT	600
	TCTCGGTACA	TAAAACCAAGT	GTCATGCAAG	ATGCCTCAAT	CTTCGTTTTAA	CCGTCCATCA	660
	AATGGCAAAT	CAACGGTTTTT	TGAAACGCCA	TGAGTGTATA	TCCACAGTTT	GCGCCCATTG	720
	TTAGTAATGT	A					

1403UP

	GATCTCAATA	TCAACCAACT	TGTGACGTCG	CTTAAACAC	CATATGCGGA	GGACATTATG	60
	TCCATCACCG	TGTACAAGGA	CAATGTTTTT	GCCACGCACA	AGCAGGGCAT	TACGCGGTTT	120
35	CACCAAGGGA	ACGTGAACCT	CTGGAATGCT	CACCAGGGAC	TCGTCTTGAG	TAGCGAAATA	180
	TTGCGCAAGA	GCTGTACCAG	TAATCGTATA	GATCGGATGG	TTACTGGCGG	AAATGATGGG	240
	TCATTAGCGT	TGTGGAATAT	TAACGAATGG	CTGAACGGTA	CAGCGTCCCC	GGGTGGATCA	300
	GCCCCGACCG	AAGAACACTC	GCTTCCCTCT	GGCGAGCGCC	GAAATTCCTG	GACCGAGTAT	360
	CAACAAATCC	AGTTAGATAA	CGATCACATC	ATTGCAACAC	TCGGGGAATT	CATTAGTTAC	420
	CAGACTGTTT	CCCAACTCCC	AGAGCCCCAA	AATATCATCG	ATTGCGGTAG	GTGTGCGAAC	480
40	TTCCTGCAAA	ATCTCTTCAC	TAAGCTCGGT	GCTAACCAT	GTGGGCTTAT	ACCTGTCAGT	540
	ACAGGCAGCA	ACCCGGTGGT	TCTCGCGCAG	TTCAAGGGCA	ATGCAGCCGC	GCCCAAACGC	600
	ATACTATGGT	ATGGCCACTA	CGATGTGATA	TCCGCGGACC	ACCGTCGCAG	TGGGACAACG	660
	ACCCCTTCACG	CTCACTTGCG	AAAATGGGTA	TCTTAAGGGA	AGAGGCGTGT	TGATAAC	

1404RP

	GATCTGCAAC	GTTACTGATT	ATCCTGTAAAG	CCCTCTTTTG	GGTTAAAAACA	TCCTGTGAGT	60
	TAACAGTCGT	GTTGAAGATA	GAAAAATAAAG	CAGTGTATGA	TGATGCTGGA	ACAACCCCTG	120
	ACATAACCAC	CACAAGATCT	AGAAGTGTGG	CACTCATTTT	TGGCTGGCCC	TTACAGGTT	180
50	GGCTAGACGC	CTCCTTATCC	ATGGCATCTT	TTAGTAATGC	GCATACGTTA	TCAAACGTGT	240
	TAGACAGGTT	TTCCGCAGAA	GTAATTTTCA	AGTATGCCTC	GATGGTTTCC	AAAATATAGC	300
	TCCGAGCGTT	GGGTGCAGTC	TGCGTGTAGA	CATTGAAAAAG	AACGGCCAAC	ATATTGGGCG	360
	ATTTCTGGGA	GAGGTATTCT	ATGTTTTTCT	CCGCTTCTGT	CGGCGGGAAT	TGCTGTCCCA	420
	TAATAATGTC	GTCCTTATAC	GCACCATCTC	TGTATAGAAG	ATTACTTGTG	ACCAAGACCT	480
	TCAATCCATT	GCATATGACA	GTACGCAGTT	CAATTCTGGA	ATAAAGTAGG	GACGCTAACT	540
55	CTGCAGCAAA	CTCATCCGTG	AATACATCGT	TTAGATCTTT	TGGAAGAACG	CAGAACTGAG	600
	GGAAGGTAGA	CCACAATTGG	TCAACAACAG	TCTGAAGTAA	TGTGCACTGG	ATAGACTCCT	660

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TATCCAGTTT CTCAATGGTG GACTCGAAAT GACGAATGGT AGGAATAAAT

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1404UP

	GATCTTCAGC	AAGATCAGCA	CCACTTGACG	CACTACAAGA	AGTACCGGCA	CTGGCGGTGG	60
5	CAGGCCAAGC	GCAGGCTGGC	CGGCTGCGAG	TCAGGAAAAG	TCGGAGCAGG	TCGTACAGGA	120
	GCCCCAAAAC	GCCGAGCCGC	TGGCGAAGCT	GGGCGACGCG	CTGACGGTGA	CGGCGCTGAC	180
	GGGCAAGATG	AGCTACTACC	GGCAGCTCCA	GGGAAGCGTG	AGCTCGTTGC	TCAGTTCTGT	240
	GTCGCAACTA	ACGACGTCCA	CCCCGGGCGCC	AGAATGCGAC	TTCAGTGAGC	AGTTCATCAC	300
	CTTACTCGTG	AACACCTACC	ACGAGATGTG	TCTGGATGCA	ACCGTCACAC	CGTTCGACAA	360
	GACTAACCCG	CCATCTGCTT	TTCTCAACAA	GGTAGCGCGT	GCTGCGGTGG	AGCGTTCTGA	420
10	GCAGCAGAGC	ATCGCCATCG	GACGTCCGCG	CGATAAATGG	TTGTTGACCT	GCACGCGGAA	480
	GCGGCTTCTA	CAGGAAATAA	AGCGGGAGAC	CGAGGACGTT	CCACAGGGGT	CCGTGCGCTC	540
	GGTGGCCTGT	TCCATGAACC	ACGGCACCCCT	ACAGCGCGAT	CTAAGCTCCG	CTTTTGACAG	600
	GGAGGGCGAT	TTCTTCTACT	GGGATCCGGA	CTTCCAAGT	TTCCAAGGCA	TCACGGCAAA	660
	ACTTCTAACC	GACACTGGAG	ACATCTCGGG	CAAAAATACC	CCATGTCTTT	GGATC	

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1405RP

	GATCTTTCAT	ACTTTCGGGT	TCGTGCTATA	TAACATAAGAT	TGGACAGAAC	TGCAAGGGCC	60
	ACAGAGGAAG	AGCTGCTGCA	TTGCACATTA	GGCAGGAACA	GCGAATGTCT	ACAAATGCAC	120
20	ACTACACACT	ACCGCTCTCA	GCCGATCCCA	ATCTCAGATG	CGCACAGCAA	GGGACCCAGT	180
	TCTTTGCCCA	TGCCGCTGTA	CTCGCAGCGG	GGCGCAGATG	GGCTGCTAAC	CATTAATGCG	240
	AGCGCTGTGG	GCTCGCCTGT	GGGCCCCGAG	CCGGTGATAC	CTCCACTCAT	GCACCAGGTG	300
	GCGGTGACAA	AGCACGCTCA	TATCATGCCA	GGCTCGTACG	CGCTGCGACA	GAGCTCGCCC	360
	CAGGTCACGG	CGATTATGGG	CGAGTTAGCG	ATGCTGAAGA	AGTCGATATT	CCAGTCGCTG	420
	AACGGCGAGT	TGACGACGGA	GGAATACAAC	AGCATCTACC	AACATTTGAG	TCAACTGCTG	480
	GCGTCCCTCC	CACCGCCCGT	CGAGCCATCT	GCAGCGCAGC	CCCAGCTGCG	ACTGCCGTCC	540
25	ATATCTCAAA	TTATGCCGGG	AACAGAGCCC	CAGGAAGTCC	AACGTACCTT	CATCATAGCA	600
	TCCTCCGAGT	CACAGCAGGG	CCAGCCGTAC	ATCTCGCCGC	CGTTAAGCTC	GACAATGTCT	660
	ACGCACCCGC	TTTCACCGGG	CATGTCGGTA	GCCAAACCGA	ACTACTCCGT	GAGCACCAAG	720
	AAGAATGTT						

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1405UP

	GATCCAAATA	ACACCACGGT	TTTCATCGGC	GGGTTGTCTT	CGCTCGTGAC	TGAGGATGAG	60
	CTACGGGCTT	ACTTCCAGCC	ATTCCGACAG	ATAGTCTACG	TGAAAAATCC	GGTCGGCAAA	120
	GGATGCGGCT	TTGTCCAGTA	CGTGGATCGC	AGTTCCGCGC	AGAACGCGAT	CGCCAAGATG	180
35	CAAGGATTTT	CAATTGGTAA	TTCCGAGGGT	CGGCTCTCAT	GGGGCAGGAG	CGCAAAGCAA	240
	ACAGCCGCTA	TGCACGAGG	GTTTGCCATA	GCACTACAGC	AGCAGCAGCA	GCAGCAGCAG	300
	CAGCAGCAGC	AAGCCCGCCC	GCAGCATTTT	CAGCAACATC	AGTATCAGCA	TCAACAGCAT	360
	CAACAGCAGC	CTCAACATGT	CATTTCTGCA	CAGCCGTTGC	TGCAGCAGCA	ATTGCAACTA	420
	CAATTTCCTT	ATCAGCATCA	ACCTGCCATG	CCGCGAGGCT	ACGGTTACAC	ATTGGACTCG	480
	TTGAGCGGCA	CCGGTTGCAA	ACATGTTCCA	ATGCAGGGTT	TTCTTTCCCG	TAATATCGGG	540
40	TTCCAACCTT	CTACGGCAAT	TGATAGCTCT	CCAGCAACGA	CCTTGCTTCC	CAACCTTTCT	600
	TCGTTGGACT	ACTCTGGGTT	TCCACCTTCC	ACGTCAGCGT	TCATTTTTC	CCCACGAACT	660
	CTTTAGGCAC	AGCTTTTACA	ACATCGCCTA	GATTCTCAAC	AATGGCAGCG	TGTCC	

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1406RP

	GATCTCCTTC	CAGTGACGCT	GATGCACAAC	TGCGGACCTC	AGCCCGCGTG	CCTCACGTGA	60
	CCACAGTGGA	CATTTTCTCA	GTTAGCGCTC	GTTTAGCTTA	GCTATACGAG	GGATGGCACC	120
	ACTTAGCGCG	TGCTGCGGAA	CCAGATACGA	TGAAGCCGCC	CAAATTCGAT	AGAATGCTGC	180
	CTCGCTGAGC	CGCCGTCTAT	GGGAAACGAC	CAAAGGTTCC	GTCTGCCGCA	TCGTATGTAT	240
50	GTGCTGTGT	ACGAGGACCG	AAAAGTTGAC	TTTTAACGAA	GTAGATTTTT	TTATTAGATA	300
	TTTAAGCACG	TATGCGTTAA	CGAGCAGCTT	GCAAGGCGTA	TACCAAGGCT	CTGTGCGCTT	360
	ATCATTAGCA	GGGCGACATG	TCAGAAATCCT	TGCTACAGAC	AGTGGTGGCG	TACGTGGAGT	420
	TGGTGCTGCA	CCACTTCATG	GCGTTGTGCT	GGACGACGCA	GCTGTCCATA	GTAATAGTGG	480
	CACCATTCAT	ATACTCGCTG	GTTGTGCGAG	CGTTATATTC	ATTAGGAAG	GATAGAGTAC	540
	CGCTAGTGCC	GTTTATGGTA	CCCTGGGTGG	GTTCCGCGCT	CGCGTATGGG	AGGGCTCCGT	600
55	ACGAGTTTPT	TGCAAGTGTC	AGCAGAAGTA	TGGCGATGTG	TTTGCCTTCA	TGCTGCTGGG	660
	GCGTGTGATG	ACGGTGTATC	TGGGGACGAA	GGGCCACGA			

1406UP

	GATCTTCATT	AGAACGCGCG	GATTAGTCAA	AAAGTGCCGG	AATGTTCCAT	CCACTAGGCC	60
5	ATCTGCCTTC	ACCCACGGAT	TGCAAATGCA	GACAAGGTTT	ATTAGAATTA	TACCGATTGC	120
	CCAAACGTCG	CCTGCAGCAG	TAGGAGCTCG	GAGCTCACGA	CCGAGCGATC	CGCGCTCGGG	180
	TGCCATGTAG	TAAGACGAGC	CTACGCAGAC	ATTGGGGGCG	AGCTCCGGCA	CGGGTGTGGC	240
	CAGCCCGAAA	TCGCATACAT	GTACGTTGTA	CCATTTGTCC	AGAAGAATGT	TCTCCGGCTT	300
	TAGGTCGCAA	TGATAGACGC	CGAGTCGGTG	GCAGTAGAAA	ATAACCTCGC	ACAGCTGCAG	360
	GAAGACCTTC	TTAATCAGTA	GGCCATCCTT	AGCAAAGACT	TGCTCGTTGA	CAATGGCTGA	420
	GAAAAGGTCTG	CACGTGATGT	AATCCATAAC	AATAAATGTT	GCCAGGCTTG	ACTCCATCAC	480
10	CTGATGTATG	GTAACCACAT	GTTTCGTGGGT	GTGCACAGTC	AGGTGCATCA	GCAGCTCCTT	540
	ATAATGTGGC	GCGTGGGCCA	GCTGCTCTTG	GGATAATGTC	CGGATCGATT	CCAGGTCCAC	600
	AGATGGTAGA	TACAGCCGGT	TCTGGAAAGA	TTGAAGAAGT	GGTACAGCTG	CGTGCGCAAA	660
	ATTGTTCGACC	GGCCTGACGC	CTCGTCTGCG	CTGCCGCTGT	GCTGCTTCA		

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1408RP

	GATCCCGCTT	ACCAAGCAAT	TACAGGAGAC	AGAAAAAGAAG	GATAATAATT	TACCACAGAA	60
45	CTCCAAGCCT	GACAGAGCAG	CGATTTACAT	TCTGAGTCAC	ATGACAGCAG	ACTCTCTTTG	120
	CTTTGGAGCT	TCAATAAGCA	CCAATATGAA	TATGAATAGT	TTTAGATGCT	TTGTATAATT	180
	ACCACTATTA	ACTTTATCTT	GATTAATATT	TATTATTTTG	TTATTTTATT	ATTTTATTAT	240
	TTTATTATTT	TATTATTTTA	TTATTTTATT	ATTTTATTAT	TTTATTATTT	ATTTTATTAT	300
	TTATTTTATT	ATTTATTTTA	TTATTTTATT	TATTATTTAT	TTATTTATTA	TTTATTTATT	360
	TGTTTGTTTG	TTTATTATTT	TTTTATTTAT	TACCTTTTTA	TTTTATGTTA	TTTTATTTTA	420
	TTTTATTTTT	ACTTAGTATA	TAATATTATA	TTATATCATA	GTATAGTTAT	ATTATGGTGA	480
50	CTTTATTTCAT	TATATAGATT	GTATTTTGTG	AACATAATAT	ATATGCTATT	TCTATTTCTA	540
	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	600
	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	TTTTCACT	

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1408UP

5 GATCCGCCTT CCATCGAAGA GGGTACTGTT TGATTATGGT GATTTCTTGG TGTGGGTTCCG 60
 ACATTCAAGT GCATAGTTGG AGGTTACCGA TAACTTAGAT TTTCTTATAA ACGGTTACCC 120
 TACGTCTTCG CGGTTCGGCG ATATACTGAT TAACAGTTGG AGAGCCTTGG CGGGATACTG 180
 TGAATGCCTT CTCCTCAACA TTATTTGAAT ATGCAAACGT TATTTAAATT AAGTAACACA 240
 CTTGTGCTTA TATATTCAAT TGTTCCAAGC GCGCCATCCA ACATGGCGAT TCTCATCTAG 300
 TTTGAGAAGT TGCCTCTATT CTTATTCTGT GTACGGCAAC GGTATTAGGA GAGACTTCGA 360
 GTTTTTGGAA CTTCAAAGTC AATACTTCAT CATCGTAAGT AGCAGTTACT TGGCCTAAAC 420
 CAGTGCCAC CTTTGTAGGG AGCCTGATTG TTCGCCGAAA CTCCGGGTTT GTGGGTTCTC 480
 10 CAGTAGTCCA CGCGTCTGTA TTCTCATCCG TATTAATGGC TGGCACGACA ATAGAAAGAA 540
 CTGCATCATT CATGTCTCGA TGCAGGGCAA TATCTATGTG GTCCTGAGAC ATTACGCCAG 600
 GAACTCTGAT GTGGATCTCA TAGGCGTCCG AACGCTCCAA AATTAATAAT GAAGGAAGAA 660
 CGTCAGAATT TGC GCGCGAG AGCTTGATT CTGAAC TAGC CACACTC TCAGCTTTGT 720
 GT

1409RP

20 GATCCTGGCT ATCTACCTGC TGCTGGGCGC GCTGCACGCC ATACTAGGGG GCACATTTCAG 60
 CGGATTAATG TATGTGGAAT ATGCGCGAGT AGAAAACGCA CGTKCATGTG ACAACAAGGC 120
 CACCGGACTA ACCAATTTAC AGAACC GCGG CTATTTACAG GGCTGCCCTG ATCGCGATGA 180
 GTACTTGGAT TCCGCTTGCA TCCGCAGTCG TACAGGCCCT GTACCTGCTA TCGCAGCAT 240
 TTGTGGCACA ATCCAAGCTG ATATAGGATA CAGACATCCA GCAAGACGCT GGATGGATCG 300
 TGTGTATCCC TCTGCTGCAT CAATACGCTA TCGCGGGCCG GCAGCTTATT GTCACGTGAT 360
 GCGCTATCTT GTGGAGCACC CAGACATATG TTGCTGAGCC TCCCTCAGCT ATATAAGCGT 420
 CGAAGAAGGG CGCGAGTCGA ATACATGTCT CTGGCGCTGT GTGCCTCGTG CAGTCTCCG 480
 25 CGATGTCGTC AACTCTCATA AACCGTTCCT TGGCAACTAT CCGTACAGAG CTTGCCTTTT 540
 TGGTTGATT CCGGGTCATT ACGCGGCAGC AGTCAGAGCA GATTGAATCT AATCTTCCAA 600
 ACCCTAACGA AGCCCTCCGT GCGCTCCCG CAAATAACGC AGGGCCTGTG GAGTATGTGG 660
 AGGCACTTTA TGC GTTTCAG GCGCAACAGC CTGGTTGACC TAGACTTCAA

1409UP

30 GATCGGGGAC CAGAAAACCA CACAACCTGGT CCTTGAGGCG GCGGTGGGCG TATACGCTGC 60
 TACTGTCTCT TCTTGTGCTA GCTGTGGCCT ACGGCTCTGC GTGCGTAACC GCTGGCATGT 120
 GGCTCATCAC CAGAAAATAT GATGTCTCAA CCGAAGTTGC AATATTGTCC TGTTCCTTGG 180
 35 TGGTCTGTTG CTACGGTGTG GGACAGCTGG TTTGGGCGCC TCTGTACAGC CTGTACGGCC 240
 GCGGATAAAC GTACTTCACA TCTCTATTCC TTTACGTGGT ATTTAATATT CCATGTGCGG 300
 TGGCTCCCAA CATCCAGACG CTTTTGGTTT GCAGGTTTAT TTGCGGCGTC CTGTCTGTCG 360
 CTGGACTATG CCTAGTCGGC GGCTCTCTCG CCGATATGTT TCCAGCCGAC CTGCGTGGGT 420
 TGACCATCGC GTTCTTTGCA TTTGCACCAT ATGGAGTCC GGTATTTGCG CCACTTATAA 480
 ACGGATTTCAT GCTGTCTGCA ACAGAGAGGC TTGACCTTAT CTTTGGGTC AACATGGCGT 540
 TAGCCGAGAT TGTTTGGCTG TTAGTCGCAC TGGTGCCCGA AACATATGCG CCAATTATTT 600
 40 TGAAACGGCG CGCAGAGAAG CTGAGGAAAC TAACAGGCAA CCAGAATATA ATGACAGAAC 660
 AGGAAGCACA GGGACTCTCC CTGTCCGCAT GGTGCAGACT TGTCTACTGA GACCG

1410RP

45 GATCAATTTCG TCACATTTTCG CGTATGCAAT TTCTACCATC TCCTCTTTGG TAGCCTTTAA 60
 TTCCACTCCT GGTGTAACAT CACTAATGCC AATAGAAAAG CCTCTATTTC CCAGATAGCG 120
 CGCACAAAGC TTTGCCATCC TATTCATAGC CTCGTTGCT TCTGTGGCC CGAAATCTCT 180
 CAGAAATAGTA TAGAATACGG AATGTTTCTT ACCATCACCA AGCACAGACT TATCCATGAC 240
 ACCAGACAGA ATATTAGAGC CTCTGATAAC TACATAACCA TCATTAGCAG ACATCTCATT 300
 50 TGGTAGGGCC TTATTCTTAG GCGCAATATA AACCTTATTC TTTGCATCCA AATTAATAAT 360
 AACGGGAGAT TTCTTGTTCG GTTTTATCAA TAGAGAGAAG AGCTGTTTC CAGTCCATAA 420
 GTAGTGTGGT CGCATAATG CAGGCGGCGG TATGTCAAAC TGCAGGTTGC CGTCAGACAT 480
 CATAGAAAGC ATTTGGACAA AAGTTGCGCG GTCGAAGAAG GAGTCTTTGT GAGAAATCAA 540
 ATATGATCCA GTGATGAAAT CCTGGGTAGC TGCAATGATC GGTTCACCGG ATTTCCGAGT 600
 CAATAAATTG TTTTGGACAC CCATAAGGTT GATTGCTTCC GGGCGAGCCT CTTCGTTG 660
 55 AGGAACATGC AAGTTCAATT CGTCAACATC AAAATCGGCG TTGTAGGGG

1410UP

	GATCTGAGCC	CTAGCATCTT	CGGTGGAAG	CGGGAAGTCT	ATTTTCCTAT	CCAAACGACC	60
	GGAACGCAGA	AGCGCTGGAT	CAAGGACATC	GACTCTATTC	GTAGCAGCCA	AGACTTTTAC	120
5	CCTATCGTCA	GAACCAAAGC	CATCTAGTTG	GTTTAGCAAC	TCAAGCATGG	TTCTCTGCAC	180
	CTCTCTATCA	CCGGACTTCT	CCGAGTCAAA	ACGCTTAGTT	CCAATAGCAT	CCAACTCATC	240
	GATGAAGATA	ATGGTAGGTG	CCTTTTCCTT	CGCCAAGGCA	AAGGCGTCGC	GGACCAGCTT	300
	CGCACCTTCA	CCTATGAACA	TCTGGACCAA	CTGCGGAGCG	GCCAGCTTCA	AAAAAGTCGC	360
	ATTGGTCTGA	GCGGCACAGG	CTCTTGCCAG	AAGCGTCTTG	CCGGTACCCG	GTGGACCATA	420
	CATCAGAGCA	CCTTTCGGTG	CCCTAATACC	CATATCCTTG	AACTTGTCCTG	CCTGCTTCAT	480
10	GGGTAAACAG	ATTGCTTCGA	CTAGTTCCTC	GATCTGCTTG	TCTAGCCAC	CAACGTCGGA	540
	GTATGTTTCC	GTAGGCTTGT	CATCCACTTC	CATAGCTTTC	ACTCTAGAGT	CAAACCTCCGA	600
	AGGAAGCGTA	TCCAAGATCA	GGTACGAGTC	CTTGTTTACA	CCCACCAGGT	CGTTCGGCTT	660
	CAACTGCTTA	AGGGTCCACT	AGCCCAACCA	TGGGGAGAAA	AACGGTTTGT	CGCGACGAAG	720
	TTTCACA						

1412RP

	GATCTGGAAC	CAGGATGACT	GTCTGGCAGT	TAAC TCGGGC	GACCAGATTG	GCTTCCTACA	60
	CAACTTCTGC	TCCGGTGGCC	ACGGTATTTT	CATCGGGTCT	GTTGGCCACA	AGAAGGGCGA	120
	CTCAGTCACC	AAC T T C C T C G	CACAGGACAA	CCAGGTCTGC	GAGTCGGACA	ACGGTCTAAG	180
	AATCAAGACT	TTTCGTGGGCG	CCATTGGCAA	GGTCGACAAC	ATCAAGTTCA	TCAACAACAA	240
	GGTCAAGAAC	ATCCGCAAGT	TCGCTATCGT	CATCCAGGGC	GACTACAAGG	ACGGCACCAC	300
50	CACCGGCACC	CCAACCGGCG	GCTGCCCAAT	CACCAACCTA	GAGGTCAAGG	GCAACACCGG	360
	TAACACCGTC	GGCAAGGGCA	GCAAGCTCAA	GATTCTCGTC	AAGAATGCGT	CTAAGTGGAC	420
	CTTCGCCGAC	AACAACATTT	TGGGCAAGAC	CTTCCCAGGC	TGCTCTGGCG	CACCTAACGG	480
	CATCAAGTGC	TAAGCGCCTT	TTTTTTTTTT	GGCTGCGCCT	CGAAACTATT	ACTATGAACA	540
	TTGGCGTCCA	CCGCCACTAC	AAAAGCATCG	GGTCTATCCC	ATTATAACAT	TAAAATCTCA	600
55	GTTGATATTA	TATTTTACAT	TCGAATGTCC	TTAGGGCTTT	TTTATATTAT	ATAAACTTTA	660

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GATTAAAAAA ACGAGGTACA AGCAGATCAA CGAAGCTTTT CGGCCAGCCA

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1412UP

	GATCGAACGA	GATAAACAGA	GGTATTGGTT	GTTATCACAA	ACATATAATC	CTGGGGATAC	60
	AACGCTGTCA	AACTCTGGGC	CTTCTGCTTT	GTGTCTAGAT	TCCTTTTGCA	GGCTTGAGAA	120
5	TAACCTGTAC	AATTTTGTGA	TGTGGTTAGT	AAGAGACGCA	TCAACGATAT	CATCGCACAA	180
	AGTTCGGTTT	CTTTCCCTG	CAAGCGGGAA	TGCGCCTTCA	TTACTTCCCG	AATCTTCTCC	240
	ATGAGTCGAT	GGTCTCGGCG	TTGAAGCTTG	TAGTGTCAAA	GGTCTATTTC	TTGGAGAAGG	300
	TTCTATCTCT	ATTTTTFGTC	CCCAGAAAGA	ATCATTGAC	ATCCAATATC	TTGTAACTTC	360
	CCTGGGATGT	AATCTTTGAA	TAGCGGGTT	TCGGTACAAG	CTGCTACCTG	CCAGATTATT	420
10	ATTTAACGAT	TCTTCTGGTC	CGTGAAGGTG	ACGTATAAGG	TGGACGCTAT	TGGGTTTCTT	480
	TTCCAACATA	GGTTGTTCAT	CAAATGAGAG	GTAAAAATG	TCCTGCTGGG	AACGCGACGA	540
	AGGCTCCTTT	ACTTTAAGTC	TTAACAAGGC	GTCAACATAT	TCTTTTGTGA	TCGTTCTAGA	600
	AGTGGTTACA	AAATCCATAT	TGCGTCTTAG	ATCTGACTCC	TGAACGCCTT	TGTCTAGTTT	660
	CTCATCCCCC	AGTGGTAAAT	CTGAACGAGG	GACAAAGTAC	ATGCAACTGT	CCTCATCATT	720
	GTAAGTCA						

1413RP

	GATCTGCTGG	GAGTGACTION	GGAAGCTTTG	TCAGTACCTG	GAATGAAAAA	ACAGTCTCTG	60
	ACAGAGCGGG	GAAGCTGGGC	CTGATGGTCG	TTACAGCGGA	CCAGTTCAAA	GAATATGAAC	120
20	AATTGAAGAC	TGTCAGCCCC	AAGGATCAAC	TTGCTCAGCA	GGCGAAGGAG	CTAGATATGG	180
	TGCTAATTGA	TGCTGCTGAA	CTATACGAAT	TAAGAAGCAA	AGTTTCCGAT	GGACTGTCTG	240
	GCGATTTGAA	CTCTGACTTT	GTCTTGAGCA	AGGAGATCAT	TCTTGAGAAT	GCTCATAGTT	300
	ATGGTTTAAC	GGTTCTTCAA	ACGGAAGAGT	ATCTTCAATT	ACAGAGTAGT	TTGGAGAGAG	360
	AACAGGTAAC	GTCCTACAAC	ATTGCCGAGA	AAGCAACTAC	AATTGGCTAC	GTTGCACTTC	420
	CAAGAACCGA	GTACGATGAA	CTTGTAGCTT	CGCAAGCTTC	TACGAAAGAA	CAGAATTTTG	480
25	AGGTATACGC	GGCGGAAAAT	GGCAAGGTCA	TAGTGGATAA	ATCTGAGTAT	CACGATTTGA	540
	AGATCAAAGC	TATCCCAGTG	ATTTCAACCAT	TGCCTCAAAT	GAGCAAAGAG	CAGATGGTTG	600
	AAAAGGCCAA	GGAACCTGGA	ATGGTAGCTT	TGCTCATTGA	CGAGTATGAG	AAGTTAAAGA	660
	GCCCTATTTT	CGATAACGCT	TTGAATGCAA	CAGCGAAGGG	ACCGTGGAAA	GTTTGTCTC	720
	CTAAAGGAGA	GT					

1413UP

	GATCCAGTTT	TAGGTCCACT	TCAAACCTGGA	TTTTCCGGTA	CTCCCCGCAC	ACCACCGTCA	60
	AGTCATCGGC	ATAGATGGAC	TCAAGCACTT	CCAGCTCCTG	CTTTTGCTCC	TCCTGATAGT	120
35	CCATACCTAT	CCGCTCGACC	AACTATGAGC	CCACGCGCAG	CTTAGGGCTA	GACCGTTACA	180
	GCTGCAGGTG	ACCGTCCGGG	GGACGATGCG	CTATCGCTGG	CGAAATTTTT	CGCCTATACC	240
	ACCACCTTAT	TTACCCGGTC	TATAGTGCTG	CTCTCCGACC	TCACTGATGG	TGCTGTCCCG	300
	CGGGGACTGC	TGCCTCGTGC	GGCCAAATCC	CCACCGCTCT	GAACGCTCGT	TCCATCTGCG	360
	TCACGGGTTG	ACCGAACGGG	AATTGCGCGC	GCCGAGAAAT	CTTGCGCAAC	CATGCTGCAC	420
	GTAGCCTTAC	TGCCAAAATT	AAGCCGTCAA	ATGGCTGGCT	ATCCTTCCAC	GCACGCCCAT	480
40	AGTCACCTGA	AGCTGGCTGG	AACAGTGGTC	ACGCAGCTTT	CTGACGCATA	CCAGGAACAG	540
	GTGGCCGAGC	CCGAGGCCAA	CGGTGGGTGA	TTATGTCAGC	GACTTTTGGT	GGATTACGTA	600
	AATCTGGGTG	CATGCCTGGC	ACGACAGCGC	GCATCGCACC	CCAAGACAAA	CGTGCCACAC	660
	CCATTCAATA	TTAGAGGACT	TTGCTGCACA	CCCTAATCAT	CCGTTGGGTT	GTGAGATACG	720
	C						

1414RP

	GATCCGTAAT	CGAGTTTAGC	TTCCGTGTG	CATCATCGAC	AGGTGGAAAT	GCTCGCTTGT	60
	CGGCCGTCTG	AAAACGAGTC	AGATGTGCAG	AGAGGCTGAA	GTCCAACATT	TTAACCACCG	120
50	CTGAAGACCG	GGAATAGTAG	GGCAACGTAG	TTCCGCGAAC	TTTCAGTTTG	TTTTCTTTTA	180
	ATTTAATGGA	CTACACAAA	AAAAGCTCAA	CAACAGTCCC	AATTAGTTCT	GCTAGAAGAT	240
	GCAAACACGT	TAGTGATCAG	TAAGTATGTG	TACTCGTGTA	CTCGTCTGTC	ACTGCAAAAT	300
	TCGCGTCACA	ACTAGCTGTG	AACCATGGTT	TGAAAAAATA	TAATGATAAT	GATTCCGCCC	360
	AGGATCGAAC	TGGGGACGTT	CTGCGTGTTA	AGCAGATGCC	ATAACCGACT	AGACCACGGA	420
	ACCACCTATA	AGCCCTTAAT	TATACTCAGA	TACTAGTGAC	CATTTTCTAG	TCACATGATG	480
55	CTAGTTTCCT	GAATAAAAGA	TGCACGTGAT	TACCAAATCT	GTATTTACTA	GGTAAATGTC	540
	CTTGGTGAAT	AAGTACGTAG	ATATTATATA	TGTATACATA	TGCATTTTAG	ATGCAATAAA	600

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AGCTCTATTA TGTATGCGCG CGGAGCTTTA AGCCAGTGTG TTTTCCGATT GTTTTGTGGA
TGCAATGGTC TTTGCATAAA AGCCTGACTT TCATCTTTTT CGTGCTTGGA TGTTAAC TTC
CAACTCTGA

660
720

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1414UP

	GATCTGGCCC	CGCGGGCGCA	CCGCGGCCAG	GGGCCAAAA	GGAGAGCGCC	CGCGGTGGCG	60
	GCCGCCACTG	CGGCGGTTGC	ACAAGACATA	TATGTCGGTA	TATAAGACCG	CGGGTGCCGC	120
5	GTGGCTGCCG	TGCAGAACCC	GCCGTGCGCG	CGCGGGCAGA	GATTTCTAAT	ACTCTGCGTT	180
	TTCTTTTTCG	AGCGCCTGGT	ATATAAGTTC	GGGCTGTGTC	GCGGGCCGTC	GGCGCCGTTT	240
	GCCAGGGAGA	TAGGGGAGCA	TTCCGCGAGCA	GCCGTCTGTA	GCCGGACCAG	TACGACAGGG	300
	ACGCAGGACA	CAAAGCAGGC	GACGGCGAGT	GCGCGGGATC	AGCAGCGCAC	AGCGAGCCAG	360
	GGGTATAAGA	GCCGCGGTAC	GAGGCGGCTG	GTAGGTATAG	GGCCAGATGG	AGGTGGGTGC	420
	TAACGGGATT	TTTCTGCACC	AGAACGACTC	TGCGGAGACG	ATCAAGCTGG	AGATGTCCGC	480
10	TGTCGGCGGT	TCGGGGAGCG	CAGGCAGCGG	CATCGCGATG	GGCAGCGCGG	ACGACGAGCT	540
	GACGAAGTGC	ATCAGCGACC	TGAACATCTT	CGATCTGCTG	CACAACAACC	CGCCGTCGAG	600
	TTCGGACGAC	AACAAGGAGG	GTGGGCGGCG	GGCGGCTGC			

1415RP

	GATCGTGGTT	CTGTTATCGA	AACGTTGGTT	GCTAGAACAT	TGCGCCAGGT	TGAAAGTAGC	60
	CAGAGCATGA	TACGAATTCT	GGGATTATCG	GCTACATTAC	CTAACTTCTT	CGACGTCGCA	120
	GACTTTTGGG	GGGTAAACAG	ACATGTGGGA	ATGTTTTATT	TTGATCAATC	GTTCCGTCCA	180
	AAACCCTTAG	AACAGCAGCT	GCTTGGTTGC	AGAGGCAAGG	CGGGCAGCAA	ACAAGGAAGG	240
20	GAAAATATTG	ATAAGGTTTC	ATATGAAAAG	CTTTATGAAC	ATGTCTTAAA	TGGCTCCCAG	300
	GTCATGGTTT	TTGTGCACTC	AAGGAAGGAT	ACTGTGCGCA	CTGCGCGGAA	TTACATTTCT	360
	TTTGCCCAAG	CCAACCAACA	GTCCGATGTT	TTCTTAAGTA	GCGATCAAAG	CGTTACCAAG	420
	TTTCCCGAG	ACATCTCCAA	ACATAAGGAT	AGAGATATGA	AGGAGCTCTT	CCAACATGGG	480
	TTTGGTATAC	ATCATGCTGG	TATGTCTCGA	TCTGATAGAA	ATCTAACAGA	AAAGATGTTT	540
	AAAGAGGGAG	CTATTAATGT	GCTTATCTGT	ACAGCGACGC	TGGCCTGGGG	TGTGAACTTA	600
25	CCGGCTGATG	TTGTCTTGAT	AAAGGGAACT	CAGATATMTG	ACTCTAAAA	AGGTGGTTTT	660
	ATAGATTG	GGATTCTGAT	GTGATACA				

1415UP

	GATCATCAGG	AGTTCGTCAC	CTTGGAAC	AATTGCGAAC	CACAATTCCT	TCTGAGCCTT	60
30	TGGAATTTTG	TCACACCAAA	CTCTGAAACC	GTCTTTGTAA	CTTTCATTAT	GGCGGAATGC	120
	TACAAGTGTC	AACTTATCAG	GGTTGGATTG	GTCCCTAAAA	TGTACCTTAT	CCAGAACAGG	180
	AAGCATCGAG	GCTTACGTA	TAAACTTATC	TTTCGCCGCT	CCTTGAATGT	TATGCACGCG	240
	GCACACTGAG	CACAACGCAG	CATAGCCCAT	CCGACCTAGC	TTCTCCAACG	TCAGCATCTC	300
	GCCACTATAC	TCATAGGGAA	AGCCATCATC	CCCGAATAAT	TCGGGGTCTA	AGCGTTGTAG	360
35	CGTAATTCCA	GGCAAAGCAG	TCACCGGGTT	GTCCCTCATA	CATGTTCCCT	GCTTAATGCA	420
	CTGCATGGCT	TTAATCATAG	TCATAACTGT	CCTGAGGTAC	CCAGATTCGC	TTGCAATATC	480
	GATATAGGCC	TGTAGAATAC	GTAGCGCCTG	GTGAGAACT	GAGATCGTAT	CTTGTTAATA	540
	ATCTGCAATT	GCTAAGTCAG	CTCTACTTAG	GTAAGCTTGT	AAAAGCAAAA	AGGCTTTGAC	600
	ATGGGGGTCC	CATATTGGTA	ACTCTTGTTT	TCCTGTAAAA	GTACTTTCAA	CGGAATATCT	660
40	AAGAGTTTCT	GACATTTCAA	CATTTCATGAT	AGTCTCGCCC	CCC		

1416RP

	GATCATCATT	ATTTCCCTGCG	TTCGTGCCGA	CGATTCTGAAG	GGCGGGGTCG	GTTTCTTGAA	60
45	GGATTTTCAGG	CGTATGAATG	TTGCTCTCAC	CAGAGCAAAG	GCCAGTCTCT	GGATCCTGGG	120
	TCACCATAAA	TCTTTATACA	AGAACAAGCT	ATGGATGCAT	TTGATTTTCAG	ATGCGAAAGG	180
	GCGTGACTGC	CTCCAAATGG	CATGTCCGGG	CTTCCCTTGAT	CCACGGAACA	GAGCCGCCCA	240
	GGATGCTCTT	CATAGGTTCA	AAAATCACCA	TAATTATATC	GAGAACGCAG	ATGATTATGG	300
	GCCTGAACCG	GTGATGACTA	AATCAAGAGG	ACGCAATAGA	TCATCCAGAA	AACGCAAACA	360
	TATGGAAGAT	AATCCAGATG	ATAACTACGA	TCCCGTTGCT	GAATTCAAGA	AGGAAAATCA	420
50	AAGAGAAAGC	AACACAGGCA	CCGGTGGTTA	CCGTGCGGAT	ACATCTAACC	ACAGATTGGC	480
	ACCTGCTAGG	AACGATAGCA	AGAAGGCCAA	GACGTGCTCC	AATGCCGCCG	GTATTTCCGA	540
	GGCTACTTCA	GAGGATGGTG	ATCGAGGTCA	GAAAGGACAT	GGAACATAAG	AGAAGTCTTC	600
	CATATTCCGG	AATTTTATGC	CCCCAGTTGA	TGACGCGACC	CCTGCTGCCC	ATGTGTACGA	660
	CCCTAAGGAA	CGCAAGCCCA	AGAATGCTGC	ATCCGCTTAA	GCGGCTGGCC	TTGGGAAC	

1416UP

	GATCTTGCCC	GGCAAGACCA	GGAAGTCGTT	GTACGTCAAC	CCGCCCCGCG	TCTTGAGTCT	60
	CATCAACTGC	TCCACGGGAC	AGCCCGTCCT	TCTCGGCGTA	CGTCGCCAGG	TGCTCCAGTG	120
5	CCGTGGCTGC	GTCTCTGTAA	GTCAATTGCGC	TTTGTTCCGGC	GTGCTATGAA	GAGAAGGAGT	180
	CAACACTAAA	CCCAAGCTCT	CAAGTTGACC	CATCCATCAA	GTAACATATCC	CGAACAGACG	240
	CCGGTAAACC	CAGCTGGGAT	TTGGCGCATC	TAGAAAACCT	ATTTATACTG	CAGCTCATCG	300
	CTGCAAACTT	TTCACGTAAA	AGAAACGATG	ATCCAGCGGG	GGCCAAAAAG	CAATGGGCCCT	360
	GCGCCGCACG	ATGCGAGCCC	TACCGGCGGC	CAGCACCAGG	TAGGAGCTGT	CAGGGGCCTA	420
	GAACGCGCGC	ACGCTAGACG	GGCTCCTCGG	GGGCCGCGGC	AGGCGTCCGA	CGGGCGCCTC	480
10	GCAGCAGCAG	GCGTGCCAGG	CGGACCAAAA	GACCGACCAG	CCAGCGCAGC	AGTCTGTAGA	540
	CGGCGCGGAG	CAGGCGAACG	GCCAGGAATA	CAGTCCAGAG	CACGGCGGAG	AGCAGCAGGA	600
	AGTTGAACAC	GCCGTCCATG	CCCACGCGCG	CACAAACGGG	AACAGCGCCA	GCGCGCGCTC	660
	GCAGAGCGGC	TGCAGGAATG	CGACGACGGA	CAGGAACGGC	AGGATAGGAC	TA	

1417RP

	GATCCCCCTTG	GCGTCGTCGT	TGACCAGGTA	GCGGCGCTGT	AGCCCGAAGA	AGCCGGACAT	60
	CGGGTCTGAC	GCGGTCTGTA	GCGGACGCGC	CATCATGCGC	GCGCTACTGG	AGATCACGCG	120
	CCGGTACAGG	GGCCAGTCCT	TGTCGATTCC	GACGCCGGGC	GCGTAGCGCG	TGCCCAGCAC	180
20	GAACGGATGT	GTGCGTAGTG	AGTCCAGAAG	CAGCGGTACG	CTCTCTGGCG	GATGCTGCAG	240
	GTCCGCGTCC	ATGCACACCA	GGTACTCGCC	CTTGGCCTCG	TAGAAGCCTT	TGAGCACCGC	300
	ACTCGACAGC	CCGCGCTCGT	CCGTGCGCAC	GATGATCCGC	ACGTTGTAGC	CCTGCTTGGC	360
	CAGGGCCTCC	ACCTCTTCCA	CAGACCCGTC	CTGGGAGTTG	TCGTGACAAA	AGATCAGCTC	420
	AGTCTTCTTG	GAGTCCGCGT	TACCGAGCGC	GGCAAACAGC	CGCGTGGCAA	GGGGCTTGAT	480
	GTTGGGCCTT	TCGTGGTAGG	CCGGCACGAC	CACAGAGTCT	CGATGCTCAT	GGCGCTCGTA	540
25	TGGTCTTTAA	TGTAGTGAGT	AGCGAACGTC	GGTAGCTGTT	TCGCAAATAA	GTGAGGCCTG	600
	CGCGCCTAAT	GTGCTGTCTT	TATCGTTGCT	TTTTGGTTCTG	TGTCACGGGG	TTACCCGGCC	660
	ACCAGGCTAG	ACAGCGAGAC	CCGCGGTGAG	CAGCCCACGA	CCAAGAAGCG	CTGTA	

1417UP

	GATCTGCGTA	GGTAGTAGAT	GAATTGAGGG	TATAGGGA	AGTTTGGTGC	CAAGCGGAAG	60
	GAGCGGGGGT	CGCCCTTGTT	GATGTCGGCG	TACTTCTGGC	AAAGCTTGAT	CAAAGTTCTA	120
	TCGATCCACC	GGATGACGTC	AGCGCCATCA	TCGGAATCTG	CCTTATCGAC	TGCAACACGC	180
	GCCATTAGTA	CAGCAGCGGC	CTCCTGGTCA	AAGGAAGCAG	CGATTGCCGG	GTTACCGAAT	240
35	GGCAACATCT	GGTTAGCAAC	TGTAGTCACT	CTGACACGGT	TGGTACCAGA	TGCATGCTGG	300
	TATGCAGTAA	TGAATTGGGT	GTATGCCAAT	TTTGGTCTGT	CCCCCATGAG	GCTGGCAGTT	360
	GCAGCGGTAT	TTGCAATCTC	GAAAAAGATA	GCGTAAGAGT	GGTGAGGGCT	CAAGGACGCC	420
	ATTTTCCATG	TAGAAGTGCC	CCCAATACCG	ATTTCTGAAT	CGCTCACGTT	CTGTGCATCA	480
	ACGTTAACCG	GCGAAGCATG	GCCAATCAGT	CCCTGCAGCT	TTAGATCTGC	ACTGGTTTTA	540
	ATGCACATGG	AAGCATTGAA	CGCCATGGTT	AGGTACCCTC	CTCATCTTTA	GAAAACAGTC	600
40	TGATGAAAGA	TTGCTTGAAG	ATGGCCGTCG	AGAATGCGTC	AGTCAACAAC	AAAAACACCAC	660
	CAGTGGAGTC	GGTCAACTTC	TTCATCTCAG	ACATACAACC	TGGTCGTAGC	ATCCA	

1418RP

45	GATCCGCGAG	ATTCATCGTG	GACCCGCCAC	AGGCAATTAC	TATAACAACA	TCCTGCGGTG	60
	TTAAAGGACC	TAACTCACGC	TCAAGTATTT	CAGGATGATA	TCCTAGATGA	AGAGCTGCGC	120
	CACACGCTGG	TTCCGGTTACA	ATATTGCTCT	CTTCCGCAAA	ATTTAAACAT	GTCTGTACTA	180
	CAGCGAGCTG	GTCAAGCACA	ACAGATTTTG	TCCTGTATTT	TTGGGCCTAA	CTCAGAGTAA	240
	GATCCGATTC	GAAAGATGTG	CATAAAGAA	TAGCAACGCT	TTTAGGATTC	ATCGAAACGT	300
	TCCTGCCAG	CAGCAAGAT	CTGTGCAAAA	CCTCGCACCC	CTCTGTTTCC	ACTGCTACAA	360
50	CAGGGATAGA	GTCTGCCAAA	CCATGTTTTCT	CCAGCCCAT	TACAATCCCA	TTATATAACC	420
	CCCCGCCACC	TACGCTGCAG	ACGATACCTT	TCACGCTCTC	CAATTGACAG	CCTTGAGAT	480
	GCACTGCTTC	TACTACTTCA	TCTACCAATT	TTGCATGCCC	TTCCAGATG	AGTGGGTGT	540
	CGAATGGATG	TGCATATATC	GGAGCGACTT	TTTCTAAATT	CACATTCCTC	ATCAACTCGG	600
	AACGTAAGTA	GTCATCGCTC	TCTTTCAATA	CACTTCCCAT	TGATATCACA	TCTGCCCCCG	660
55	TTGACCGTAT	CCGCTCTACC	ATCCGCCGTC	GAGTAGTTTC	AGGCACTACC	ACTGTGCAAG	720
	GTATCCTA						

1418UP

	GATCATCTGC	GTGCGATACT	GGCAAAAAAT	GAGAGACAGC	ATGATGAAAA	TATAGTTAAT	60
	AAGATATTGC	ATGATATAAG	CACAGGCGGG	TTTCGTCGAA	GAGGAAAGGG	TGCACTTGAT	120
5	CTGGAAATGA	GTGAAAATGA	AGACCAAGAG	TTACAACAGT	TTAGACAGAA	AAGACGAGAA	180
	CTTTTGAAC	AAAAGATATT	GGAAAAATGGT	GATACTAGCA	AGCTCGTATC	TAACCCCAAG	240
	TCATACGCCT	TTTTTCAGAC	GATGGTGGAC	GATGTTACTG	AAGCATCATT	TGGAAATACA	300
	TTTGATGCCA	ATATAGATGA	AAAAACAGAT	CCATCTGCTG	CAGGTCGGAA	AATTGTCATA	360
	TCAGAACAAT	TTGTAAAGGA	AACCTGTCA	TTCTTGTCGA	GCAAGAGTGG	CGACTCAGAA	420
	ATCCCTGCAG	AAACTAAATC	TATTTTCATCC	AGCACAGTTG	AACGTGAAGA	AATTCAAGAC	480
10	CTTCCATACA	TTGAAGCAAA	ATAGTAACAT	TAAACATTTG	AAAGGAATCT	AGAACTTCCT	540
	GCTCAGATGG	CTGAACTCAG	CAGTGGAGAT	GAAGGTGATT	ACGGCTTTTC	TTTAGATAGA	600
	TTGCTCTGTC	GGCAAAAAGT	TTAATAATGG	AACTAACGTC	GACGATAAGT	TTAAAAGTGG	660
	CACCAAGGCA	GTGCGAATCT	TAAAGGCAAT	AAGACAATTG	GCGGTCAAAA	GCC	

1419RP

	GATCTGGGGA	GTCTCATCGA	AACGTATTCTG	ATGAGGCTTG	GTGGTGGCAG	GCGGCTCCTC	60
	GCTCGATTGG	CGAGCTGGTG	ATGACTTCGC	ACTTCTCCGG	GCCGGAAAAT	TCGTGTCAGA	120
	CAGTCGGCGT	TGGCGTTGAA	GCTGCCGCTG	TTGCTGCACA	CGTGGTGGCG	CCCTTAGCTG	180
20	AATACGTAAAC	GCTGGCGCGG	TGTCCCGCGC	ATCCAGGTAT	TCCTCGAGGC	TTTCTCTTTC	240
	GGCGATGTCT	GAGATATCTG	GAGCACCGCG	AGCATTCCTGA	TACACGTGGC	CCGAAGATGT	300
	TTGCTTCGCG	GTGAAGTCTC	CCTCAAACCC	GTAGAAGTCA	TCGGGGTATT	CTCCATCCGG	360
	CATTGTCAAT	GTAGTAGTGG	TCTCCACATA	GCGTACGCCA	TTGATGTGCT	TCACCGTCTG	420
	GCGAGTCACG	GTCCTGTGAT	GGCCCTGGAG	GTCCTTCGTT	TCCGTCGTCT	TCACCGTTAT	480
	CGTATTGCCA	GCTGCGACAG	CAGGAGGGCC	AAAGCCGTTG	TTGCTGCGTA	GCGAATTTCGC	540
25	GCGTCGTTGC	GAGCTCATAC	TGTAAGTCCG	CGGAGGCGCA	CCGAGGTAGC	TGGGCCGAGC	600
	AGCTCCTAGC	GACCGCGTCC	GCCCGTACCC	AGTCAGTGAC	TGAGTCCGCC	CCATCCCAAC	660
	CCCTGGTCTT	CGGAGTGACG	CAACCGACGC	CGCCGCAGAC	GACAAGCCGC	TGCCTGTTGA	720
	ATA						

1419UP

	GATCCGTCCG	CGCCTGCGTA	CCCATAGGGG	CGAGGTCGCC	GCCGGCCCGC	CAGGTCACTG	60
	CGCCCCAAACC	GCACCTGCAC	CTGAACCGAG	CCTGCAGCCC	ACGAAGGAAC	GCCACGCTAC	120
	ATGTGCCCCG	GCAGAGCACC	GCCCTTGCT	TGCGGGGCTG	AAGTGACTGT	GGCAGCTCC	180
35	GCAGGACATA	TCTTTTTAAT	GAGCTGTGTC	ATGCGCACAT	TCTCACCGTC	GCGCTACCGT	240
	AGCGTCGCCC	TCTGTCAACG	TGTGAGCTGC	TGCCAAAACA	AACAAATCGG	GACGGGCCCCG	300
	CATGCAGTAA	TTACCTCCTC	CCGAAGGCAA	CGCCTTGCTT	TTGTTTACGT	TGGCCAGAGA	360
	TTTTCTCTTT	GGGGTGGATT	AGCTCACGCG	TCATCCGCGT	GGCAGAGGTG	CCTGCCCTGA	420
	CAGTTCTTCG	AATATTAGAT	GCTGGTATGC	GGGCACGCC	AGCGCAACCG	ATTGTAGTTT	480
	ATTGTTTCGT	CACACCCGCG	TAGAGGGCCG	AGCTACAGGA	TCGCCGATGT	GGCGTGACGG	540
40	ACAGCGTCAA	CGTTACGATC	TCAACGGTCG	CTCGTGCGGG	CCCGTCTGTG	GTAGGCGTTG	600
	AGATACGCTT	AGGATGAAAG	CACGAAAATT	AAGGTTGTCTG	TAAAAACACA	AAGTCAACTG	660
	GGGTTTCCGA	ATGGGTTAGA	GTGCCATCGT	AATGGCGGAC	GGAGAGTGTC	CATGGTGCGA	720
	G						

1420RP

	GATCAATTCA	AGGTTGCTTT	CCCAGACATC	TACGCTGTTT	TCCAAAAGAT	CGCTCAGCAG	60
	CACCCCGACT	ACGAAGTGAC	TGTCACGGGT	CACTCACTGG	GTGGCGGTTA	TGCCTACTTG	120
	ATGGGCTTGG	AGCTCCAGCT	ACTTGGCCAC	AAGCCACATG	TGATCACCTA	CGCCGGCCTG	180
	CGTATGGGTA	ACGCTGACCT	CAACAAATGG	TACGACAAGG	TGTTTCGACAA	CGTCAAGAAG	240
50	GTCGAGGACT	TGAAAAACGG	CGGAAACCCA	AGAAACGCCT	ACATCCGTGT	GGTTCAAGAGC	300
	CGTGACATTG	TTCTATGGT	TCCAATGGC	CCTATCTACA	CGCACGCGGG	TATCCTATTT	360
	ACCATCACTG	ACGTGGACAG	CGAAGTACCT	CTACAATCGG	GCGTCAGACT	TGATGGCTGT	420
	AACACCAAGC	TAAAGGAGTT	GGTCGGCGAC	ATCCTCTTCA	GCGGGAAGTT	GCTAAGCTTG	480
	GTGCGTCTCC	TGAACCACAA	CAAATTTTTC	AGAAGAATGG	CTTTGCCATG	CACTGATAAT	540
	TCCTTGAAGC	TATAATTCCG	AGGAAGTAAT	GAATTTTAAG	TACGGAACGT	GCAGTCGCTG	600
55	CAGTCTTCTG	CCTCTTCCTT	ATGCCCTATA	TAGTTAATTT	GATGTTCTGT	TCTATTTTTT	660

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TACATTTTCC AAACACTGGG AATGCCACCT TGTAGATGTT GTTCCCAAGA TGGATATTTA
G

720

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1420UP

	GATCCGTCGC	GAGGCGCGCA	CCAAGCGCAA	GTGCATGGTG	GTGTGGCCG	GCCTGGAGGT	60
	CTTCGAGATT	GACATGAAGA	AGCTGGCGAA	GACCTTCGCG	TCCAAGTTCG	CGACGGGTTG	120
5	CTCTGTGTCC	AAGAACGTCG	AGAAGAAAGA	GGAGGTCTGT	GTTCAGGCG	ACATCGCGGA	180
	CGAGGTCGAG	GCCTACATCC	ACGCGCTGCT	AGAGGAGAAG	GGGATGAAGG	GTGTCAAGGT	240
	CGAGCAGATA	GACGCTGCCA	AGAAGAAGAA	GAAGACGCCG	ACGACGACGA	CGCCGCCGCC	300
	GTCGTGAAGA	GCGGGTCCGG	ACATGTGTAT	CAGATTTCGT	TGTAGTGATT	AATGATTGCC	360
	GCGATTTCCA	GTGTCTTACC	AGTCCAAGAG	GACAGGTGTC	TGGCATGCTT	GCACATTGCT	420
	GGCGTCTGCG	TGGGGACCAT	GAGCCTGGAG	ATGGATCTAA	TTGAATGGGC	GCTTAACCTG	480
10	CGTGCTGCGG	GAGGCGGGGT	ATTGCGCAGT	GGCAGCGAGG	AATTGGACAG	AGTGCTAAAA	540
	CTGCACTACC	GAGTGACATA	CCATGCGTTT	GACCGGGGCA	CCAAGCGGTC	GGTGTGGGAA	600
	GTCTGCTGGC	GGAGGCCGAG	AAGATC				

1421RP

	GATCCCTCAG	TTCCCCATCT	TGCCCTCACA	GCCAGGATGG	ACCATCCGTA	ACTGGGAGTT	60
	ATGCGGTTTC	ATTTGTCTTT	TTAGTACAGT	ATTATCTCTC	TGGTTTTACA	TCCTACTTGT	120
	TTTATCGTTA	CTTGGGTATG	TATGGCATCT	TAAATTTTAT	CGACTCTAGT	ATTTTTATGA	180
	CTGTGTAAAC	TAATGAAAAA	TAATGAATCG	AAGTCTCGTT	TACCTAGAGC	TGATTATGCC	240
	ACATGCGTAC	TATCGGCGTG	CCACCGCAAT	TATGTATCTA	TCCTACAGAT	AATCCTTTCT	300
20	ATTAGCAGTT	CTCACGAAAC	GTCTCAGTTG	CCACTCGACG	TCAGCATCCT	TGTTCTCCAA	360
	GGTGCCCACT	GTCAGCTCGT	AGAGCTTCAT	TTGGAACCGT	GGTCCCACCT	CGGCCAATTC	420
	AACCTCATCT	CTCGTCTTGA	CGTATACGTG	CTGCCGCACA	CTAATGAAAT	CGCCGCGGTT	480
	CGCAAATGTG	ATGACCCTAG	GGCTGTCTTT	CTTGACTCCG	GGCGGGAACA	TGTGCTTCAG	540
	TATTTTAACG	ACCCGTTGCC	CCAATGGAGT	ATTGAAATTA	TC		

1421UP

	GATCATCATA	CCGTGTCCAA	CATCGCCAC	GGAACCACCA	GTCACCTGAA	GTGGAACGCA	60
	GGTAACATAC	GCGATGGCCT	CCACGACGAC	TTGGCCAGCT	TCAAGGACGC	AGTCGTGCAC	120
30	TGCTCACGT	TCCGACGCGG	CCAGTCCCGC	GACTACCGCC	ACCAGTCGTC	CATGTTCCGGC	180
	AACGGTTCTG	CTGGCAGTGC	CAAGTCCGGG	TCGTGGTTCTG	GTGGCGCGAC	TGACTCGCGC	240
	GATGGACTAC	TGCAGCGCGG	GCGCGAGGCC	GGGCGCGAGG	CCGGTCGCGA	GGCCAGCTCG	300
	TGGTTCCGCG	GCGACAGCCG	CACCGAGGAT	TCCGGCCCGT	CGTGGTTTGG	GCGCGACGCC	360
	CGCGACACCC	GCGACACTCG	CTCGGACCGC	TCGTGGTTTG	GCCGCGACGC	ACCGGAGGCC	420
	CGCACCGACG	GCACCTGGCT	CAACGAGAG	CGCGACCGCT	CGTGGTTTCG	TCGCGAGAAA	480
35	CACGCCACCC	TGCACGAGTC	CGACCGTGTC	TTCCGGAATG	GCGGCCGTCT	CGGCGTCGAC	540
	ACCACGCGCT	AGGCGCCGAC	GCCCGCGGCA	AGGTCGACGA	CATcAagcaG	GCAGGTGCAG	600
	ACCTCGGCGG	CTCCGCGCAG	GCCAAGGTCG	ACGACTTCAA	GCAGGCCGCG	GCTGACCTCG	660
	GTCGCTCTGC	CCAGGACCGC	CTCCAGCGCG	GCGTTGCCGA	CGCCAAGCAG	ACGCTCTCAG	720
	GCGCCGCGCT	CACCGTCTCC	GGCGCCGCGG	CCTCCGCTGC	TGGCGCCTCT	CGCGACGCGC	780
	CCTCGTCCGC	CGCCGACAAG	ACCCAGTCCC	TCTTCAACTG	GGGCTACAAC	AAGGCCGAAA	840
40	AGTCGAAGGC	CATCGCCATC	GGCGAGTACG	ACAAGGCCAA	CAAGGACTAC	CAGCAGGCC	900
	TCGACGCCTA	CAACCGCTCC	AAGCGCCTGC	TCGCCGACGG	CGACCAGCAC	CTTCGCACCG	960
	GCCTCGAGAG	CGCCAGGCC	CAGCTGCGTG	ACTGTGCGGA	CAAGCTCGAC	GCCATCTcCG	1020
	CGGAGTTCGA	CCACTACGCC	CGCGAGAACA	TcTcCGACAT	CTNCCGGCGN	CTGGACCACG	1080
	AGGACCGcGA	TTCCGCGGcT	TCCGGcCTCT	TTAGCTGGTT	CCGcTTCAAG	GCCCgGcTGT	1140
	cGAAATCGAC	CT					

1422RP

	GATCCGTGTC	CTGGGGCTGG	TCGAGAACAT	GAGCGGCTTT	GTGTGCCCAT	CGTGCGAAAA	60
	CGAGTCGACC	ATCTTCAAGC	CAACAACAGG	TGGTGGTCTG	GCCTTGTGCG	AGGAGCTGGG	120
50	GATAAAGTTT	CTTGGAGCCG	TGCCGATTGA	TCCGCGAATT	GGAAGATGCT	GCGACTCTGG	180
	CGAAAGCTTT	TTGGACGCCT	ATCCGGACAG	TCCAGCGTCG	ACCGCCATCA	TGCATGTGGT	240
	AGAGGCTCTC	CGTGACGCCG	TCGGCGACGT	ATAACGCCCC	TAGCAGTTCC	TGCCAGTGAC	300
	AGACTGATAC	CAGTTTATAC	ATACATACAT	ATTTGTAAAA	AAGACGCTTA	GTGTTACGTG	360
	GATGCGAGCG	CCCGTTTCAG	GTAGATAGTT	TCCGGCTGTC	CCAGCGGCAA	TGCAAGTAAT	420
	CTGTCTTTAA	AAGACGGGGT	CTCCAACGCT	TGTCGATAAT	TCTCAAGGAT	GATATGACAG	480

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ACAAGTTTGG	ACATGACACA	GCAAACGACG	GAGAGTTCTC	GGTGGGAGCC	GAAATCCGTG	540
GCCAGGACGG	GCAGAACCCG	GACCAGATCG	GAAAGCAGCT	CTTGTTGTG	GTTGTTGTCA	600
AGTGCTATCT	GGAGGTACTT	CTCAAATACC	CCCAGGCCGT	GAGTCCAAGT	TTCCATCTGT	660
TGTGCGGGGA	AAGTCTCCAA	TAATTGACGC	AGTGTCTGCA	AGTTAGCAGC	TGA	

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1422UP

	GATCTCCTAG	GCGCCAAGTC	GACGACTACA	GGCGGGCTTT	TTGGGCCAAA	GACGGAACAG	60
	AAGCCCGCAG	GCGGCCTTTT	CGGACAGAGT	AGTGCCGCTC	CCAATGGCAC	TGGCGGCGGT	120
5	GGTCTCTTCG	CTAGCACGGG	CAACAGCGGC	AGCACCCAAT	TGGGTGGGCT	GTTTCGGCAAC	180
	AGTGCTGCGG	GCGGTGGTGG	GAGTCTTTTT	GGCGCCGGCT	CGGCCGCGAA	CAACAACGCA	240
	TCCACCTCGT	TGGGAAATCT	CTTTGGGAAA	CCTAATGACA	CGGCACCGGC	AGCTGGTGGA	300
	GGTCTTTTCA	GCAATCGGCC	GAACACAGCC	ACCACAAATA	CCGTTTCTTC	CACTAACAGT	360
	CTTTTTTAGCA	ATAATCAGGG	AAATGGTGCG	CAGAATAATG	GGGGGCTCTT	TGGTGCGAAA	420
	CCTACCGGGG	GGCTCTTTGG	AAACAGCACC	GCTCAGCCAC	AGTGCTCGCT	TTTGGAGCT	480
10	TCCTCCTCAC	AGAATAATCA	GCAGCAGCAG	CAGCAAACAC	AGCAACTGTC	CCTTCTGGGT	540
	TCCAATCCAT	ATGGCCTGAA	TCTGACTGGT	GTTCTGTGTA	CTACCATGCC	GGAATCTATA	600
	ACGGCAGCAA	TTACGTCTAA	GAAGAAGACG	AAGCCTACCG	CT		

1423RP

	GATCGAACAC	AAATTCATCT	ACGAACACAA	ACTTGGAGCG	GTTCTGTGTG	GTTATATTGG	60
	ACAGGAACAT	TGACCTACCT	TCAATGTTTG	CGCATTTCGTG	GATCTACCAA	TGTTTAGTAT	120
	TTGACGTATT	CAATCTCTCC	AGAAATACGA	TTTCAGTACC	GAATACTGAT	GAAAAGGGAC	180
	AACCCACATA	TAAGAAGATG	GATATTGAGC	CTAAAGACTT	CTTTTGGACG	ACAAATGCGC	240
20	ACTTGCCGTT	CCCAGACGCA	GTGGAGAATG	TGAAAAATGC	ATTGGCAGAC	TATAAGGCCG	300
	AGGCGGAAGC	GATAACCAGG	AAGACAGGCG	TTGACAATAT	AGGCGATTTA	GATCCTAACT	360
	CTCAAAATGA	TACTTTGCAA	ATTGAGGAGG	CAGTGAACAA	GTTCGCCGAA	CTGACTGCTA	420
	GGAAGAATAT	CATTGATACA	CATATGAATG	TTCTGGCTGC	GTGTTGAAA	GAGCTAGAAA	480
	ATAAAGGGTT	GGATTTCGTT	TTTGAAATGG	AGCAACAAAG	TGACTCTGCT	AAGGTGAGGC	540
	AAGCATTCAT	GGACGTTTTG	AAAGATGGCA	AGACCAATAA	CCTCAAGGAC	AAGTTAAGGA	600
25	CATACATAAT	CATCTATTTG	ACTAGTTCGG	AGAAGCTTCC	CGATCAATTC	GTCCAACATG	660
	TTGAGAGTTA	CTTCCAAGAT	AATAATTTTCG	AAACGCCAGC	GTTGAAGTAC	TCTATAAGT	

1423UP

	GATCATCCTG	TTGAACTGCA	TGCTCATGTC	GTCCGATGAG	TACACATGAT	TGAAGTCAAA	60
	CAAATGTTTG	CCCGACTTGA	CCTTGCCGCC	ACGCAACGTC	GCAAACAATC	CGTCGCTGGA	120
	CCGAAAGTCT	GGGATGCCTG	CAGCCACAGA	GATCCCCGCA	CCCGTGACCA	CCACGATGTC	180
	CCGACTGTGC	TGGAGCGCAT	ACCGAATGAA	GTCCGGCGTCC	CGCGCGCTCA	CCAGCTCCGG	240
	GTCACGTAGC	TAATGCGCTA	GCTGAAATAC	CGAGTTCTGT	GCAGGCCGTG	ACGTGAGCCG	300
35	CGGCTTCCTC	CGCACCGGAG	CCCGCGCCTT	GCGCAGCGCC	GGTAACAGCT	CCTTCGGTGT	360
	GACCTCCTCG	GACACGCTCG	GCCCCGCTGT	GCAGGCCCTC	GTCTGCTTCT	TTTTGACGCT	420
	CGACGGCGGC	GTGATCGGCA	GCTTCACCTT	CATCGGCGAC	CGGTACCGCT	TCACACCGAT	480
	ACCACAGTGA	GCCCTCCGTA	TCCCGCACGT	TCCACAAACC	TCTGCCGCTT	GCTGCATCG	540
	TGGTTGCCCC	GCTGCGTGGC	GTGTAGCGGA	CATGAAATGA	GTGACGGCGG	GCCCAATTTT	600
	GCEGGCGTTC	GCTTTCGACC	AATCCGGAAA	ACTTATCCCC	CGTAAAACAA	AGGCAGGACT	660
40	TCCGGTGTGG	CGATAGCGGC	TTTTGTGCGA	TGGGCTCCTG	GTCCCGTTAC	GCCTACATT	

1424RP

	GATCTCATCT	GTATTTGGAA	GGGAACGCAC	CAGACGGGGG	TGACTCGCAG	AAGCTGCCAG	60
	AGGAGAGAGA	AAACATAGAA	AATATATTTA	TATTATCTAT	ATTGAGTTTA	CATAAGAATG	120
	TGTCTAATTT	TTATTGTTTT	TAGATTTTCA	CTTGCGAGTG	CCCTGCATAT	GACTATCCTT	180
	TTATTCTAGA	TTTCTAGTCTA	GCTAGTCGCA	AGGAAATCGA	TATCGTAATT	CCCATTTAGA	240
	ACAAGATACA	AATTAGCGAA	TTTCCCAGAA	AAACCGGTCT	TATAATACAG	CATCATTGCC	300
	GAATCCATAC	CAGTCCCTTCA	ATTAACTTTC	CGAATCAAAA	AAGGCCCGGC	GCGGTCTCAA	360
	GAATCTTTTC	GCCAGTACTC	GAATGGTGAC	TATCAGCAAG	CGACTCTTCA	CTACCCGAAA	420
50	CGACAGTAT	ATTGTGTGTC	AGCAAAATGAT	TTAAGGCTCT	CGAGACACCT	CTTATTGGCG	480
	TCCTATGTGT	TCTGTGCACG	CCCTGGCCCC	GATAAAGAAT	GCAGGTGCGC	TAATAGTAAT	540
	TACTAACCGT	TTTTTAAATC	GCCGTCTTGG	TTGAGACCTG	TGAAACGATA	ATCCCATTTA	600
	TACCAGATGA	ACTCGCCGCA	CTATAGTGTC	CGTAATTTCAG	CACTGTGGAT	TCCGAGTTAG	660
	GGTGCGCGAA	GTAGCAAAAT	TGTGTATCCT	CCATAATAAG	GATATCCAAT	GCCAGTATAA	720
55	TAGT						

1424UP

	GATCATCGTA	TGCACTCAGT	TGTATTCTAG	CATAGCCCGT	GCGATTGCCG	TGATTTTCGAA	60
	CGATGATGAC	AGGCAAATCA	CCATGAGGAG	CCGAGGATTG	TCCGCTAAAT	TCAGCTGTCAT	120
5	TTGCAACAAA	GATGGCGTGT	TTCTATGCGA	GCCCCCTCAC	ACGGGCGTAA	AACATGTTTCG	180
	AAATGCTGCT	CGCTCTGCCT	TGCGCTGCGT	GTGCCCTCAG	CCAGACGGTC	TGTTTGCTTC	240
	TAATGTGGGG	GAGAGTCGTT	CTACTCACGT	GTTTCAGCGTG	CTGAATAACT	TGCCTATCCT	300
	TACAGCTGCT	GACCTGAGGC	AATGCACGTT	TCCAAGTCCA	ATAGTCTACG	GGCCCCGAAGG	360
	TTGTGCGGAA	TGCACAGTGA	TGGTAATCT	ATTACTACAG	CCCACTGCAA	GCGTACAGAC	420
	AACCTACAAT	GACGGCGCGT	TGTACAATAA	AATCAATTCC	GCTTGCTCGA	CCGTAAACCC	480
10	AAAGCTATAC	CGTACCTTGT	GTCTTCCCT	GTTTCCATTA	GCCGTTGTCAT	GTGCTTTTTT	540
	ACTGTGATTA	CAGAGCCTTT	CTGTAGAATG	TGTACGTGAA	TTTAATACTA	GAGAGCTATA	600
	AAGCTCTCTT	GTTCTTGTA	TGTCTGTTTC	AGAAGATAAA	AGGTAACACC	AGAAAACGAG	660
	GTACGACCCA	ACGGCTATTG	GACTACGAAC	TGGACAAAAA	CTAAGAGTCG	TAAGTAAGAA	720

1425RP

	GATCAGCTCC	CACTTGGTTG	CAACAGTATT	GCTGAGACTA	TCATTCTTGT	AGAGCGATTTC	60
	TTGTGAAGCA	GTTGGCCCGG	TGTATGAAAC	CGCGTGTTTA	CCAAGTGGAG	GCCTTTGTTC	120
20	AGAAATTTTA	GTTCTTTCTC	GAACGTATTG	GTGGTCCCTG	AGAAATAAGT	TTTGTGCTC	180
	GACATAGTCA	GGGTCAAAAA	CATTACAGG	TGTGTCAATCA	TATGGCGGCC	GGCTGCCGGA	240
	GGTTGTGGGA	TCAGCCTTTC	TGTTGGCTTC	CGAGTCTCCA	ACCCTCGAGA	TAGCTTTTGA	300
	TAAGTTGTAG	AAGTCGTCCA	AAATATCGTC	TTCGCCGAGA	GGAGCAACGC	TCGAGCCCCC	360
	GAACAGTGAT	CCACTAGAAC	TTCTTGCAGT	AGCCTCGCCG	TCAGCATTAT	TGCTATTGTG	420
	TGTACTGCTC	GAGTTGCGCA	GATTAGATAT	ATCAAACGTG	TTCGATTGTG	TGGAACCTTT	480
25	ATATTCAATC	TATGCTCCAA	AAGAATCTCT	GCTTTGCGGA	GAGCCTCGCG	CTGCATGAGG	540
	AGGAGGAGCC	ATAAAAGATG	AATCCCTGCC	AGGAGAGTTG	TGTAACCGCC	CAAATGGTGA	600
	TGCAGCGTAG	TTGTCATAAA	TTTGAACCAG	ATCTGCACGC	GACTTGTACA	GGTCCCTGGG	660
	GTTGTATCCT	GCCTTGGGGT	CGCCAACCTC	TTTAATGGAC	CCGAAGAAGC		

1425UP

	GATCATACAC	GCGCTGCGCA	TACAGTTGGC	CAGCACCAGC	ACCCGCGACA	GCCTCCAACG	60
	GCTAGAGACG	GACACCGCAG	GCCTTGTCGC	CCACGACCTT	TCCCGCTGGG	CCGACAGCAC	120
	CAATGCATAC	ATAAACGGCA	CAGAGGCCCTC	CGTAAATGCC	GGCCTCCTCG	GCTGGGTTAC	180
35	CACAGCCAAT	ACAGCCCTCA	ATACCACCGT	CGCCGCCCTG	CTCGCCGACA	TCGATTCCAC	240
	CGTCGACCGC	GCGTTGCGAG	ACACGCCACT	TCACCGCCCC	ATGGTGACCG	TTGTCTCCTG	300
	TGTAATCGGG	AACAAGTTGC	GCGCCATCGA	GGCAGGCCCTC	ACCCTGGACCC	ACGACCACGT	360
	ACGCATCGCC	CTGCCCGCGA	TCCATACCGC	CCGCCCTTCG	GACGCTGTG	CAGAACCAGA	420
	CCTTCCAACC	CATCCCGCCT	ACACAGCCGT	GCTCCAGTCC	CTCAGTGACC	GCCTACGTCA	480
	TTCCGGTTGAC	CGTGTGCTAC	ATCAGTGCTG	TGCCCGCGTC	CGCATTGAAC	TCTACGTATC	540
40	GCTTGCCCTG	CTCGGCCCTC	GGATTCTGCA	GACACCTCTC	GGCTTGGCAA	TGCTGCTATT	600
	CAAGTCGCAC	TGCCGTCGCA	GGAACCTGCG	CCGCAGAATG	CCTTGAGCCT	AATTCTTACA	660
	TAATCTTAAT	TCGCCATTCT	GCTGCTCGAA	CACGAACCTC	GCGTTAGCCG	G	

1426RP

	GATCTTCTCT	CCGCTCGACG	TCAGTGGCGG	CATGCACGAC	GCCATGAACT	GCTGCTGCCG	60
	CTCCTGATCG	CCCTCGTGCA	CTGCTAGCCG	CGACTGGCCC	TCCAGAAACC	GGCCCATCTT	120
	GTTGCGATCC	TGCAGCAGCA	CCACCACATG	CGGAACCACC	GGCTGCCTGG	CTGCTTTTCG	180
	TAGCTGAAAC	GAAAGAAGAC	GCCCTATAGG	CGCGCTGCCT	AGCATATACA	CCCACGGGAC	240
	ACCCATAACA	GCCCTTCTAA	CCCTCAACCG	AGTCACTGAG	AACTGGCGTA	GTGCGCATCA	300
50	TCGACCTCGC	GATTTTTCAT	TCTAGTTAAAT	AATCCTTACA	CCGCCAACAC	AAAGCCAGCT	360
	TCACCACCAT	TCTGGCTCAA	CTAGGAGGCG	TGTCGGGCGA	ACCAGGAACG	CGTTACTCGG	420
	TAAGCGGGCA	TCTAGTCAAG	TGGGCAGTTG	CAGGCGACTT	CTTTTTGTGT	GTTATTTCAGG	480
	GTGTAGGATG	CTTGTATATG	GGTTGACAGG	AGGTATTGCA	TGCGGCAAGT	CGACGGTGTG	540
	GCGGAGACTG	CACGAGCATG	ACCGGATCCC	GGTGATCGAT	CCGGATGCGA	TTGCGCCGGA	600
	GATTATGCGG	CCGGGGGAGC	GGGCGTACCA	CGGGTGGTGG	AACGGTTTGA	GCAACGGGTG	660
55	CCGCAACTGG	TGCAGGCGAA	CGGGGAGCTG	AACCGCGCGG	CGCTGGGGGG	GTGGATCTTC	720

CA

5 1426UP

GATCTGCTCC	AGCGCCTGCT	TGAACCAATC	TCCAGAAGAG	TGTCCGCCTC	GTCAAGAACC	60
TTGAAGTCAA	CCTCGGTAAA	GTACTTTGGA	CCGCAAGCCT	CGAGCATGTC	GATCAACCGG	120
CCGGGCGTGG	CAACCACGAT	ATTGGGCCTC	CTGCGCTCTA	GGGATCTGAA	AGTTTCAGTC	180
CGCGAGGAGC	CGCCCATCAT	GACAACCGCA	TTGAAACGGC	GAAGCTTCCT	GTTGGCGTTG	240
CGCATCTCGT	TGATCTCGTT	GAAGATCTGC	GCGGCCAAGT	CCCTGGTTGG	TGCAATCACA	300
ACAGCCTTGA	CATTTTCCGA	AGGAGGCCCC	TCCAAGAGCC	GCTGGAACAG	CGGCATCAGA	360
AACGCAAGTG	TC'TTACCTGT	TCCAGTTTTC	GCCCGTGCCA	CCACATCGTG	CTCCGTCTGC	420
AGGATCGGCT	TCAGCGTCTT	CTGCTGCACC	GGTGTTAGTT	TATCGAAGCC	GCGTGACTGC	480
AGCATCTCGT	ACAGCTCGTT	GCTGAGCAGC	CCCTCCTCCA	CCAAGGTCCG	CGGTGTGCTT	540
TCGACCCCGG	CAGCTTCGTC	GGCCACACGC	ACCACCTCGG	TGTTGGGGCC	GAGGCTGAAT	600
CCCTCGCGCG	CCGCGCCGTC	TGTACGGCCG	CGTCTGCCCT	GTGGCTTCCG	CCACATGCCG	660
CCGCGGGGAC	CACGCTCACC	ATCCTCCCCTG	TCGCTGCCCCG	GCT		

1427RP

GATCTTTCTA	TCCGGGAAAAG	AGTCCATCGA	ATACAAGGTG	CTTCTAGAAG	GGCCCTATGG	60
AAACACCATT	CCGCGGCTTG	CTGCTCCTGA	CCGGCGCTAC	GTGGGCGCCA	GCGCAGGTCT	120
TGGCGTAGCA	GCGGTCTACC	CACACTTCGT	CTCTCTGTGT	GACAAGGAAA	GCCAGTTCAC	180
CCATTCAATC	TACTGGATTA	TAAATGACCT	TTCATATCTG	CATTGGTTTT	CGCATGAGCT	240
GAGGTAACTG	GCGGACCGGA	ACTGCGACAT	CAAAATTATT	TACACGAGGA	GCAATGAGTC	300
GGCTAAAGAA	CTGACCCGAG	ATGTTGCCGA	TTCCGCCTCT	GCGAAGTTTCG	TGGATTCTGT	360
GGATATCTGC	AGGCTCCTCC	TGCGCCGAGA	TCTCAAAGAG	ATCGTGGAAG	AGCAGATCCT	420
GCTCTCGTCT	AACCAGGCAC	AGGACGTCAC	GTTTATTAGC	AGCGGCCCTT	CGACCTTTAA	480
TGACCATTTT	CGCTATGCTG	TGAAATCTAG	CATCACGGGC	AAACTCCAGT	GTGATGTCGA	540
CCTAGAGGAG	GAAAGCTACA	CCTGGTAGAT	AGATAACATC	TTATTAGTTA	ATTGTACTTA	600
TTTATTCCTC	TTCTGTATC	TTAAGCAAAT	CCCGCCATGT	CTCAACCAGC	TTCTGCATGC	660
TTTGCGGATT	GAGCCCTGCC	TCGACCACGT	CCAGAGGTAC	CTGGTTTTTC	G	

1427UP

GATCATCTTG	TCCATGCCCT	TGGGGCCCAG	CGACGTTCTG	ATCGCATCCG	CGACTGCTCT	60
GGCAGCAATA	ATGTTTCGCC	TTCTCACTTC	CTGCGGCTTC	TCGCGGTTTT	TGAACGTCCG	120
ATTGCTGGCA	CTGACCTTCG	GTGGCATCTT	AATATACTTC	CTGATTCCGC	GCCCCAGAAG	180
CCTTACTTGC	TGCTAGAGAA	GTTAAGGTTG	TTTGTTTATG	CTGACAACGC	CTAAGTTACC	240
GTCAAACGAT	CAGATTTTTG	CCACTGGAAT	TTCCCTTCGT	ACAAACGGAT	ACTTGATCCT	300
TTGATCTCCA	AGAGCTGTTT	CATCGGGATG	GCCTGCTGAG	TAGTGCCGGG	TTGAAGGGAA	360
AATCGGGGCT	CGACAACCTG	GGAAATGTCT	ACGGAGGACG	CGGCGTTAAC	AGGGATCGCG	420
GTGACGGCAG	AGCTCAAAAA	AAAATGCCCG	TTTTCCAGCT	GGTATGAGGC	GTTCAAGGGC	480
CACACTCCGC	GGGCCGAGGT	GATTCGGCCG	CTGCCCGAGG	AGTTCTGTAG	CTACGTGGAT	540
CAGCGCGGGA	TCAGGCTGGC	GCGCGAAGAA	GGCTCGAAGT	ATTTCTACGG	CCAGGAATGG	600
AGCCTACGAC	GGACGGAGAG	TACAGCGACT	GGGAAGGCGG	CGACAGCGCG	AGTGAGCGGT	660
CGTTCGTGCC	GCTGGACCGG	TGGCGGACTT	CCCCGAAGTG	CACGCGCGGG	TGAAGCAG	

1428RP

GATCATACAC	GCATTGCAAG	TATACATTAT	AGTGCTCATA	ATTATCGGAT	TGCAAAATAGA	60
ATGGGGCCCT	TACCGTAGTA	CTGTCTTGGT	AATGCAGCGA	CGCTCAGGCT	TAAGAAGCTT	120
TTTGTTCTCC	GTGTATTACT	AACAAAATAA	TTTCCTCGAG	CACAGGGAGT	AGAGATGAAT	180
TACATAATCC	ATATGGACAC	CTCGTCACCT	TCCAGCGACA	TTAACATTTT	CTTATGAATG	240
CCCAATAATG	GTGCCTAAAT	GATGTGCTTG	GTGTAATGCG	CATTATAAAA	TGTATGTGGA	300
TTATATATTG	TTTGTAGCAT	CTAGTAGAAC	CATGGTAGCG	AGGTCTTTGG	CCATACCCTT	360
CTGAAGAGAG	ACATAGCAAC	AGTGTCTTGT	GCAGACAGTC	TGCCGTCGAA	TGTTGCCTTG	420
AAGTAACCAT	GAGTACCAAG	ACTCTCCTTA	ATGAAGCCAG	AGCGTCCAGA	TTTCGTGAAT	480
AGTGGGATCG	ACTTGAACCA	CTCGACATCT	TCTGGCCTAA	AGAACATATA	GCGCACTGTG	540
ACGACGCGCT	TGTGGAACCT	GAATGGATGG	CCAGTTAATA	TGATTCTCTT	GGCCAATATC	600
CGTGTGTGGT	CTGCGTTTCA	GAACGTGCCG	TGGCCACGGA	ACGTCAGGCC	CTTTGGATCA	660
GAGGGGTTTT	CTTTGAAGTA	AATGGCCGGT	GACTGGGTCA	GGTCCAAGGG	AAGCATGCAT	720
GTC						

1428UP

	GATCAAACCA	GAGTGCGAAG	CGCACACGCG	GCACTGGCGG	GAGCCCTTAC	CGTAGTTTCT	60
	TGGGTGGGAG	AACCAAACGT	TTTCGTGAGC	CATCTTGTCT	GCAATGCGTT	AGTACTCTGT	120
5	CTGACCGCTT	GGAAGCGCTC	CGGCCCTCGT	GAGCTGCCCA	CACGCTCGGC	GTCTGCGGCG	180
	TCCTCATTTGC	CCGCACCGTA	TTCTGTCTGC	ACCGACAGCT	CTAGACCACA	CTTCGCCCCA	240
	TCCTGTGCAC	ATACGATTAT	GCTTTGTCTC	TTGGTATTAT	CCTTAGATTTC	GCTAGACTTC	300
	GACACTATGG	TTATCACCAC	TGTTGAAGTC	TGCTTCGGTT	GGCACCACAA	GTCTCGGGAC	360
	TGTAGTTGGA	AAGCGCAGTT	CGCGGCCAAAT	CAAGCATCTC	ATAATGTGTG	GGTGCAACCG	420
	TTGAATGTGT	GGGTGCAACA	GTCAATTGTA	ATTTCTTTT	TTGATCGAGA	GATGGGATGC	480
10	GATGAGCTAG	TTGAAAAATT	TTAGTATGGC	AAAACTGGCA	TGCATATCTG	AGATGGGCCA	540
	TCAATTGCGG	CAGCTTAGTG	TTAGACGACC	AATCCAGAGG	TGGTAATTGG	GCTATGGCAG	600
	GCTACTCGCA	CAGGTCGTCG	GTAAAAAAGG	GCCACAAAAC	GTTCAAGTCG	AAGCATGCGA	660
	GCAAGGGCGC	GTTGAAACGG	CTGCACAAGG	GCAAAGTGGA	ACAGGAGACC	GCTGCTGGGG	720
	TGAAGG						

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1429RP

	GATCAAAGTT	TAGCATGTAA	ATGTGCAACA	AACTATTTAT	TACCTCTGCA	CTGCCCATGT	60
	CGCTTTGAAAC	CGCCGAGGAT	CCAAACCAGT	GCTTTCATAA	TGGAATTGCA	AAATTGAGTG	120
20	CAGTAAATTGA	TAAGTATCTT	GAGAAAAGCC	CTCCCGACTT	TACCCTAGAT	GATTGCTTAA	180
	TATGTTTCAAA	AGCCTCCGAG	TTAATAAAAA	GGCTTGCTAC	ATCCAAGGTG	CATATAGATG	240
	TGATAGATGA	GACTAACAGC	ACCAATTCATA	AAAAGCGGAA	CGCAATTTT	CGAATCCACAT	300
	CACCCAGAGC	AGTATACACA	TCCATTGGA	ATGTCGTATT	AAGAAAGTTG	GATAGCGTTG	360
	TCGACCAAGG	AAAGGTAGAA	ACCGTCCAAT	CCTTTGATCA	GATACCTGAG	AATTTCCTTA	420
	TTAACTTGAA	AGAAGTCGAC	TTTACTCTAT	CTGGGGTTGC	TCTGATGTAT	AGCACTATTG	480
	ACTACTGGAA	CCCCACATG	ATCCCAGGCT	ACGGCAAAGT	TACGACTGTA	GAGCATTTCC	540
25	TGGTGCAGTA	TATCTTACAT	CGATATGAGG	TATTATATGT	GGCCGGCGAT	GAAAGCCTAC	600
	TAGATAGTCT	GGTTGGTGCC	ACTATTTCGGA	AGCTATTTGA	ATGCATGCAG	TCACAGCATG	660
	ACCACCAGAG	CCTGGTAGCG	AATAGCCAGG	CTGATACCGC	ACGAAGAGAT	AT	

30 1429UP

	GATCAACCGA	TAGCGGAAGG	CGGACGAGCC	TCGGAAATAG	TACTAGGCAG	TGGTTGGCTT	60
	TTGTTTTTAG	CTGTGTTTCA	AGATGTCAGC	GAGAACAAGC	AGGGAGGCAG	GCGCCTCCAG	120
	GGTGATGGGA	GGTCGGAGTA	GTATGGATGG	AAAGTCCGGG	ACAGGAACAG	GGTATTTGGA	180
35	ACAGCTGAAC	TCGCCAAGCA	TTCAGAAGCT	CATGCACTCG	GACGCTTCCA	CGACAGCACT	240
	ATTGGAGAGG	TTGAAGATGT	CCCTAGTGAC	TTGCGTGGAG	TTACAGAAAT	TCATAAGAAA	300
	GAAATACTTG	CTAGAAGAGG	GCCATGCGCA	GGAGATGGGC	AAGGCTTATA	AGAACTTCTT	360
	TCCGGAGGGC	GCTTGCAAGT	GCTTGCAAGT	TAGCATACAT	AAGGTTTTTG	AGTATGACGG	420
	AAAACCTTGG	CAGGTGAAAC	TTTCATATGT	TGCTGCGTTG	CAGAAGATGT	ACGATGAGTT	480
	AACGTCGCTT	CTTGCAATCCA	TGACTAAAAT	GCGCAAATCC	CTCAAGGAGA	GCAGTCGGCG	540
	GTTGGAAAAA	GAAGTCGCAG	ATGCTATACA	TAGCGCCGAA	AAGGCAAAGG	CAAGATATAT	600
40	GTCTTTGTGC	ATGGATTGGG	AGAAGCTCAA	GCTTGTAGAT	CCTGCAAAGA	CGAAGTTGAC	660
	ATTGCGGGGC	TCAAAGACCA	CTCGAGAGCA	GGAAGAGGAC	TTATTAGAAA	GATTGATA	

1430RP

	GATCGCAGAG	AGACACAATG	TCCCTGTGCC	CACTTTGTCT	ATGCTTTATC	ATTTATTGAT	60
	TCTTGTGCAG	GGGAAAACCTG	AAGGCCCAAC	AGGGAATTGT	CAACCATGTT	TAAACTTTTC	120
	CATGTGCATG	GAGCTCCGTA	TGTAGCAATA	TATTCTCATA	GCTAGAGATC	TCACTATATA	180
	TTAGCTTGGC	ACATTTATGT	CATATCGACG	TTGCTTTTTG	TACACCTTTG	TGTCAGGTAG	240
	CAGGGGCGCG	ACATAAATAG	TTATAAAAAAC	GATGCGCGCG	GAGAACGAGA	TCTACTATCT	300
50	CTCTGAGTAG	GCACAGTTTC	CAACGTATTA	GTCCTTAATG	AGCAAGCGAA	TCATTCAACT	360
	CATACTTCTC	TCTGCCTTTG	CGCGAGCTAA	TTACGTGGAG	CCCTTCAAAT	CAAATCCATA	420
	CATTGCTTGC	TCAGAGGCAA	GCCATTGCCC	AAAGGAATGG	CCATGCTGCT	CGCAATATGG	480
	ACAATGCGGG	AGTGGGCGCG	TATGCATTAG	TGGCTGCAAC	CCAAAATTCT	CGCATAGCCC	540
	TGAGAGCTGC	GTGCCAGTGC	CGGCGCTACT	ACCGCAATTG	GAGATAGTGG	CCAGCGATGA	600
	TAAAGGAGTA	TACCTAGAGA	TGTCGGGTCA	GCCTGCCTTG	GTCACAAAGT	TCCAGCGCAA	660
55	GAGCTCGGCG	CAGTTGTTGG	AGGTACATCA	CGAGGAACAG	CAGTATGGTG	TGTCGGCATT	720

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AGAGCAGGAC

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1430UP

	GATCGATTTG	GTTACCTTGT	TGTCCAACCC	ACGTACTTCA	AGAGATTCCG	ACGCAGAGTT	60
	GTAGACAGCG	TACCTATTCC	GAGCGACAAA	AGTCGCAAAG	CTTCCCTTAT	CCTCAACTAT	120
5	ATTTGTGGCA	TCAACAGCAC	CGCTAGCCTG	TTTTGGAAGC	AGGCAAAGAG	CATACCTATC	180
	GCCATCCCTG	CTACTTGAGT	TCACGAGGAG	AGAGTGTTCG	GAGGGATTAT	AAGAGATGGA	240
	CTTGAACACG	TTATATGGCT	TTCCAAAAGTT	TTTTAGAGAA	ACAAATGGCA	GAGAGGACAC	300
	CTTCTTTTCA	TAGTCAAACA	TTTGGACCTG	CTTCTCTTTG	TTGACAAAGT	AAAGCTGGTT	360
	CTGGTTTACA	GCCACAGGTG	GTCTCTCACG	GTCCAGTTTA	AAGACCATGA	TACCCGAGTC	420
	ATGCGCCGCG	CCAAAGAGGT	TCACATTAGG	GTGCGCCCTA	ATCGACCAGA	ATCTGTCTCTG	480
10	TTCTCTTTTG	AACTGTTTTA	CAGGAGTGGC	CTTGTCTAGA	TCCAGACCC	TAATGGGTAGA	540
	ATCCTCGCCG	ACAGAGATAA	TTAGGTTTTG	AAATGGGTGA	AATATTACAC	TGTCGACGTT	600
	GTTCGTATGA	CCCTGCACTT	GTCGACCTCC	CACGCTTTGG	TGGAGCTCAT	ACGCCACAAC	660
	TTGACCTGTC	TGTCTTCAGA	ACCGGAGACA	ATCAAGGGCA	GAATCGGATG	GAACGAAGG	

1431RP

	GATCATGTTA	TACAGACCTT	CAAAGTTGAT	ACCAAAACCC	TCAATGGACT	CGCTGACCAT	60
	ACTTGGTACT	TCCTGTTTAG	AGGCCCTGCG	GCACACTTAC	TGCCTCTACA	AGAAAAAACT	120
	GTTCCTCTCG	AATTGGATCA	CCCTTTTTCG	GACACTAACC	ATTTGCAATA	CAATGCTATA	180
20	TTGCCTCTAT	CAATGGTCTA	TTGACCTTGT	TGAATCCAAG	CTCGAAATCC	AGCAATGTGT	240
	AGAGATACTG	CAGCATTTTCG	GTGAGAAATG	GGTTMTTGCC	AAGGAGTGTG	CGGTTCGTCTT	300
	TCAAAATATT	GGAAATGCGA	TACTAGATAT	AAGTCTCTCC	CGAGGACAGG	TAGAAAACGT	360
	TGATAAATTG	ACTAGGAGAC	TATTTGGAGC	TAGCAATGAA	TACCAAGATA	TATTGGACGA	420
	AAATAACGTA	GATATATCCT	GGATTGACCT	GGCTATCTAA	TTTCTGAAAC	CATTGAGAAC	480
	CTGTTTAAAC	TATTTGGCAG	TAATTCATAA	TGTATTGGTT	GTTCATAGC	TGAATTGCTA	540
25	TTGCCGCTAT	GGAGTTGCTT	ATGCAATACA	CGGGTTAGTG	GGTGATTGTC	GTGTTCTTAT	600
	ACCCAAACTA	ACCGAATCCG	GTCTTAATCG	ACTCCGGTAG	ACTTTGTCAT	CCAGTAAGAC	660
	ATGTCCTTACA	CGCCCGATTA	ATGGTTGTAA	TCTTTAATCG	ATGAATGAGA	AATGGTATAT	720
	GTATGTGACT						

1431UP

	GATCTCCTGT	ACCATCATGA	AAGTCTTTTT	ATCACGGGAA	AACCCGTTTC	TCAGGCACAT	60
	CTGACGCAGT	GCTTGTCGCA	CATCAAAGGT	CAAGTTCCGA	TCCCTTGTGA	GCGCTTCCAA	120
	CTCCAGAAC	TCCTTCTGCA	GATTTTTFAC	TGGGCGCGG	ACAACCTTCG	CCTGCCCTCG	180
35	GGGCACATAT	TTCTTTAACA	CCTCCTTCGG	AATCTTAAAG	TCCCTCACAT	TATAGCGACT	240
	TACGAGACCT	TCGAATAAGA	AGAGGCACTT	TATATATACG	TTTGACATAT	CCAGTTTCAT	300
	CTCGCACCCC	CGCACGATCA	GGTCCCGGTA	GTCCAAGTGC	GCCTTTCTTC	TTGAATTTCGT	360
	AGAGCTCGCC	CCCGAGGATG	AGCCTCGCTG	ATCAGAGGTG	CCTGTCTTCA	GCGAGAGCTG	420
	TGGCATACTC	GGCTGTGTGG	CAAGCTCCAC	CTTCACCTGC	TTGGCAAAGT	TCACATTTAG	480
	GCCCTGCGCA	AACGCGTCCA	GTCGAGCGAA	GATATGGTTC	ACCAGCTCGA	GTGGCATCGC	540
	CATCTTGTTT	ACGTCCAGTG	ACACGTTCCC	TTGGCCTAGC	TGGTGCACTA	GGGCCGCGCT	600
40	CTGTGTGAGT	TGTCGCTGCC	ACACAGAGTC	CAATTCCACT	CGCATCATGC	GCATCGCGTG	660
	CTTCAACGCA	CGCTCACTGA	TCTCCCTCG	CTCAGGCATC	TGTGGAGCCT	CTTCTCGGCT	720
	TC						

1432RP

	GATCCAGGAC	TGCCGTGCTT	GGTTGCGCTC	AAGGGAGACT	TAGAAATGAG	GTGTTGGGCC	60
	GCATTCTGCG	CTGCAGATAG	AAACGAAGAC	AAGATGCCAC	CGTTACCCAA	TTCTCAGCC	120
	CCAGAGAAAA	AATTCCCGTA	CCGGTGCTTC	CCAGTACCAT	CCTGGTCAAA	GGGTGTGATA	180
	TCCGAAAAAT	TATCCTCAGT	GTCTCTCTTG	TATCCTGCAT	CCGAGCGCGT	GCTTTGGCCC	240
50	GCCCCCGCGG	GCTCGCCGCC	CGCGCCAGAC	CGCACATGCG	AGTGCCGCGC	GCTCATCTCA	300
	ATTGGCATGC	TGAGCGACGA	CGAATTGCTG	TGCCCCCGCG	TATGCCAGCT	GGCGGCGTCC	360
	CGGCCACCCC	ACCCAGGCG	GAGCGACGAG	TTTGTGCTGT	TCGCGTAAAC	CACCGGTCCG	420
	GACATGAGCC	ACGATTCTGC	TCCTGACACC	CGGCTCTCCA	CATCCGAGCC	CTCCCCCGCC	480
	GCCACCTCGA	CATCACCCGC	CTCCGGCCCC	GTCCGCGCGT	CCCCATTCCG	CGTCGCTACC	540
	CGTCTTTTGG	CACTGCTCGC	GCGCCCCCTC	CGCCGCCCCT	CCCCCGTATG	CTTCTTGAAA	600
55	AGTGCCGCGC	GCTCTCTCTG	AGCGACC GCG	ACCGCTTCCG	CTGCTCTGCC	ATCCTTGCTA	660

GCCTCTGCCT GAGAAGAGCA TCTACCTCTC CTCCCTGTTT ATTCCGCCGC CTTTTTGCGA
AACA

720

1432UP

5	GATCCCGGTC	GGCCGCTCCT	CCTCGAACAT	GTCTGTACC	CCGCGCAGCG	GCTGGAACAT	60
	CCCCCCCACC	CCACCGTACT	GCCCCGGGAA	GAACGTGTGT	TCCACCAGCT	GTTCGTGGCG	120
	CGCTGGTCC	GGCGGCCGCA	TATTCTCCTC	CTCCTGGTAA	GCCTCCTGCT	GCAGAGACTC	180
10	CGCCAACTTC	TCGTCTGTCG	ACTCCGCGGC	CGGCCGCGCG	CTTGCAGGCC	CACTGCGTGC	240
	GCCAGCCTGC	GTGTGCGCCG	CGTGCTCGAA	GTACAGCGAG	ATTGCCGTTT	CCACGTCGCC	300
	ACCTGCCATA	TCCAGGAACT	GCCGCGCCAG	CTCCGCGTCC	GCCACACCGC	AGATGCTTTG	360
	GAATACGCCG	AGCTGCTTGT	CTGAACATCAT	GCTCCTACTT	TCTGGCGCTG	CCGTGCTGTG	420
	TGGCACACTC	AGGAGTTTGT	CTGACGTTGT	CGCTGGCTCC	AGCCTTTTAT	ACCGGCGCGT	480
	GCCACACATG	CGCCGCGCCC	AAACGCTTAT	ACATATACAT	GCTACTTAGT	CCGCCGCTTG	540
15	GTACCCCGCC	CGTCTCTGAA	GCGCGTGTGC	GTGCCCTGGA	AGTGCACCGG	CTGATCGCCG	600
	CGCGCTCGGG	CGCCG					

1433RP

20	GATCGATGCG	GACCACCGTG	CGGAGGAGGC	CGCAGGTGGA	TATGCAGTTT	GCGGCGCTGA	60
	GCGCGCCGAT	TTCGAGAGCT	CGCGCGTCCG	CTGGCGTGCC	CGCTTCGCGC	AGCCACGGAA	120
	CCAGCTGACG	CGAGGTGTCT	CCCCCGCGGC	TGGCCGTTTG	CCCGACAGTG	CTCGCCGCTT	180
	GGTAGTTCTG	TAGCCACGCG	GGCCCGTTAA	TCTCGCCAT	TACGTAGCCG	AGCATCTGCA	240
	CGAGCAGCGG	CGACTCGCGC	ATCTTCTGTA	TTTGTAGCAG	CTCGCGCTCG	ACCTTCTCGT	300
	CTGGGTGCGC	CATGTCCGCG	CCCAGCCGGT	ACTGTTCTTG	CAGTCCAGCG	TCTGTACAGT	360
25	ACCGTGCTAT	TTGCCGCTCG	TTTACGACTT	CGTCATTCTC	AGCCACCGGT	ATTCCCAGGA	420
	GCTTGCATAT	TGCCCCCGCT	TTCTGTAGGA	GAACGTGGTA	GCGCCGGATG	ACCTTACGTG	480
	CTTTGGATGG	TTTGATTGCC	GGCGTATGTT	TGACGGCGCT	CTTGCCCGTA	ATGCTTCTTC	540
	GCTTCCCTGGC	CAGCATGTAT	GAAAGTTAAA	CCGCAGTTAC	TACTGGTACT	AGATATGCCC	600
	TCGGAATGCC	ACCCGATGAC	CTGCTGGTGT	ACCTTGCTTT	TGTCATCAGC	ATGCTTCGAG	660
30	CTGAATCGTT	GAAGAATTTT	GAGTGAAA				

1433UP

35	GATCACGGAA	GAAGGCAAGG	TCAAGAAGGT	TACATTTGAT	ATCGAGCCGT	ACAAGCCCAT	60
	CAACACTAAG	CTATACAAGT	GTGACAATAA	GTTCCGGACG	GAGGTGCTCT	CGGAGCTGCT	120
	GGAGGCTGAC	GAGAAGTTTC	GGTTTCATTG	GATGGATGGT	CAGGGGTGTC	TTTTCCGTAT	180
	GTTGTCCGGT	AACACCCGGA	CTGTTCTACA	AAAGTTCACT	GTGGACTTGC	CGAAGAAGCA	240
	CGGTAGAGGT	GGTCAATCCG	CGGTGCGTTT	CGCCCCGTTT	AGAGAGGAGA	AGAGACACAA	300
	CTATGTGCGC	AAGGTGCGTG	AGGTGGCAGT	CGAGAACTTC	ATCACAAACG	ACAAAGTTAA	360
	TGTTAAGGGG	CTAATTTTGG	CTGGTTCTGC	GGACTTCAAG	ACGGACTTGG	CCAAGTCTGA	420
	ACTGTTTGAC	CTGAGGTTGG	CAGCCAAGAT	TGTGAAGATT	GTAGATGTAT	CGTACGGTAG	480
40	TGAAAATGGT	TTCAACCAGG	CTATTGAGCT	GTCCGCCGAG	GCGCTGGCCA	ACGTTAAGTT	540
	CATTCAAGGAG	AAGAAGTTGC	TCACCGAGTA	CTTTGATGAA	ATTCCCAAGG	ATTCGGGCAA	600
	ATTCTGCTAC	GGTGTGACG	ATACTCTGAA	AGCGCTAGAT	TGGGTGCGGT	GGAGAAATTG	660
	ATTGTGTTTG	AAAATCTAGA	GATTGTTCCG	GTACGTGTTT	AAGACTTCTG	AA	

1434RP

45	GATCAGATGC	TTCTGTGGTC	CTAGAGAAGA	CTGCTATTCT	TAACCCCTCG	TCAACGAATA	60
	TAGCCGAGGA	CGAGTTTGTC	GATGCCATAG	CGGAACCTCC	ATCGGCGTCC	GTGGATAGTA	120
	CGCCTTATGT	GACCGCGGCG	CGCGATTATT	CCTCGGAAGA	CACCGGGGAA	CGTTCTGAAC	180
50	CTACAATAAC	GGAATACAAA	ACTGCAATTG	AATCACCATC	CACCTTTGGC	GACGATAACG	240
	AGAGTGATAT	TCTTGTAAC	TCTGCGGACC	TGCATCCATC	GGTGTCTCTT	GCGAGTCAAA	300
	CATTAACAAC	GGAAGAGCTT	CAAGCCGTTG	CGAACAGCCA	CCAATATAAG	ACCGAGGTGC	360
	AGATTGTAAA	ACAAGACGAA	GATGAAGTAA	AGGATGTTCT	AGAAATTGGAC	TCGCCACCAG	420
	CATCTCTGTA	TGATGGTGAT	GTTTGAAGG	AGGCAGAGAA	AAATGATAGT	AGCAATGTTA	480
	TTCTGTATGA	TCCATAGAT	ATCGATGAAT	ACCTCGATGA	AAACTTGGTT	AAAAACTTCA	540
	CATTGGAAAA	CGCTCTTTCT	TTAGATGAAA	TCTTCGACGA	TGATAATGTA	GTTTTTGGAG	600
55	AAGAGAAAGCT	GCTTGTGGAT	CCAGACCTAG	AATTCCCGGA	ATTAACCTGA	ATGGAACAAG	660
	ATATGGAATC	TGACTATCTG	CCGCTGATTG	AAAATGGTAC	GGAGGCTGTT	CTACAA	

1434UP

	GATCAGGTTT	TCCGGTACGT	GAGAACGTAT	CTAAGGCACA	AAGGGCTTTG	GGCGACTGTG	60
5	CGGACGCTTG	AGTTGCGAGA	TACAGGACAA	AGCTGTTACG	GCGGCAACTG	GTGCAGCACG	120
	AGCAGCCGAG	GAGCGATTCT	GCGCGAAGCG	ACGGTGAATT	CGAGCCAGCT	GGTAGCAGGA	180
	GTGCCGGATC	GTCTATTTAG	TTGCGACGGG	CGTCGGAACA	GGATGCACGT	AAACGTTGCG	240
	GTAACACGCG	ACGCTGACGC	GACGGCTGCT	ACGCCGATAG	CACGGGAGCG	CAAACGACGG	300
	CAGCCGCTGT	CGCCAGAGAT	GTCTTCACCA	CTGCGCGGTA	GCAAGCTGCA	GCGGCGGAAG	360
	CAGACACTTG	AGGCCGGTCC	GGGTGCGCGC	AGTGGGACAC	ACACGGTGGA	CGAGCTGGCC	420
10	GCGCAGCTGG	AGCGCGGCTG	CGAGCAGGCG	TCCGAGCGGA	AGCCGCCGTA	CTCGTATGCG	480
	GTGCTGATCG	GCGTTGCGAT	CCTACAGTCG	CAGGAGGGCA	AGCTGACCTG	TCCGAGATAT	540
	ACCGGTGGAT	CTCGTCTTTC	TTCCCTTACT	ACCGGCTGTG	TGACGCGGGG	TGGCAGAACA	600
	GCATCCGGCA	CAACTTGTCT	CTGAACGAAG	CGTTTGTCAA	GCGCGGCAAA	TCCGCTGATG	660
	GCAAGGGCCA	CTTCTGGGAG	ATCAAGGCAC	TGTGAAGGCG	CTTCTCCGCG	ATGGG	

1435UP

	GATCCGATGC	TACCCGTCGC	CCTGCCAACC	CGTTGCGCTA	GCGTTGACGC	CTAGGTCTGA	60
	AACTGAACAA	CAGGTGGCAT	TGTGGGCGGG	CCAGCAGGCC	CTGGCGCGAC	CATGCCGCCA	120
20	TGGGCGGCGA	ATAATACCAC	CAGTTGTGAA	GCCCAGGTGT	CTGTAACTCTG	CACCGAACAT	180
	CTTTATCTAC	CAAGGAGGAG	CCTTGAAAT	TATATATCTA	CCCCTCCCCC	TAATATATTT	240
	GACCAATTTC	CTCTCCGGAA	ACCGAATGAT	CGAAGACGCC	ATCAGGGCAG	CGGACAGCAC	300
	AGGAAGTGAG	GAGTGATCTC	GCAGGTACGA	TGGAAGCACA	GTCTATACAG	TCTATTCCGGT	360
	CGAACCAAAG	CGTACGGAGC	ATCSCGAGCA	CGAGCGGAAC	CGCAGACGAG	TCCGTAATCT	420
	TTGAACGGAG	CGTTGAGGAT	CGTTTGGCCC	CGTGAAGGAC	GCGAAGGGTT	GCAGCCTGTG	480
25	TGGTGTCTCC	CAGGCAGGGT	CTCTGCACGC	CGGGGTATCG	GCGACTGGGG	GCGCGTCT	

1436RP

	GATCAACCTC	GGAAACGTAT	TTAAAAGCTT	GTACTCGACA	TCATTAAGTC	TTCTCCTCGT	60
30	TTCTTTTGGT	AAAGTATWAG	CATCCAGTAA	AGTAACAACG	AAATGCAATG	CTGAAAGATC	120
	GTATACCCTA	GACGACCTAA	ATGGGGTATT	TTGATCATCC	ATACTAGCTT	GAAGATCAAT	180
	GAAGTCAATA	ATAGTGTTGA	CAGACTCAGG	GGAGAGTTTG	GACTTGATGT	ATTCTCATAA	240
	GCCAGTCCAT	CCCACCTTCC	TAGCACTAGG	AGTAATCTTC	AGCGATTCTT	TAAACGGAAT	300
	ACTTCTGATA	AAATCCTCCA	GCTTTTTTTC	CTCGTAAAGG	ATCTGTACAA	AATTAGCAAG	360
	CGGGGTGGTA	TCCTTGTTAA	TTATGATTCT	TCCAACTTCA	ATGACCTTGT	GGTTGGGGAT	420
	TTTCTTGATA	AGCTCACCAA	ATACCATCGG	AGATTTTTTCA	AATACTTGGA	CCATTAGAGT	480
35	GACCAATAGT	TCGTTAATAA	TCGCCTTATT	TTCAACCATA	AGACTGAAAT	GCTTCGTTTC	540
	TGAGATCAAA	GTCAAGGCCA	AATATTCCGG	AACAATATTG	TAATCATCGA	AGAAACAATC	600
	ATGGAATAAT	TGGAACATAG	GACTGGAGCC	AAACTCCTCT	CTTGATAAGA	ACAGTTCAAT	660
	ATCGAGCTTC	GATACCGATG	TGAGATATAA	CAAGGAGTTC	TTTGAGTTTG	GGAGTACTTT	720
	AGAGACTT						

1436UP

	GATCCAGAAG	ATTATCCGAC	AATATTAGTG	ATATCAAGGC	ACAGATCGCT	GCCAACACTA	60
45	GAGGTATTCA	ATTGCTTAAC	CAACTGGTTG	ACGTTTTTCG	TCTAGGGACT	GTTACAAGGT	120
	ACATGGACGC	AATTCAGGAA	AATGCAGCTC	TTACTGTAAA	GAATGTCTTG	CGAAAGATTA	180
	CCAAGCATTT	TGGCAAAACC	GTCTATTTCG	CCGAGGATTA	TATGGATGAT	GGCTCTGTTA	240
	TAAAATCTAG	GGTGGAGCTA	AATGCTAAGG	AAGATAAGTA	TATTTTTGAT	TTTACGGGGA	300
	CTTCTCCACA	GGTCCACGGT	AACCTCAATG	CACCTGTTGC	TATTACCAAC	TCTGCCATCT	360
	TATACTGCTT	ACGTTGTTTT	GTAGACGAAG	AGATTCCGCT	CAACCAGGGC	TGCCTAAAGC	420
	CCATTACTGT	TATTATTCCA	GAGAGCTCTA	TCCTATGGCC	GACCAAGGGT	GTGCGGGTAG	480
50	TGGGAGGTAA	TGTCATGACG	TCTCAGCGTG	TAAC TGACGT	AATTCTCAA	ACTTTTAAAG	540
	TCATGGCGGA	CTCCCAAGGA	GACTGCAATA	ACTTTACTTT	TGGGACAGGT	GGGAACGACG	600
	CTTCTACCGG	TGAATATACT	CAGGGTTTTG	GATATTATGA	AACCATATGT	GGCGGGCATG	660
	GTGCAGGTGG	AGATCATGGC	GTGGTCCGGG	GTGGCATGGA	ACACATCCTG	TTT	

1437RP

	GATCGCGCGC	GAGCTATCGC	TTCCGCCGGT	CAAGCTGCAC	TGTAGTATGC	TCGCGGAGGA	60
5	CGCCATCAAG	GCCGCCATCA	AGGACTACCG	CAGCAAGCGC	AAGGCGACCG	AGCTGCGCTG	120
	AGCGCAGGCC	GCCGCAGCCT	GTCGGCGGCC	GGCCGGCGCC	AGCCGCAGAG	GGACGTCCGC	180
	GGGCCGGCGA	GAGCCGCCCG	TTTTCTATGT	AGCGACTCKA	GCATCTAATA	GACATGGTAA	240
	TAGCTTCTCG	TTTTCTACGT	TTGCACACAG	TATACAAAAT	TTTCACGCAG	CTCATCGCCA	300
	CTTCCACTTG	CTGAAGCGCA	GGTACGGCAC	CAAGACCTCG	GCTATGTCCT	CGACTCTCTT	360
	TGACGACATC	TTACACGATC	AGGAAGTGGA	CCAGGGACGG	TACAATAAGG	TATCGCGGAT	420
10	TGAGGCCATC	TCCACGTCCG	AGGACACGTG	CAAGCTGACG	CTGGATGTGA	ACACAGAGCT	480
	CTTCCCCTG	CAACCACAA	AGCAGCTAAC	GGTGATGCTG	GCGACGACAC	TCAACCTCGA	540
	CGGAACGAG	GACAGCCACG	GGTCCTGGCG	GCCTCCGGCC	CCTGGGG		

1437UP

	GATCCGGCGG	GACCGCTACA	ATATTCCCAT	ATGTATTAYA	GGCAACTTTA	TACCCATCTC	60
15	CTAAGTGCGA	TACGTACTGT	TTGTCACTCT	AGCGTCTCGC	TCGCGGTGAG	CCCCGTGTTG	120
	CGGTCCACCA	GCGCGCCGAC	CGCGCGCCCG	GGCCCGACGT	GCAGCGCGGC	CGTCGCGCCC	180
	GCCTGCACCG	CCGTGCGGCA	GGCTGCGACG	AACTCGACCA	CGTTCGTGCT	CGAGCGCACG	240
20	AACTTCTCCA	CGGCCACGTC					

1438RP

	GATCTCTTTT	TAACGGCTGT	TACCAATAAC	GATACCGCAG	CTACATCTGG	AGAATAGTCT	60
25	GCATCCCATG	CCTCCAAGTT	CCTGTGAACA	TACTCCTGGG	GATCGACCTC	GAAGCTCTCC	120
	AAGGTCTCTT	CGCTAGGACA	AAGAAGCGGG	AAGATAACAT	GTTCCTAAAT	GGTTGCATAA	180
	TGTGGGTCAA	CTATCGGCCA	AGTAGACTTT	TGGACCACTG	TTTGTTCAAT	GAACCTCCAAT	240
	ATGTAATATA	GCGACTCCTT	GCTTAACCAC	AATTCGCCCTG	CACCCACCT	TTCAATCTGC	300
	TGGAAATGCA	ACTGCAATAG	TTGCGGCAGA	AACTGCCTCA	CATACAGCAT	TTTAAATTCA	360
	GTGTACTCAA	ACTTTTTGCT	GAGAGATTCT	GAGGCATAAC	GTGGAATAA	TCGATACATG	420
30	TTAGCATATG	CCCACTTTTT	GGCTCTGACC	CATGGATGCG	CCCGCCTATC	ATCGACCGCC	480
	AGCGCCATCA	CATGCTCCGG	CAGCTGGCTT	TGTATCACAG	AAACATGGAA	GTGCGCCAC	540
	GGAAATGAAGT	TTTCCGACCG	TTGGAGAGTG	AACGGCAGGT	CATTATATGT	CACAACTTG	600
	TAGATCTTCA	GCACAAGCTT	CAACATATT	CCCACGATCT	CGTTGTGCTT	TCCTCGCTGT	660
	ACAAAAGCGC	GTTTGCGTAG	TGCAGCAAGT	CTGGGAAATA	TCTCATGATC	AGCATCTCCA	720
	GCTCCTGA						

1438UP

	GATCGGCAAA	CCTAATGCGT	CTGGACGTAA	TGTAATCCAA	CAGCGACTGT	AGAGCTGCCT	60
40	GCGGTTCTCC	GACAGAAATC	AGCTCATCTG	CCCGCTTCAA	GGCGTTTTCA	GGGCGCAAAA	120
	CAGGTGGAGC	CATGCTGAAT	TAGAGCTATT	TGGTGACCTG	TTTGAGTAGT	GTGGACTTCC	180
	TTTGAATGTG	GTGAACCTTG	AAGTAGGTTA	TTCAACTAGA	AAATTTTTTCA	CCCAGAAGGA	240
	TGCCCTCTAT	CAGCGGCCGT	GTCTGACGAT	GATCTCAACC	GCGTAAAGGA	CGAGAAGTCG	300
	TAGGTCGAGT	CTAATCTACT	ATTGGTACTG	ATGAACGGGA	CTGGCCAGCT	AACGTGAAGG	360
	CACGTCTGTC	GGGATGAGGC	CCCAGCGCCA	GCGCACGGGC	CCTGCGATGA	GCACAGGTTG	420
	CCTCGAGACG	ATTGCGATCG	GCTGACGGGA	AGCCAGGTTT	CCACAGCGTT	GGCGGACTCG	480
45	CGTCGTCAGG	CTGGAACTGT	AGAAGGGTTG	TCTTGAGCTC	CGCGCACGCC	GCACGCTGCC	540
	CAGGTAGCTG	GCGGGCCGTG	TTTCATCGCGC	ACAGCGGTGG	GCTCGCTGTC	ACGTGGCATC	600
	GAATATGTCA	CGTGATTACA	CGCAGCAGGG	CATCGCAGAC	AATGCGCAAG	CAGCAACAGG	660
	AGGAGGGTGT	GATCGGTGGT	GTGCGTTTAA	GAGTATGTGA	GCTGTGCAGC	TGGCTCCCCA	720
	TCTCTGGGTT	TACTCGTACC	TGTGCGCTTA	TATAGGCATT	GCCAAAAGGT	TTCC	

1439RP

5	GATCCTGTTG	GACGTCCTGC	AAAGTCGTGG	TCACCCCGAC	CAACTTCTCC	TCTGTAATAC	60
	CGCTGTACTT	CGTTAAGTAG	TCCACAATGG	GCTCATCTGG	CTTGACAAAC	TTGTCATAAA	120
	CTAAGTTACA	ATCAAAATCG	ACGACGCTCA	CACGCGTCAA	CACGTATCCG	TTTTTTGAAA	180
	GGCACATCTC	ACAGTCGATG	GCAAACGTGT	GAGAACCGTC	GTGTTGGAAA	CTGACAGTGT	240
	CCACCCACCC	ACTGTACTTC	TCCTTATTCT	GATACTTTAG	CAACAAAGCC	TTTTGGTACT	300
	CCTCCGATAA	GCCAGGTGTG	TTTAGATGGA	TGGGGTACTC	ATTATGCAAT	AAGTCATCAA	360
	CGGTCATTAG	CAAAATCAAGC	AAAGTGATTT	CCTTTTTGTT	CAATTGTTCC	ACCTTTGCGA	420
10	TCTTCTCCTT	TTTTGACAAG	CCTACATTGA	CAAAAGAATT	GTATGCAGAA	AATAGGGAAT	480
	TCTTTGATCC	CGGCGCTGAT	AACGGCAAGA	TACACATTTG	CTTGACATC	TGTTCAATTT	540
	CACTAATCGA	GTTTAGATGT	GCGTCTTGCA	ATTTTCGGAAT	ATTTTTATGA	AACAATGAAT	600
	CCTTCGGTAG	ACTGAAGTCC	TCGGGTAAAA	GGCCTGGAGT	GAATAAGACG	ACCACCTTCT	660
	TCAAAGAGGC	CTATTTTCTA	TCGTAATCCA	GTTGGGAGAG	TTGTTCTGAT	CGTGGAATAT	720
	GTACTGGA						

1440RP

35	GATCTATTCT	TCATTTCAGCA	ATCAACAAGA	GCTGGTGAAA	CTTGGGCAAG	AAGCTGAGCA	60
	AAGCGGTAAA	TACAACCTGG	CATTCAATGC	ATACTGGATT	GCAGGAGATA	TCAACAAGGC	120
	CAGGGACGTG	CTTTCGAAGA	GCGGACGCCA	TTCCGAGGCT	GTGCTTCTGG	CATCCACATA	180
	CACCTCAGAC	AATGACGCCA	TCAACGCTGC	TGTAGAAAAA	TGGAAGGAAC	AACTGAACTC	240
	AGCTGGAAGA	GTATCTATCG	CAGAAAGAAT	TATACTTTCC	GGAGAAGACG	ACTTCCCTGC	300
	AGCTCCCCAG	ACTTTGGTCG	AAATGGATGA	CGGATCAGAG	TCCGCGTCTA	AATAAACTAT	360
	AATTTTAAAG	ATAACAGCAG	GAATAAATTA	ATTACCACGA	AGGAAATTTG	TATGTACATT	420
	CTAACTAGAC	CCAATGGTAG	AATTTCAATG	CGTAAACACG	GCAACCTTAT	CAATATCTTT	480
40	CCGTTTGTCC	AGTCCGACAA	AGTAAAGTTC	TTTGGATTCA	GATCGGCATG	CTTCCGGCTT	540
	AAAACGCCGC	ACTTTGGTGA	ATACCTTTCT	CAGACGCCGT	TCTAATAGCT	GGTCTTCCTT	600
	GCCAGTGTAT	AACTTGCAAA	CGAATGAGCC	ACCGGGCCTC	AACAATGCAA	TTGCACATAG	660
	CAGTGCTGCG	TTACACACAAG	TCCATCGACA	TGTA			

1440UP

45	GATCCTACAG	AAATAATCCA	GTACAAGGTA	CCTCTAATCT	ACTGTGTTAA	CATGGAAAAC	60
	ATTTTCGCCCTT	TAGGCTTTTTT	CTTTTCACCG	AAAAGGTAAC	GTGTTTCGAAA	CATATATCAC	120
	GGGTTTCGAAA	CTGACTAAGG	TTGCTCATGC	CTAAACCAGA	TAGGCAGCAA	TGGCAAGGGG	180
	CTTGAGGTGG	TACCAGAAAA	GCTGCCACCT	CCTGCTGCGT	GCTTACTCTC	GCAAACGGTG	240
50	TATACTATTA	GTGTTGGAGT	ATTTATTGCT	TATTAATAA	CCGAATTGTG	GGCCTAGAAG	300
	TGGCGATTAT	CACGTAGCAG	CAGCGGCTGG	CAGCGCAGAC	TGCTCGCGAA	GCCGAGCAG	360
	TGCGTTTGAG	GCAGCGTTTA	GAGCTGCAGC	CGTGACCATC	AAACCTTCGC	CGCGGAGGAC	420
	GAGTATGAGG	GCTAGCTCGA	GGCGCATCAA	GAGCTTCTTC	GATATGCCGC	AGACCTTGCT	480
	GAAATACTCG	TGGGAGTGCA	CGGTGTCTTC	CACAATCTTG	GTTGAGACAC	GTATCAAGGC	540
	CACTATGAAG	CGATGCACAT	ACCTCTCGGC	GATGGGCCAG	CGGATCTGCA	CCGGACCGGT	600
55	TTCCGAAGGA	GGCCATTTTA	GCGTGAGGCG	GAGTAACAAG	CAGCCCGCGG	TCTGGTAGAC	660

TATGGGCGCA AACATGCATT TGGCGTTGAT GCCGTCTAGG TACTGCGTAT AC

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1442RP

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GATCAATTGC	GTCTTCATCC	GATGAGACAT	TTTGAAAATT	GTTGGAATAT	TGGGCAACAT	60
CAGGGTATGG	TAACACCTCC	GGTTCTAAAC	TTCTAATCGG	TAGCCTCGTC	GCGCGTGTA	120
CGCATGGATC	ATCAATGGAC	GGTGCTGGGG	GCGATCTAGA	CACGCCCCGA	TTGGGGCTTG	180
GTGTGAGGTT	TTCTGTCGGA	CTTCTCACTT	TATCAGGTAT	GACTATCACT	TGATGATTCA	240
TTAGATTCCG	TGTATCCACA	ACATGGACGT	GGCTTTGGTG	TTCCGAGATA	AATAGTAGGT	300
CATCAAACGA	GCGGCTAAAC	TTGCACACCC	TAAAGGACCC	GTTCTGTGCA	TGCTTTCGAG	360
TTGAAGGTAT	CTCCGCAAGA	GGCGTGTCCA	TTTTTCTCAT	ATCGTACACC	AGACAGAGGC	420
CGTTTTGGAA	TATCGTAGCC	ATGTGCACGT	CGTTTTTCGCT	ATAGCTTGTG	TAAAAGCCGT	480
TATCACCACC	AGGCGAATCG	TAAATACGAT	CTAGGACTTC	GGATCTATCG	ACCGCGGCAT	540
ACCTTGGAAC	GCACTTTGTG	CGCGACCATT	TTGAACCCCA	CTCAGGAGCG	GCGTCATATT	600
GTAATGAAAA	ACAACCGCTT	AGTTCATCTG	TCTATAGACC	GCAAACCTGC	TGGAATCTCC	660
CGAAACCACC	ATCGTCTTCC	CATCGTGTGA	TATTGCCGAG	CAGTTTAAAG	CAAATTTTAA	720
GT						

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1442UP

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GATCAAGGCT	GGGAAGTTGG	CGTTGACTGG	CTTGCCCTGC	GCAGGCTCTC	TGTTGCCGCT	60
CTTGCCGCCCT	CTGTTGCCGC	CCTTGCCGCC	TCTTTTGTG	TCTCTCTGGT	CGCGAGACTT	120
AGGAGCAAAG	GACTCGGTGC	CATCAAACCTC	TAGGAACCTGC	TTGGCCTTCA	AGTGCTTCGT	180
CTTGACGTTT	TTGACCTTGG	TAGCCTCCAT	GAAGACCTCC	TGCTTCTTAA	CGAACAACTC	240
AGCGTCGTCG	AACCTTCTCGA	CCTTTCTGGC	GACAGGGGCC	TTGTTTCAGGT	CGGAGTTCTG	300
CTGCTCCAAG	TACGCCCTCCA	AGGTGACGGC	AGCTGCAGTG	GCTTGCTCCT	CCTCGGCAGC	360
GTCGGCGGCC	AACCTCCGCCT	CGGCAACAGC	GGCACCAGCC	TCCTCATCGG	CCTGCTCCTT	420
CTCGTTGTGCG	CCCCACGCCT	GCTTGATCTT	CTTGCCAGAG	TCAGTCTTGC	CGGTTCTCGA	480
GTGGCGGTCA	AAGGTCTTTC	TGCTGTCTCT	GGCTGGCTTG	CCTGGCGCAA	GAGCGTCCTT	540
GGACTTGTTC	TGCGAACGGC	CGGCCTGCTT	GTCTCTGAAC	GCAGCCTCGT	TGCCGGTTGG	600
CTTTGGTCTG	TTGTTCTTGG	CACGCGATGG	GTCGGCAGAT	GGAGGAGGCA	CGTCCGCCCT	660
CTTGGAAGAG	GTGGTCTTCT	TCACAAGCTC	CTTTGGAGGA	GACACAACAA	CGGTGGCGTC	720

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1443RP

	GATCTATGCG	GTGCTGTGCG	CGTGCATCGA	CCAGCACAAG	AGCTTCGAAT	TCGATAGCGG	60
	GAGCTTCTTC	TTTCAGTACG	TCGAAGGCAT	CTACTCGTAC	AGGACTGCGA	GCCTTCTTGC	120
5	GGGCTATCTG	CGGACGCACT	CCGTGCCGAC	GGCCAGCCAG	TACGCCAAGG	TCCTTCTTAGA	180
	CCGCGCGCCC	TCGCCACGTC	AGGCCGAGGT	GCTGCTGCTG	GGCATAGTTG	CGGATGCCGA	240
	CGCCATGCAG	CGGCTAGTGC	AGGAGTGCAA	AACGAGTGGA	GCCGTGACAT	CTGCGAGCTT	300
	CTCGCTTCTC	ACAGAGTGCC	TCGACATATA	CCTGTCTGAT	GTGAACGATA	CCGTTTTGCT	360
	GGGGCCCCAAG	AGCAACTTCC	CGCTTGAAGA	TCTCGTGGTG	TTTTGCAACT	TGGTGCCTGA	420
	CGCGATATCT	CAGGCTTTGC	GTGCTGAGCA	TGATTATGAG	GTGAACAAGA	TGCGCCGCGC	480
10	GCTCTCCTTA	CTCCAAAAGC	TGTATATTAG	GGATAGAAGG	ACCAATTTCC	TCTCCGCGGC	540
	CAAGGGGGAC	GACTTCTGGG	TCATTGCGGA	TACCACGGTG	AAAAACTGCG	ACATTACATC	600
	TCTCTCTCTT	TACTTTGATG	AGTTCTACAG	AGAACAGTTG	GATTTGTTC	TGGCGCAGGG	660
	CCGTGCTCGG	CACGAGGTCC	CAGCGCGCAT	CTCGTAGCGT	GGGAAAACGA	TATAAA	

1443UP

	GATCCGGCAT	TTACATCTGA	CATGTAACCG	GGTGGTTCTG	TAGGTAGGGT	GTTCAATGTA	60
	AAGTGGTCGC	AGTTCGAAGT	TGGGGTAGTA	CTAAATTCGA	ACCCCGGTGG	CGGTGGTAGA	120
	AGATGGCCAT	CGTGAAGGTG	TTCCACAAAA	CTATTCTGTT	CACCCCTCGA	TACTTCATCT	180
20	TCATAACTGC	TTTCTAACAA	TACATCTCGG	TCATAGTCTT	CGTAGGCTGG	TGGAGGCAGC	240
	TTCATGCCGT	TCAGCTTTGC	ATATCCCCAT	TTCTTTACGT	TTGCTTCAAT	GTAGACGAAT	300
	CCGTAGGTCC	CGAAATTAAC	GTGTATCTTG	CATGGGACAT	TCGCACCAAC	AATCGGGTAA	360
	AGATACTTAA	TTTTCCAGCC	CTTTATGTGG	CCACCAATGC	GTTTCTCATT	TAACCTCTTG	420
	CCATTGCGCG	TGAAGAAAAC	TGTGCCGCTC	CGAGTTCTGT	AGCCAATCCC	GATGACGTCG	480
	CCCTTTTCGC	AGCGGGGGAA	TAGTGAAGAG	AGTTCTTGCG	GGAGCTTAA	CGAGTTGTTT	540
25	AACCTACGTG	CTCCATTAGA	GTCATATGCA	ACTGAGTGAT	GGTGTCTGCC	GGGAAGCCTA	600
	AAATAGGGAT	ACGGCGATGT	AGCAAGACCA	AAGGAACTA	TTTGGTTTTT	TGAGAGATGG	660
	CTGACCGGGC	GGCCAAGCCT	GTCACAGAGT	CGAAGATCTT	GCACTCGAAG	T	

1444RP

	GATCTGGTTT	TATAGGTTCA	CGAAGGGACT	CTGGACGCGG	ACCCTGCTGA	AGTGTGCCAA	60
	CATGCTGTAC	TTCGTGGCCG	TGATGCATTT	CTACGACGAC	TACGAGCACG	CGCCGGTACT	120
	GAGGAACATT	GGGTACTCGA	TCTTTATTCT	GAGCATTTGG	ATGAATCAGG	CACTGCATCA	180
	CGGCGGGCGG	CTATTACAGG	GGCGACGCGG	CGCGCGGTCC	TGGTGGTGGC	GGTCCGACAC	240
	ATTTGTGCTG	CAGCCCGCAC	TATATATCAG	CCAGTTCTAC	CTGCTGCTAC	TGAATGTACA	300
35	GAACCCGAGC	TTTCATTCTGA	CGCCGAAGCT	TGACATAATT	AATCGCACGG	TGCTGGTGGC	360
	CTACGTGCC	CTGGCGCTTC	AGTGCTTTTC	TCGGCAGCTG	ACGAGCTAAG	TCACTCGGGC	420
	AGGAGTGCTC	CGTTCAGCTC	GTGTGCTATG	CGTGCGGCTG	ATTGCTCAGC	GGCATGAACA	480
	TCTGTTATCT	CTAAATAGCG	TTCTCTAGCT	TGCTTAATCC	TGGTTACCAC	ACTGTGAGAC	540
	GGTATATCTG	CCTGCAAGGG	ATCCAGCTCT	GCGAAGGCTG	CAGCGGTCTG	CGCGTGCATA	600
	CGCAGCATA	GCTCGCTCCA	GGGGATGGAT	ATCCAGCAGC	TCGCGCACAC	TTCCCGCCCC	660
40	TGCTGTTCCC	CCAGCTCGTT	TGTGCCGCGC	TCGCGCCATC	TGAGAAGCGC	ACGTCGTGCA	720
	CTTCGAGGGC	ACGCTC					

1444UP

	GATCCAAATA	CATCCGGTAT	ATATGCTACT	TGTGCCAGAA	GACATGAAAA	GCAAGCATCA	60
	AGGGAGCTAA	TGAGCATTCT	ACAGGAAAAAG	GCGGAAGAAT	ACTACGTTGA	TGAACTCAAA	120
	GCTATCGCAG	AGACTGAACT	CTTGAGCGAC	AAAGAAGATG	AAGAAGAACT	ATCTGTGGAA	180
	GAGCAGGTGC	AGAAAGAGCT	AGAGCAATTG	AAGAAAGGCA	GTGGTCTCTG	GGATACCAAA	240
	AAGAAACCGG	TCCTGCAAGA	GATTCAGTTG	GGATGTGAAT	GTATGGTCTT	CATCAAGACT	300
	AGAAGACCAA	TCAAGCCGGA	ATGCTTTGTC	AAACGCCTAG	TACAGGAACT	TGCATCGTCA	360
50	GAAATACTA	CCAAGGTTTC	GCGGTACGTC	CAGAGATGTA	CACCCATCAC	TGATTCTCTG	420
	AATGCTAGTC	TAAACAGAAAT	GGAAAACTC	TGCAGAAAGG	TGCTTGCTCC	TCATTTCCAT	480
	ACTGACAAAG	AGATAAAGTA	CAAGTTCGCG	GTCGAGGTGG	TAAAACGTAA	CTTCAACACG	540
	ATAGACAAAA	TGGATATCAT	TAAACTTGTC	GCGAAGGAGG	TCGGTAAGAG	TGGGGATTGG	600
	GGGCACTCTG	TGGACCTAAA	GGACTACGAC	AAGCTGGTCA	TCGTGCAAGT	CTATAAGAAC	660
	3172700000	7070707070	0000000000	7070707070	7070707070	7070707070	

1445RP

	GATCATCTTC	CGAACATACT	CGAGGGAGTT	CGCGTTCGGG	AAGTTCCTGT	ATCGTTGCAT	60
	GTAGTGGAAT	TGCTCGTAAT	CGTCTGTAAA	TAGAAAATMG	GCGTCAATCA	TGTTGTCCCC	120
5	GTGGACGCG	CCGGAAATGA	ACATGAACGG	TGGCAGCCCC	TAGCGCACCT	TCTGGCCCCG	180
	GCACGCGCG	AGAATCGCAT	CGTTGGTGCG	CAAAATATCG	CTGTACGCGA	CCGGCATCTT	240
	CTCTCTTCG	ATGGGCTCCA	ACACCGCCAT	CTTCAACAAC	TCGCGCCCAT	AGCTCATCTC	300
	CATCTCCCG	GAGAGGAGAT	TGTAGTGCGC	CTGCGGGGGC	CGACTCGTGC	CCGACTGCTC	360
	CGAACGCGC	AACGTCGACG	TGCTATTCAA	GCTAGTGTTC	GAAAAGTGCA	CATGCTCGTC	420
	ATACGAGGAA	CAGCTGAGCG	CCATCTCGGT	CACGCTGAGA	AGGTACTGTT	CTTCCCCGCT	480
10	GTACAAAGAC	CCCGCCTTGT	ATGTCGAGCC	TCTGGTGTCAT	TCCATTGGTG	TCGCCATTGC	540
	TCTGGCGCAG	CCTGATACAC	TCGCCGTGCA	AATACTACCG	CACCACCGCA	CGAACGACCT	600
	TTCCGCCATT	CTTTTGGTTT	ATAAAACCCG	ACTACGCATA	TATTTTCATCC	TGCTCTGGCA	660
	TGTCGCCGATG	CCGTCTCCG	TGTGACATAG	CTGCTTATTC	ATCCTGGGCG	TTCATTT	

1445UP

	GATCCTTACT	GACGAGGAAG	AATCGAGCAA	TAAAGTTGAC	GCCGCTTCGA	GCTCTAATAG	60
	CGGTAAGAGC	ACCGCTAGTA	AACGTCCAGC	CAAAACTAGG	AAGCCTAAGG	CTGACACTGC	120
	GGCTACGAAA	AKCGGAACCA	CCTCCCGGAT	GCCCAAGACT	GCTGCTTTGC	AGGCGCTGCT	180
20	GAACAAGAAA	AGGGGGGCTT	CGGCAGAATA	GACTACTGGT	AAACGTAAGT	AATAGTATAA	240
	ACTTGGTTTT	TTAATCCCTG	GCTATCTCAG	ACTGCTAAAG	CATGGCCGTT	TAGGTGTGGC	300
	CTCCTCGGTA	GATGGTTTGC	ACCACGCAAG	GTGAAAAAAA	GATCACCAC	CCTGAAAAAC	360
	GTTTAACACT	TGTCAATCTC	TAAAGGCGCT	GCAATCAAGG	CATATTACCA	TTGTGGAGCC	420
	ATGAATCTTG	CCAATGAACC	GAAGTTCCAA	ATACAAGTTG	ATGAAACAGA	GGATACAGAG	480
	TGGAACGATA	TTTTGAGGCA	GCATGGTGTC	ATCCCAGAAC	GGCCACCTTC	ACCGACCGCA	540
	CAGCTCGAGG	AAGCGCTCGA	GGAAAGTGCTA	CNGAGACCAC	ACGAGAATAG	ATTAGAGAAC	600
25	AAAGACTCTC	TGAAGTGGAG	GACTGGAAGA	TGAAGAAGAT	GATGAATTTT	TGGAGTTTTA	660
	CCAACGTAAG	AGAATGGCAG	AAATGCAGAA	GCAACAAAGA	AGCGCAAGTA	TGGGGAC	

1446RP

	GATCTGCAGG	CTGCTACGGA	GGAACTCGTT	TCCGAGGTTG	CTCGCCTGAG	TAAAGACCCA	60
	AACTTTCCTA	GCATTTTCGC	GCAGGAGCTA	CAGAAGCTTA	CTGGTGAGCC	CCATATAGGC	120
	GGCAAGGTGG	ATGATATAAC	GGTAGTGATG	GTGAAGGTAG	ACTAGTAGAT	TGCACATATG	180
	TAGAATTACT	AATATCATTC	GAATTTCTGG	CTTAAGACAA	TGTTCTTAAT	CCGCTCTCTC	240
	TCGCTCTTCA	ATCTCTGCTC	GCCTTCTAGT	ACGTCATGAA	CAAACTTGAC	GTCGGTCGGC	300
35	AGGCATATCG	GGCGGAGTTG	AGTCCGCTTT	CCTGATTGTC	TGAGAAACGT	AAAGGGCACC	360
	TTACCCGCTT	CGACTTTTGA	TGACAGATTG	CTGTTGACCT	GTGTGCTGGT	CCCAGATCCA	420
	ACGATAGGAA	TGTTGTTTCAT	GGGGATTTTC	TCATTCTTGC	GGGATTCTAA	AGATTGTTGC	480
	ATCACAGCTT	GGTACATCTT	TTCCATTTCA	TCTTCTGCTC	TCCGCTCCTC	CTCCGACTTT	540
	AGCTTTCTTT	CGTATTCTTC	GTTTATCTTT	TTGCGCTCTA	GATCTCTGTC	AATAGTAAAC	600
	ACGTCGTGTG	CGTCGTCAGT	ATCTTCTTCA	CTTTCACCTG	TTGACGGGGA	ATCACTATCG	660
40	TCGTCATCCT	CATCGTTATC	TTCTCTGTAT	AAGTGCTATT	AACGTCCTCT	TCTTCTACCT	720
	CGCTGGAGTC	GGCACTGTCT	CCACTACTAG	ACTCGTAGCC	ACTATCTTTC	TCCTC	

1446UP

	GATCAATTAC	ACTACTAGCA	ATCTACTTTT	CAACAATCTG	ACTGTCCGCG	AGGTAAACT	60
	CTACCGTGAA	CAGCTGATGG	TACTCAAAGA	GCAGAGGTTT	ATAGTGGAGG	GCATGCTCGA	120
	GAACGCCAAG	AAACAGCGGC	GTTTTGAAGA	GGTTAATACG	TTAAAGGAAA	ATACCAAAGA	180
	GCTAGACAAT	CAGATAGCCC	AGCTCGAAGA	AACCCTAGGC	GACCAGGGTT	TTGTTTAGTA	240
	TCTAGCATGG	AGTTTTTTGC	TTAACTATAA	TTACTGTGTA	GATGCCGCGC	ATAGCATGTC	300
	GTAGCATAAT	TGCGAATTTT	CACCAACATG	AAAAAGTGTA	TGTGTATAAG	GCATCCAGTG	360
	AACTCCTAAC	ATGCTGATGA	GGTTTTAAGT	AAAGATATCA	CTAGCAATGA	ACGTAAGTGC	420
50	AGTTTTTTGAG	CTTTATGTCC	TCTGTAGAAC	ATAATATTAA	CGACAGGGGG	ATAGGATGAA	480
	AGAAGACAGC	AGTTATTGGA	GCTGAACAGT	GAAGCCTGGT	CTGGAATTGA	TGCGTTCCCG	540
	AATAAAACCA	GCAAGCTTGA	CTCAAGCATC	AAGAGAAACA	CAGGGTTTAT	CAAAAAGCTG	600
	AAACAGGGTA	TCACGAAAGA	CTCGAAAGAT	C			

1447RP

	GATCCAGGAT	GATGAATTTG	ACGAGGAGGG	GGGTGCAGAA	GAGAATGACG	ACTACTCACG	60
5	GTTTAAAGA	TCCTGCATGT	CCTCCACGT	CCCCGCGTTG	TAGTAGGCAT	AGCGCTCGTG	120
	GTACGCGCCG	TGCGCCATGG	CCGGCGCCAT	GGGCGCGGGC	CCATGCGCCC	ACCCCGTGCG	180
	GTACATGTCTG	TACATCCGGC	GCCGCGACGC	GTCCGAAAGC	AGCGCGTAGG	CCTCGTTAAC	240
	CAGCTTGAAG	CGCCGCAGGC	GTTCGTGCTC	ACCCAGCCCC	TGTTGGGCAG	CCCCGCGCGT	300
	GTCCGGGTGG	TACAGCTTCG	CGAGCTCGTG	GTACCGCTTC	TTTAGCTGCC	GTGCATCGAC	360
	GCCGGTCTTC	ACCAGTCCCA	GTACCTCGTA	GGGCGTCCGC	TGCTTGCCCT	GGGGCCACGA	420
	TAGCCCCCCC	TGCCACCCGG	CGACGGTGCT	AGCGCACCGC	ACCGTACTCC	GACCTGACGC	480
10	TGTAAGCGAG	ACCGCCAACG	TGCGCCAGTC	CTGAGCAGTG	CAGTCGGACG	CGACAACATA	540
	ACACTTAAGC	TCCTAGTTAA	CGCTTTGGCG	ATGGAGATCT	TGTCGGTGCA	TGCACATATC	600
	CAGGACGCCG	CTCCGCCTCC	GCTCGACTGC	TGGCCGTCCA	GGCTCCAGTT	GCGCGCTTGA	660
	GCCATATCGG	CGAAAAATA	AAGTCCTGCT	CGAGGCGCGA	TGA		

1447UP

	GATCCAGCAG	ACGCTCCGGC	TGGCTGTTGG	AGATGCACTG	GCTCTTCGCG	GCCGAGTGGC	60
	GGCAACGCGC	CCGCGCGGCG	AGACGCGCCC	GCCGCGCGCG	CGTGCGGGTA	CATCCGCACC	120
	AGGTTCTGCA	GCTCAAACCT	CAAGGCCAGC	TTGTTTCTGT	TCTTCTTGCG	CTTCGGCTTG	180
20	TACTTGTAGC	CCGGGTACTT	CTTCGCGTGC	TCCTGCTKCT	CCAGTTCCGC	CTTGTCGTGC	240
	CACTCCTTCT	TCTCCTCCGC	CGTCAGTTTT	TTCCACTGGT	AGCTGATGAT	CTTGCTCACC	300
	TCGCAGTTGT	GCGGGATGTC	CTGGCCGGAC	TGCTTCCAGT	AGTCTGTCTG	CAGCTTCTGC	360
	TGGTGCAGCC	GGAAACAGAT	GAACGCGTTG	CGCGGCCGCG	GGATGTGCTG	CTTCTGCTTG	420
	TAACCAAGCG	CCCCGCGCG	GCCTCGCGCG	CCTCGCCGTC	CTCGTCCGCC	ATCCTGGTGC	480
	GCTGCCACTC	CTCGCCGCCG	GGGGGCTGGT	GCGAGAAAAA	CTTCTGTGCC	AGAGGCGCTG	540
25	CCGCGCTGCC	GCTGGCTCGC	CGGCTCGTCC	GCCGCGGCTG	CGCGTTGCCCT	GCGTTGGTCA	600
	AAGGCAACAA	TTGCCCGGAT	CTCCCGCCGC	TGCTGGCGCT	GGTGTACGAT	CCGTGTGATG	660
	GTCAGCTTCT	GCTCCAATCA	CAGA				

1448RP

	GATCCGCTAC	GTATACAACG	ACATATTGCT	ACGTATCGAA	TGTGATGTGA	CAACATGCAA	60
	GATTCTCAAC	AACAAGCGCA	AGTGGTTTAG	TGGTAAATC	CATCGTTGCC	ATCGATGGGC	120
	CCCCGGTTCG	ATTCCGGGCT	TGCGCATATT	TTTCACAACA	TGCACACACT	GTGTGGCTAT	180
	CGAGACGGAG	TCCACTACGA	GCATCGTCAT	TTTTGTCTAT	AATTTACAAG	CATATTGTAA	240
	CTATPTGTCT	ATTGATCTAA	ATGTCGAGTC	GATAGAATCC	TTTCACTCCT	TGTAGCTAAT	300
35	GATAATGACG	TTCATCTCGT	CCGGTGTAC	CAAGATTATC	TTTTTCAGATA	CGCCGGTGTG	360
	GAGTTTGTTC	AGGCACCGGA	GTACGTGGGT	GAGGTCCATC	ACGGATTTCG	CGTTCTCGTC	420
	CACCTGGTGG	AACACGTAAT	CGTAGAACAG	AATGATGGGG	AACTTGTCCC	CCGCCTCAGA	480
	CCAGTGGATG	TCCATGCTGG	ATTCCATCCT	ACCAAAGATG	AAATTTAGCT	TGCACATGAG	540
	CCTGAAGAGC	CTGCCATTCT	CTAACTCCCG	CGACAAGTGC	TGCTCGATGT	TCTCCGAGTA	600
	GGTCTGCGAC	GAACTGATTA	TGTCTAACAT	CTTGTGGCTG	AACAGGGCGG	TGAACTCCCG	660
40	AATCGTCTTC	TTCTCGTCCG	ACAAAAGGTA	CGCCAGCACC	CGCTTGAACA	GCGGGTGC	

1448UP

	GATCTCGCCA	GCGCTGGCAT	CCGCAGCGCC	GCAGGCGCCG	CGCGCGCGCG	CGCGGCCGCG	60
45	GCCACTGCGC	CACAATGCTG	TCCCATAGCC	CTCAACATCC	CAACTAGCTA	GTCACCTTGT	120
	GCAATCGGTC	TACCGATGGT	GTGTGCGGCG	GGGACAAAGC	CGTGGTGAAA	CGGACACTTT	180
	TCAAAATGGG	CTGATCTGCA	GCAGTACACG	ACCGATGAGC	TGCGCGCACG	GCGACAGCAG	240
	TCGCGGTTCC	GCGCCTGGCT	GCGCATAGGG	AACTTACGTA	TAGTATAGAA	GGGCCGTCTA	300
	CTTGGCGTAG	GCAGCGAGGA	TGTCGTCTGT	TGAGCGGAGG	TATTTGCCGT	TCGCGCAGTC	360
	CGGGATGCCT	CTCAGCGCCA	GGTTGGCGAA	GATGGTGGCC	GGGATCTGCG	GGTCCAGCAG	420
50	CTCGCTGTTC	TTCTTGAGCT	CCGTGAAGCG	GCGCAGTGCC	TCCGGCGCCA	TGCGATGGCC	480
	GAACTTGTCTG	CGGATGTCTG	TCTGCATCTG	CGTGTGAGCC	ACGCCCCGCG	CCACGGCGAC	540
	CGCGCGCACC	GCAGGCTCTT	CCGCGGCCAG	CGTCATCGCA	AAGTGGTTCA	GCGCGGGCTT	600
	CGACGAGCCG	TACGCGCCCC	ACGCGGACTG	TCTCCGAGTT	AGTAGCTGCC	CCTGCCCTGC	660
	CTGCGTCTGT	ACATACATAT	GCTTCTGTGC	TGCGCCCCGA	GCTCACGAAC	ACCACACTGC	720

1449RP

	GATCCAAAGA	CCGCGTGCTC	GCACTTCCAC	ATGTCTCCAA	GCTGGACGCG	AACAACGATA	60
	TCTTACTGGC	GGTGAAAGAA	AGCCCGAATC	ACAAATGCCC	ACGATGCTGG	AAGCACGCAT	120
5	CTCCCGAGGC	CGACGCTCTA	TGTAATCGCT	GCGCCAGAGT	CCTCCAGTAA	GCCAAACCTG	180
	AAATTTTCAA	AAATTGAAAA	CTTCACCATG	GCTCACATGC	TGACTGCTTT	AATATCCTGT	240
	AAATACAACC	GGACTCTGCA	GGTCGATGCT	CCCTCACCTG	GGCCCCAAC	TCTCCCTTGT	300
	ACCGGGTCGC	GGCGTCGCTG	CCTCATTCCG	CCTGCATCTC	GCTTCCAGAG	GCGGCGCTTC	360
	TGGGGTGCGC	GCGCGCCTGC	CGGCATTACAT	CGCGCGCGCC	TACGGCAGCC	CACCGGGCGA	420
	CGCGAGGCAG	ACCCGCGCGT	GGACGTACCT	CGCGCGCTCG	CGGCTCTTCC	AGCGCCTTTA	480
10	CGCGCGCCCT	TCGTTCGCCG	CGTACATCGA	CCGTCTGCTG	GCCAAACGGGC	CGGTGCCAAC	540
	ACTCGCCGCC	TTCTTGTGTC	TCCATGAGGC	CACCGCCATC	GCTCCTCTGG	CGCTGCTGTG	600
	GTGGGGGGTC	TACAGCTGCG	ACGTGGTGGC	GCTGTTGCCG	CAGGGCCTGC	TTGACTACCT	660
	GGCCGAAGCA	CGCATCTGCG	CGTCRAGAGG	TTCTGTGG			

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1449UP

	GATCGGCTCA	ATGGGTTGCT	GAAGCCGTGT	CTTTCGTAAG	ATGACCTCAA	CTTAAAGGCA	60
	GGCTCTCGAT	ATCTCGTTTC	TTTTTTTAAAC	AGGTGAGCTT	TGGAAAATTT	TTGGTTCTCA	120
	GCTCATCTCA	TCTACAATAG	TATGTCTAGC	ACGCCAGCAA	AGCTTGCGTA	ACCGCTCTAT	180
20	TCAATATGAG	TAAGCAGGTA	AATGATACTA	GCAAGAATGG	TCTTGACCTA	AAGACGCTGT	240
	TTGTCCGGAA	TATTCGGTTT	GATGCTACGG	ATGCAGAGCT	GACAGACTTC	TTCTCGCAGT	300
	TTGCACCTAT	TAAGCATGCT	GTGATCGTAA	AAGATAATGC	GGGCTCGAGC	AGAGGGTTTG	360
	GGTTTGTGTC	GTTTGTGCTG	GAAAGTGATA	CACAGGCTGC	ATTGGACAAG	GGACGGAAAA	420
	CACAGTTCAA	GGGCCGTCTT	CTGAGGGTGG	ATGTTGCCAA	AAGAAGAGAA	CGTTTCGAAAA	480
	AAGGCGATGA	GGCCGAGGCA	CAGACCTCCG	CGGAGGACGC	GGAGAAGCCG	ACTACTGCTC	540
	CCGAGGGTGA	CGAGGCGCTC	ATGCGGGGCA	AGCCCAAGCT	GATCATTAGG	AACATGCCGT	600
25	GGTCTTGCCG	CGACCCGACC	AAGCTGAAAA	AGATCTTCGG	TAAGTTCGGA	GTGGTTGCGG	660
	AGGCTCCATC	CCGCGCAAAG	CGGATGAAAA	GCTGTGTGGG	TTGCATTTGT	CACGA	

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1450RP

	GATCAATTCT	GTCTTGAAGT	AGGTATTAAT	CAATGGGTCA	GGCTGGGTGG	AATTGCTTAC	60
	AAAAATACCA	ACCCAATCAT	CTTGTAAGTT	GGTGAGCGAT	ACGTAGACAA	TTTGCCTCAC	120
	ATCAATCTTA	TAATCGACAG	CATAGGTGAG	TGATTATTA	ACCAGTGCT	TTCCGATAAT	180
	GTAGAAATGG	GATGGCGTAA	GTATAAAGGT	TTTGGGTAGC	CTTTGGGCCG	ACCTACCAAA	240
	TTTTGAATGT	AGCGCTTGCC	CATTGATAGA	GAATACGACA	TGATCATTAA	TTCCAGCTTT	300
35	CCTTTTGACA	AACGCACCCT	TCGATTTCAG	CTCATTACAA	GAAAGGTAGT	CTCCCAGGAA	360
	TGCCCTGTAA	CCTAACAAAG	ACATTGCACG	CCTCTCCTTT	CTGCCACCCA	ACAACTTGTT	420
	ACCGTAATCC	CGGAGTTGTT	CGAATTGGTT	CCCATGTTTC	ATCTCACGGA	TAGCACGCTG	480
	GATACGAATC	GCAGAATCGA	TACGCCGTTG	TAAAAACCGC	CGCCAGGCTC	TCTGAATGCG	540
	AGATGCCATA	TTATGCCAAT	ACTTATCCCT	CATGTTTTTC	AAAGCAAACA	AGGTCTCAGG	600
	TGTTTTAATA	AATACCTTCG	TTACACCCAA	CTGATATTCA	GTACACAGGA	TTGAAGTATC	660
40	TCTCAAAATT	AAATTGACAG	CATCTAAGGT	ATTACCTTGC	CATGT		

1450UP

	GATCGCAAGT	TGGAAGAGCG	AGTATCCATA	TGATTACTCG	CGCGAGACGC	CCGGCTCGCG	60
45	CATCAAGCCT	CAGACAGTTA	TCACTCGGCT	CTCCGAAATC	GCAAACGCCA	CCGGAAGGGA	120
	GGTCATCGTG	ACGACCGGTG	TAGGTCAGCA	CCAAATGTGG	GCCGCCAGC	ATTGGACGTG	180
	GAAGAAACCA	CGCACATTTA	TCACATCAGG	CGGCCTCGGT	ACCATGGGCT	TTGGTCTACC	240
	GGCGCCATT	GGTGCCCAGG	TAGCCAAACC	CGATGCGATT	GTCAATCGACA	TCGATGGCGA	300
	CGCCTCGCTC	AACATGACCT	TGATGGAGAT	GTCCAGCGCG	GTGCAGGCGG	GCGCCCCAGT	360
	AAAGATATTG	TTGTTGAACA	ACGAAGAGCA	GGGAATGGTC	ACTCAATGGC	AGTCTCTATT	420
50	CTACGAGCAT	CGTTATTCTC	ACACCCATCA	GCTAAATCCG	GACTTCGTCA	AGTTGGCTGA	480
	TGCAATGGGG	TTCAAAGCAA	TGCGCCTAGA	GGCGCAGTCG	GACATGGAGC	CCATGCTGCA	540
	GGAGTTTATT	AATTGCAAGG	AGCCCGTGTT	ACTCGAAGTG	GCCGTCGAGA	AGAAGGTTCC	600
	CGTCTCTCCG	ATGGTCCCTG	CCGGTAAGGC	CTGCATGAGT	TTATCTACTT	CGACCCAGAG	660
	GTACGCGACA	GCAAGCGGAG	CTTCGCAGCA	GGCGTACGG			

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1452RP

5	GATCAAATGT	GGCTCTACAA	GGGCGGAAGT	GGCAGAGAAT	ATTAATGAAT	CAGTTCCGCT	60
	GACATATTTG	TATTGTACAG	GTATTCCACA	TTCTTTTGAG	TACGTATGTC	CGTCTAGGAA	120
	TGGCTGGCTT	AGTAAGGCTT	AATATTAACT	GAAAAGCGCA	GCAGTGTAAT	CCATCTAGTA	180
	ACTAACACAT	ATCCATTAGC	ACATGTTTCG	TTCACTACTA	CGTCATTCCT	ACGCCGTCCC	240
	TACTGTGAAT	TACACATGGT	CCTCGAGAAG	CCTCATAAGA	TTCTTCACTA	GCGATGAGAA	300
	GGCAGCTCCT	CCATCGCTTC	CGAGAGAAGA	GCAGAAAAGAG	TTCGAACGGC	TTTCAGAAGAT	360
	TGCACAGTCA	CAAGCTGCCA	TCGACGAGTA	CAACAGACAG	TTTCGAGAATG	ACCATACGAA	420
10	GGAGTCAGCG	AACTCTCCCA	TCCTCAAGAC	AGAAATAGGC	TCGTTCCTCAC	CGGAATTCAG	480
	CAAGACGTTG	CCAGAGTTTCG	AGGGCGACAA	GAATCCCGAG	ACAGGGGAGA	TTGGCGGGCC	540
	GCGCCAAGAC	CCACTGCGGT	ACGGGGACTA	CTCATACAAC	GGCCGCGTGA	CGGACTTCTG	600
	AGGTATAACT	TGTGTTTATA	TGTTTGCAGG	TTGGTTAAAT	ACATAGCTTG	CGCTCCAAC	660
	CTCTCGCAGC	TGCAGACAGG	TTGTCGGTGC	ACTCCGTGAT	GAATTTTCGAG	TCCAGCTTT	

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1452UP

	GATCACCAAC	TCTACAGCAA	GAAATCCTAC	CCCCAGCAAA	AGCTGTCCTC	GATGTTCTTC	60
	TATTCTGTAA	ACAGTTTGTT	ACTTCTGGTC	GCTTGATATCT	GCATGCGCTA	TCATCTTTTC	120
20	ATCTGGAGCG	TTTTTCAGCCC	GAAGTTGTGC	TACCTTCTGG	GCTGGAACAT	CCTCATCCAC	180
	TTTCTCACTG	AGACGGTGCT	TGAACCTTTC	TTGCTCATGG	TGGCGGGCTG	ACTGTCTCTA	240
	GTTCCACTTG	TATAATATTC	CTTCATCAGT	GAGAATCTCA	TAGTATTGTC	ATATATTAGA	300
	TATTATCTAG	GTCATGTTTT	AGAGAATAGG	TCTCTTCCGA	AAAAATTGGC	TACCACTGCC	360
	AATCATTACA	TGTCAGAACC	GACCATCTCC	AAGTGTCGAA	CCGTCCCCAC	TGCAAAATGCT	420
	CTCACTTAGA	TCCAGCTTCA	GACGCTTATT	TTCTGTTTCC	TGCAGGGTTT	ATGACCAGCA	480
25	GGCGCAGAAG	GCCGTGTCTT	CCTGCCCCGC	TGGCACACCG	CTGAATCTGC	TTATAAAGAA	540
	GGGCGGGAAG	GAGCCGTTGG	CTCTCGAAGA	TCCGACTACC	CGAGTGOTTA	TGGAAGGTGC	600
	TTGACCTGAG	GCGCAAGCCG	CAAAGCTGGC	AGAGGACCCA	TTAAAGCGCG	GAAGAAGGCT	660
	CTGCGGCGGA	TGAACAGAGA	ACACATCCAG	CAGCAGAACT	TCCTGGCGAA	GATGTGAA	

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1453RP

	GATCTTAATT	TAAAATTTTA	ATTAACATTT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAATAAAAT	TAGTAAAATA	120
5	AATAGAAAAC	CATAAGTTAA	TTGATTCATA	AAGAAAAATG	GAATTATTTG	TGGCATCTTA	180
	ATTTTATTA	TTTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATAAA	240
	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAATTTAA	TTTTAATATT	300
	AAATATACCA	TTTTTATTAA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
	ATTTAATTTA	TATAAATTAT	TTAATTTACT	TCATTGATAT	ATATAATTAT	TAAATGTACC	420
	TTTCATAATA	TTTATTTTTA	TTAGTCTAGT	AATATTTCTA	TTTAATAGTC	TACCCCTTAA	480
10	TTGGATATTA	CTACCTACTA	AATATTTACC	TAATAATATA	TTATTAAGAA	TACTTAAATC	540
	TAATAATTTA	TTATCTAAAG	TATATAAATT	AATTAAATCT	TTTTTATTAT	TATTTAAATT	600
	ATTATTAATT	AGTAAATTAT	ATTTATTTAT	TTTATTAACA	TAATTTTTTG	ATAATAATAT	660
	ATCATAATTA	AATGGTAATT	TATTAATAAT	TATCTTTAAT	GAATTTAATG	ATAAACCATT	720
	ATTA						

1453UP

	GATCAAAATT	TCAACAATTT	CCATTTTCATT	TAGTACTACC	ATCACCATGG	ACCAATTGTT	60
	ACATCATTTA	GTTTATTAGG	TTTACTATTA	ACTTTAGCTT	TTACTATACA	TGGTATTATT	120
	GGTAATATTT	ATCCTTTTAT	ATTATCTTTA	TTAGTAGTTT	TATTACTAAT	AACCTTTATGA	180
20	TTTAGAGATA	TTGTAAGTGA	ACTTACTTAT	TTAGGTGATC	ATACTTTAGC	TGTAAGAAAA	240
	GGTATTAACT	TAGGTTTCCT	ATTATTTGTT	GTATCTGAAG	TATTAATTTT	TGCTTCTTTA	300
	TTTTGAGCTT	ACTTCCATTC	AGCTATAAGT	CCTGATATTC	TATTAGGTAA	TGTTTGACCA	360
	CCAGTAGGTA	TTGAAGCAGT	TCAACCAACA	GAATTACCAT	TATTAAATAC	TATTATTTTA	420
	TTAGCATCAG	GTCTAAGTGA	TACATATAGT	CATCATGGTT	TAATTGAAGG	TAATAGAAAA	480
	CATGCTTTAT	CAGGTTTACT	TATTACTTTC	TGATTAATTG	TTACATTTGT	ATTATGTCAA	540
25	TATATTGAAT	ATAGTAATAC	ATCATTTACA	ATTACAGATG	GTATTTATGG	TTCAGTATTT	600
	TTTGCTGGTA	CTGGTTTACA	TTTCTTACAT	ATGGTTATGT	TACTAATTAT	GTAGGTATT	660
	AATTATTGAA	GAATAAGAAA	TTATCATTTA	ACATCAACAC	TCATGTAGGA	TATGAGACTA	720
	CTACTATTTA	TT					

1454RP

	GATCATGCCT	CACCGGCGTG	GAACATGCAG	GTGAGGCGTA	TGTACCCCAT	GTTGCCTTAT	60
	TTTTTACCT	GAAGCGGATT	GGCTCTTGTT	TATACAGACT	TTTCTGCATC	CCTTGGGGCC	120
	CAGAGCTAGG	GCCTAGAATC	CGTGTCGTAA	CGGTTGGGCA	CTGATTCAAC	ACGAGCACA	180
	TTCCAGTGCT	GCTCGTAGAA	ACGAGGCCCC	TGAAGTATAT	GGTGATATCC	ACATTGCCGG	240
35	AGTATAGTTC	TCTGTGGGGG	CGACTTCATG	CCATGTGCAT	CTCCGGCTTA	CTCCACAGCC	300
	GCACACGCTG	CATTGTTTTG	GGAACATCAT	GTGAAATACT	GGTATAGAGC	GCATTTTCATA	360
	GGGGTGCCAG	AGCTGTAAAT	AGGGCGGCAT	ACCCCGCTCT	ATTTTCATGTG	TTCATGTGCT	420
	AGTTTAGAGG	TATTTTTGAG	GTGCATGGGT	TATGGCTTAC	TTTGCATATG	GAGATCTCAT	480
	TCGCTCGTAA	CGTATATAAC	TGAGGTAGCC	GTAAACTTGC	ACTGGTTCCC	ATTGCCAGAG	540
	CGAAGCTACA	ATAGCACCAT	CTGGCTGCAA	GTGTGAACA	ATGCATTGGA	ATCGCATACT	600
40	CTTTTGGGGC	TGTGCGCTTT	TGCTGCAACA	ATTAACAAAT	GCCTTTGATG	AAGGAGTGCT	660
	AAGGAAATGT	TATGAATCTG	GTGTATGCCA	CCGGAACAGG	CATTACGGAG	AGAA	

1454UP

45	GATCAAGCGC	TGTATGGTTC	CCGGAGCGCC	AGTAACAGCG	GTCCTGTACG	ATTTCAACGA	60
	TTCCAACATG	GACGATGATG	GCTCCAAAGT	TATGTTCCCG	ACCACGCTTG	AACTCAAAAA	120
	GGTTTTTCAG	GCTATTCGTT	TTGAGGCCAT	CAAACGGGGG	CTGCAAGTGT	TTCCCATTAG	180
	GAATATTGCT	CCTATCTTCC	GACAGGTCGG	ATTCAAGAAC	GTAAAAATATA	CCGTTCTGAC	240
	ATTCAAGCGC	GGCGATTTTC	TGAATGAAAT	GGGGTTCGTG	AACGAGCTAC	TTGCAACGTT	300
	TCACTACGAT	TTTCTAGTGC	GAACCTTTTT	AACTGATCGT	AGTAAGTATC	CAGTTGGAAC	360
50	TGACCCACAG	ACACTGCCGA	GGAGGTACAT	TGATGAGCAC	ATGGGCCAAA	TAGATGACAA	420
	TGCAGGATGC	TTGCGTCTTA	TTGCAATCAC	GGCGGAAAAA	CCAGAGTAGG	TTTCCACCGT	480
	TGCTATTGCT	ACCCGGGGCA	ATTCTCCCGG	TCATTATATA	TGTTAGCAGG	TGTCAATACC	540
	TCCTTACAAC	CTAATATTTT	AAAACCTAAT	ATCTTCTGCT	CCTTAGAAAG	AGCCACTTCC	600
	TTATATCTTA	ATAGTTACCG	CTAGTTCTAT	CTAATAATTT	TATAATTTTG	ATAAATCTTG	660
55	ACGTACATCT	TATCACTAAG	GAAGATCTCA	TCACAACTC	CGCAAAGTGT	TTCATATATA	720

1455RP

5	GATCTCTTCG	ACATAGTGTC	TTAATAGGCC	TGCTGAGGAC	TTCAC TGAGA	AAGCTTCAAT	60
	AGCGGGCAAT	GGCCCATCTC	ATCAACACTT	AAAATTTTTC	GTGGCAAAAG	AAACAACACT	120
	GGAATCACGT	GACCACACAA	AACTCACGAT	TTACTGTTGA	AGGGGAGCAG	GCTACGACGA	180
	CTCTTCTTCG	CATGGTAACT	CGCTGCTGTC	CACTTGCCGC	TTGCGAGCCT	TCTTTGCTGA	240
	CGCTCGCTCT	TTCTCCTCTT	CTAACAGCCT	CTCCCGTTA	GCTGTGATGT	AGTGGATGAA	300
	GAAGTCGCCA	TCCTTGCTGC	GTTTCGCATC	ACGCAGGAGC	GTCTCGACAT	CGTCGTATAT	360
	ATCAATGCGT	CGCTTTCGCA	GTTGGTTTAG	CAGCTTGTTA	TCACGCCCTG	CACATTGCAA	420
10	CTTCGCGATG	GCTTTGGTCG	ACTTGAACGA	CACCTCGCCC	GGTTTCATAT	ATCCAGATTT	480
	GCGCAGGTTG	TGCCAGGGCG	TGCTCACAAT	GCTACATTGT	GCCTGCTTGT	TCCCTTGTTAC	540
	AGACTCTGAC	TTGCACAAC	GCAGGCAGGC	ATGCAGCACA	TCCCGCGGCA	CGTCGCTGGA	600
	GCTCTGCTGC	TTTGATGTA	ACTTGAGATA	GACATGTGCG	CTGGCATACT	TGCTACGTT	660
	GGAACCAGAA	GTAGTTTAAT	CCCGGTACCC	GTGCTTGAAC	AAAAGGTCGT	TC	

1455UP

	GATCCCATCA	CATGAAATGT	CTAGAACTCC	CTGCATGACG	CGAATGAGGC	CAAGAATGTC	60
	TGGTGGGCTT	GGCTAACCGA	TGTTTCGCAAC	TGCAACAAGG	GGTACCTGGT	GTTTATAGCC	120
20	GTATGTCGTC	ATCCGGGATT	CGTGCAACAG	GAGAGAAGAA	CGGGACCACA	AGGAAACGCG	180
	GTAAGCATC	TAGAATCAGC	AACCTAGAG	AACGTTTGT	CGTCGTTGGC	GCAAGAGCAC	240
	GGAGCGTAGG	GGCTGGGAGT	TGCGGTGGCT	ATTTCATGCGT	GGGCACGCCG	GGTATATAAG	300
	TAGGGTATGC	TCCGTTGAA	CAGAATGGAT	CCGTCTCAGA	ACAATACCAA	AATCGCATTT	360
	GGAAAAACAA	CCACTAATAT	GAAGTACACC	TCCGCTATT	TACTCGCTCA	AGTCGCTTTT	420
	GTTGCAGCAC	AGTCATCCTC	GGGGTCTGTT	ACCGGCAGCG	CTGCCCCCGC	TCCGGGTGCG	480
	GGGTCCGGCG	CAAGCATTT	TAGCACCACG	ACAGTCACCG	CCTCAGGTT	TGGACCAGGC	540
25	GCGACGTCCG	GTGCTAGCTC	CGGTGCAGCA	GGCGGGGCG	CTGGCGGGG	CGCAGGTGGC	600
	GCCGCATGTG	GCGCCGAGG	TGGCGCCGCC	GGTTCTAACT	CCGGCAACTC	TGGCTCCAAT	660
	GGATCTGGCT	CCCGGCCAGA	ACACTCTGGA	ACAGAACACT	CCGGCCGAGA	ACACTCTGGA	720

1456RP

	GATCCACGCC	GCGCTGCTGA	CCAACGTCGT	CATCATCGGC	GGGACCTCCC	TGCTCCAGGG	60
	CCTGGAGCAG	CGCTCGTGA	ACGACCTCAG	CCTGCAGTTC	CCGCAGTACA	AGCTCTCTAC	120
35	CTACGCCACG	CCCGCCACG	TCGACCGCCA	GCTGCAGAGC	TGGCAGGGCG	GCGTCAACAT	180
	GTGCCACCTC	CCGACTGGA	AGCTCGGCTC	CTGGGTCAAC	AAGCAGGAGT	ACCTGGAGTC	240
	CCTCGACAAG	TAGCTGTGTA	GTATGTAACC	GTATGCCGCG	ACCCTGCGGT	TTCTTTCCCG	300
	CTCCCCCACC	CCCATGACGC	CCCCCGCCCG	CTTCGCCGCG	TCCCACGCGC	TGGCGCCCGC	360
	CGCGCCCGCC	CGCGACACCG	TCGAGCTCTA	CCTGGACTAC	TGCTGCCCTT	TCTCGCGCCG	420
	CCTCTTCCTC	GCCTGGCAGC	ACGCCCTTTT	CCCCCGCGCG	CGCGCCGACT	CGCGCTTCCA	480
	GATCGTCTTC	AACCACGTGA	TCCAGCCCTG	GCACCCCGCC	TCCCAGTACA	TGCACGAGGC	540
40	CGCCCTCCGC	GTCGCCCGCC	TCGACCCCGC	CGCCTTCCTG	CCCTTCTCGC	GCGAGCTCTT	600
	CCTCCACAG	GACCGCTGGT	TCGACACGCG	CACCGCCGAC	AAGTCGCGCC	ACGCCGTGTA	660
	CCGCAAGCTC	CGGACTTCGC	GCGCGACGCC	GCCGGC			

1456UP

45	GATCTGGAAT	ATTACCGGCA	CAAACCTGGC	GCTGTGCTTC	CACACCAGCC	TCCGGTACCG	60
	CTTCACGGCC	ACCAGCTCCT	GCAGCAAGCG	AATGCACACG	TATGCCAGCT	CCATGCGCTC	120
	CAGATTAGTC	AGAACC CGCA	GGTAGTTGGG	GTTTCGACACC	AGCGCCTCCA	CCAGCTCCTC	180
	GCTCTGACGC	CCCTCCTGGA	TCAGCAGCGA	GACAACGTTG	AAGCACGACA	GCAGCACGAA	240
	CTGGTCGTCC	CCGCGCTGT	CGCTCAGTGT	CGACTCGTAC	AGCTTGCGCA	CAAGCTCCGG	300
50	GCCCTCTCTG	AAGTACCGCA	GCACCTCGTG	CACGTACTTG	TCGCTCGTGA	ACAGCTCCGA	360
	CAGCAGGTTT	AGCACCGCCC	GCTTCGCATC	CAGGTTGTTT	GACGTTCGCCA	GCAGGTGCAC	420
	CAGCGCTGCG	ACGCCCTGTT	CCAGCGGCAG	ATCCAGCGCG	CCGCCGCGCG	CGTGTTCCTAA	480
	CAACGTCGAC	TCGAGCTTCT	TGGCAATCCC	CGCGTCAAAC	TCGCTCAGCT	CGGGCGAACG	540
	CACCAGCGCG	TCCCACGCCA	CATGCCTCGA	GCTGATCGTA	TTGCGGATAT	CGTTGAAGTG	600
	CGTGCTATCA	AGCAGAACTT	TTTGAACCCC	CTGAGCCACG	GGCATCGTCA	CAGCTAAGAT	660
55	CTACGCTTTC	ACGCCACCGT	ACTGCCCACT	TTGAAACCCG	TGGGACTAGT	CAATATCTGG	720

EP 0 866 129 A2

CGTGGTCTGG CGGACTCCC

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1457RP

	GATCAATATC	GGGACGAAAT	CTGTTGTATC	TACTACCGGC	ACGGCGACTG	CGCCCAGCGC	60
	ACCAGGATCT	CAGGCTTCGT	CAGCGAGTCC	GGATTTCGTCA	GCTAAACAAA	AGAAAGATTTC	120
5	ATCTCCACTA	CCTCTTGACT	TACCTCCACC	GAAGGATTTT	AGCAAAGAAA	TCGAGGAGAT	180
	TATAGAACAC	GATTTGACTA	AATTGGCCTT	TCAGAATCCT	CTTTTTAAAG	ATGAACTTCC	240
	ATATTGGTTA	CAGGCCAAGA	GGCCATTGAT	CCAACCGTAC	AGCACTATGT	CTGAAAGAAT	300
	GTTGAAACAG	CTGGAATCCT	CATTACTTAA	CTGCCCAGAT	TCGCTTGACG	CTGACACACC	360
	ACATCTCTAT	CAACACCCGC	TCCTTTTACC	GCAATCCCACC	TCCATTTTCT	TCCCTAGTGA	420
	ACCGATCAGG	TTCGTGGCTG	CTGGCTGGAA	TAACGATAAT	ACGTCCACTA	AAGATATCTA	480
10	TGGAAAAACT	TCTATGGTTC	AGATAATGAC	CAAGTTCGAT	TTGGATACCC	TGTTTTTTTAT	540
	CTTTTATCAT	TATCAGGGAA	CGTACGACCA	ATTCTTAGCT	GCCAGGGGAA	CTAATCATCC	600
	GTGGGTGGAT	ATTTAATAGA	GTCAATCGGT	GCTGGTTTTA	CAAAGAAGTT	GAAAAGCTGC	660
	CCCCTGGAAT	GGATCAAAAA	GAAGAGGT				

1457UP

	GATCGAGGAC	TTGAAGCAGT	TCCGGCAGGT	CGGGTCCAAG	ACCCCTGGGC	ACCCCTGAGTA	60
	CGAGCTTCCC	GGCGTGGAGG	TGACCACCGG	CCCTCTAGGC	CAGGGTATCT	CCAACGCCGT	120
	TGGCTTGGCG	ATCGCGCAGG	CGAACTTGGC	TGCCACTTAC	AACAAGCCGG	GTTACGAGTT	180
20	GTCCGACAA	TATACGTACG	TGTTCTTGGG	CGACGGCTGT	TTACAGGAGG	GTGTGTCTCT	240
	CGAGGCTTCC	TCCGTTGCAG	GCCATTGAAA	GTTGGGCAAT	TTGATTGCGT	TCTATGACGA	300
	CAACAAGATC	ACCATCGATG	GCCACACTGA	GGTGTCTTTC	GACGAGGATG	TCTTGAAGAG	360
	ATACGAAGCA	TACGGGTGGG	AGGTGTTGAA	CGTTGCCAAC	GGTGACGAGA	ACTAGAAGAC	420
	ATTGCCAGTG	CCTTGGAGCA	GGCCAAGAAG	AACAAGGACA	AGCCAACTTT	GATCAAGTTG	480
	ACGACCACTA	TTGGGTTTGG	CTCCTTGAAT	GCGGGCTCCC	ACACTGTGCA	CGGCGCGCCA	540
25	TTGAAGCGGA	TGATGTCAAA	CAGTTGAAGA	CGAAGTTGGG	CTTTAACCBA	GATGAGTCCCT	600
	TCATTGTGCC	TCAGGAGGTT	TATGACCTCT	ACCACAACAG	CACTATCCAG	CCAGGTGCCG	660
	AGTCCGAAAA	GGAGTGGAAC	GCTCTACTCG	AGAAGTATGC	GGGTGAGTAC	C	

1458RP

	GATCCGCAGT	AGCTGATTGT	TCGGGTGGCC	AGGCGAATAT	TGCTGGAAGC	GGTTCAGGCG	60
	CGTATATTTG	CTCTGCGGAC	CGCCAAAGTA	CCCCGCCGAGG	TTACTCTTGC	TGGTCGTACT	120
	AGAGAAGTTG	CGCACTGCCC	TAGCAAGTGC	GGTGTCTAGG	ACGGGATTTA	GCTTCGCCAG	180
	TAAATGGTGT	AAGACGTTGC	GAAATGGCAC	AGACGCCTGT	ACTGGTCGCA	CTTGCAAGTG	240
35	GATAGCGTTG	CTAAGAAAGA	AACACCGCCC	ATACGAGCGC	GTGAACGTAG	ATAAGCTCAT	300
	GGTCAGCAAT	CAACAAGCCT	AATGATGATC	TTCTTTACAA	AATGAGGTTT	TAAAGCGACG	360
	TTAAAAAGGG	ATGCCCAACG	CTATGTTTGA	CACCTATGGA	ATATCCGTAT	GAATGACTGT	420
	GTATCATTA	CGACGGTACT	TCCTTACAGG	GCAATGGCAG	GATGGTAACG	CCGAGTAATG	480
	TCCAATAATC	ATCATATATA	CTCTAGTTAT	ACGCTATGAG	GGGTCAATTT	ATGTATTGTT	540
	CGTTCGCCTA	TCGGCTATGC	TTCAAATTTC	ATGAGGTTGG	GCAGCTCGCC	ATTCTGTACCT	600
40	GCGGGTGGCA	TGTTCACTTT	CTCTAGTCTC	TTTTGTGGGC	GGTTGTCTTC	GTCTTGGTCC	660
	ATGTCAAGGT	CCAAGAGATC	ACAGAAAA				

1458UP

	GATCTGTTGC	ACCTGCTATT	TCAGGCAGAT	TTGTGCGTGC	AGCAGCGCAT	GGCCATACTA	60
45	TCTGCTTTGG	CGCTCGCTGC	GCGCGAGTTG	CGGGGGCTGG	AAGACAAATA	CGTGCTCAAA	120
	CCCGTCTTTG	ATTTCCCCAC	ACGCCGCCTG	CCCAGAAATG	ACGCACCATC	AAGAGCCCTT	180
	GAAAGCCGCG	AATCCGGTAC	AAGCTCCGAG	GGGACCATCT	CTGCACACCA	CACCGTCTGG	240
	CGGTCGCGCA	AACTTGACTC	AGCGCCAGCA	CCAGAACGTC	CGAACGCCTT	TCGGAAGCAT	300
	GCACCTGCGT	TTTTCCTTCC	GCTGGCGCAC	GCGTGGCTGA	ATGGCATCGA	CCTGGGCAC	360
50	TTTGACGCCC	TGTTCAAAAA	GCACTACCTA	AGCACCCCTG	GCCTTATTCT	TGCAGCCGCC	420
	AACCCGCATG	CAGAAATTGA	CCGGATGTCC	GAACCTCATGA	GCTACGTTTT	GCAGGACGCT	480
	GAGGCGCAGG	ATATCAGCAT	TGAGTAGCCC	GTCGCGCATG	TGTCAGCGCA	TCTGTGGACA	540
	ACTCCTGCTT	GCAAACTGTA	TCCCGACCAC	TACCATGCAT	TAGTATGAGA	TCTATAGAGC	600
	GCCAAATTGCA	CGCCTAGAGA	GATGTGAACC	TCGCAATGCA	TCTCTTGGGA	GTCTCTGTGG	660
	CCGGCAGTAT	CTGCTAGTAC	ATACTCTTTG	TAACCTCTACA	GAGATGTGAA	GTCTTGTTAC	720
55	CCGG						

1459RP

	GATCATGCTG	GGGCATATCT	GAATGCTCTT	GAACAACGGA	CTAGATTAAT	GGAGCCTTGC	60
	ACTCAGAGGC	TTGGGCAGGA	TGCAGCTTAT	GCGGGAGCGG	CTGTTGGAGC	TTTACAATAC	120
5	CAAGCAATAT	GTGGTGCTGC	CCCCAGATGA	GACAGTAAAA	CTGCAGCGAG	AGGTGACGGC	180
	GAGCCTGAAC	TCAGCAGATC	CAGGACTCAA	CGACGTTGAC	CGCATGGCCC	TAATGGAGAT	240
	GAAC'TTCTAT	TTGTTGGTGT	ACATTGGCGA	AGAAATAGAA	GCAGACGTGC	TCTACCGCAC	300
	ACTTGT'TGGA	CGTATAGGTG	AGAACTCGCC	CCGGATGCAC	CTCATGAAGG	CTACGTTACT	360
	GCAGGTTACA	GAAGGTGATC	CCGCTGCCGC	GAAGTACCTG	AAGAACCTGC	TTGAAAAGCA	420
	GCTTGAATAC	GATACAGATT	CCGTGGATTA	CCTGCAGGTG	GGCAAGAAGC	TAATTGCGCT	480
10	GGAACGGCCC	GCGTTGTCCA	CCGAGCTGTG	GATGAAAAAG	CTGCTGTCGC	CTGCTAGAGA	540
	AGTTTCCACT	GGACGCCGAA	CTATGGTGG				

1459UP

15	GATCACGTGC	CTGCGACATG	GCGACTTCAT	CCACTGGCGC	CCAGCTACGT	GGTATATGAC	60
	ATTATGGCCG	AGAGGTTAAG	GCGTGAGACT	CGAACTAAAT	TGAGGGATCT	CTTGGGCTCT	120
	GCCCCGCGCAG	GTTTCAATCC	TGCTGATGTC	GTTATTTTTT	GCTTGCGCGG	CCTACGGGGG	180
	CTGTGATTTT	GCTTGT'TGCT	ATTTAGATAA	ACGAGATAGC	TAAACTATGG	GTAGAACTCG	240
	CGGTACTTCC	CGTAGTAGTA	GGCTGTGCCG	AAGCCGCCGA	GGGCGGTGAG	CACCAGCGGG	300
	ACGGGTTTGG	CGAAACGCGA	TGGCACGCCT	CTGATGAGGC	CGGTCAACAG	CATCACGGAG	360
20	CTCGCGCCAA	GGGCGAGCTC	GAGGCCGCCC	TCTGCGTTCT	TCCGGAGCAA	GTACCCTGCT	420
	ACAGCGTAGG	TGCTACCAAA	AACGAGACCT	GCAGCCAGCG	AGGGCACAGA	CCCTTTACGC	480
	CAGTAGCCCA	TCGAGCCACC	GATGACGGTG	AGCGCGGCCA	GAGTGAAAGA	GGGATGTTCC	540
	CTTGCGGTGG	TGGTGGGTGG	TGCTGTGGGG	AA			

1460RP

	GATCCGGGTG	GAGACACGAA	AGTAGACAGA	CACGGACGGC	TGTTGGGTGG	AAGGAACTAC	60
	CTCGTGGAATA	CATTCCAGCT	GCCCCAAAAG	ACACATAATT	TCTATGTGCT	TGTCGACGAG	120
	CTGATAGAGA	TTTTGCATTT	CGAGGGGAGC	GGCTCTGACT	TTTTGCACCT	GCATAATCAG	180
30	CTGTACCCGC	TGGAGCTCAA	AGACAACGAG	CGGGCCTTGC	TTGCAGACGC	TGGGTTGATC	240
	AAAGGCGAGC	TGCGCTCCCC	ATACTACGTT	ACTGCACCTCT	CTTCATACAT	CATTTT'TGGT	300
	GCTGCTATTG	TGGCGAGCGG	CTGTAGGATA	ATAGATGACT	ACTGGGAGCA	GCCCTTAAAG	360
	GAGCAGGGAT	TCACCATGCA	CCACCGTGTA	TTCTCTCTGA	ACGGCACGCA	ACTTTCATTG	420
	CTACGCCTGC	TGAAACCCCC	GCGTCCAGAA	TCGCATCAGC	AGGGTGAGAA	GCTGGATACC	480
	AACTGGCTAC	AGAAGTGCGA	GGATCCATAC	CCAACGATCC	AGGAACAACC	AAATGCTGAA	540
35	GCACGGCGGG	AATACGCTAG	AGAACACGCC	AGAGGTGAGC	ACATAACGAT	GATTGTTCCA	600
	GGTCAAAGTA	TTAGCGGCAG	TATAGAACTG	AGCCTAAATT	ATAAACTTCC	TAAGTACCAC	660
	TACAAAAACT	CATTTGCTAA	TGGGT'TGA				

1460UP

40	GATCCAACAA	TTCCCGCAGC	GCCGCTCCAG	CCGTGCTCTC	CGTCGCATCA	AATGAGTCCA	60
	CGCCTGTCTC	AATCCCGCAC	AGCTGCCGTC	CATGCGCCAC	CTCGAACTGC	ATCCGCGACG	120
	CAAACAGCTG	GATAAACAGC	CCGT'TCTGCT	CGCACCCCCG	CCGCAGCTGT	CCAAAGAGCG	180
	CCTCCGCACC	AGCTGCTATA	TCATCGCCCC	AGAAACTCTC	TACGAATGCC	CCCATCGCCG	240
	TGTACCTCGT	CGTAGTTGTG	CATGTCGCTG	CCTCTTCCGG	CTGAATTTTG	ACAGTCTGGC	300
45	CCCCCACCCT	AGCTCCGGAA	CGCTACGTAA	TACAACACAC	AACCAAATGC	CCTACCCGAA	360
	GGTCGCAATC	GTCTTCTGCA	CCGGCTGCCG	CTGGGGCTTG	CGCGCAAGCT	GGTATGCTCA	420
	AGAGTTGCTA	CAGACTTTTCG	GCGACTCCCT	AGCCGAGATT	GCCCTCGTAC	CGGGTCCGTC	480
	CGGTCAATTC	CAAGTCTCTCT	GTTACGCAAG	CCAAGAACAA	GAGGCCACGG	GACAGCGGCA	540
	ACACCATCTG	GGATCGGCGC	CGCGACAATG	GTTTTCCTGA	TAGTAAATAT	CTGAAGCAGG	600
50	CTGTCAAGCC	ACTCTTTT'TG	CAGACAGCGG	AACCGCCTGG	GCGCCACAT		

1461RP

	GATCAAACCA	CCACGGCACA	TCATCATAGT	TGATTAAATC	AATTAGGTAA	GGCAACCATA	60
	GTTCGAGACT	TTGTTTCTGT	ACCATTTTCT	TGGGATTAAA	GAAGTAGGGA	GTCACGAGGA	120
5	AATGCACCGC	ACATGCTTTG	AGATTGGTGT	TTTGGGATTT	TAGAAGGCCA	GTAACGAAGA	180
	CGGTGAACGA	GCTGTCCAGC	CATAGATTAT	TTTAACTGG	ATGAACCTTG	TAGCACTCGA	240
	TGTATAGGAC	AATCGCCAAC	CAGAGCAATG	TCCTCGTGCA	CGGGTTCCTG	ATGACAAGCG	300
	CACGCGGGGT	GCTCGTGAAT	GGTAGGAGTT	GGTTGCTTCC	TATCCCACGG	TTGCTAAATG	360
	CCATGTACTC	TTGGTCCCTG	GGGTTCGGCG	CGACGCTGAC	CTTTAAAAATG	TATTTGAGGT	420
	CCAACCTGGT	ACCATAGCGG	TCCACTAGTG	ATAGCATGAG	TGCCCTCTAAC	GGCAGAAGAA	480
10	GCCCTTGCGG	AAGCGAAACC	ACCTCCCAGG	ATTTGAGCAC	CGCAGACATT	AACTCCAAAA	540
	GCGTGTGGC	CCAGGAGATC	TCCTGCTCGG	AGTCATCTGC	TTCTCATTCA	TCCCCGAGGA	600
	AGTGATATCAA	AAGCCCCGGC	AAACCCACGG	GCACAGCCCC	CCGCACATCC	GCGTCCCCAT	660
	TACAGTAGTC	TATCCCACAG	TTGTTCAA				

1461UP

	GATCGCGCAG	TTTAAACTTA	AAGTTGATAG	AGTTCCCGTC	GTGCTCTCTG	GATACAATAG	60
	AGGCCACCGA	GTGACGTTGG	CCCTGCACGT	AGTGCCCGCC	GTCGCGCCTG	TCGTCCGAGA	120
	TGGCCCTTTC	TAGGTTGATC	TTGGAGCCAG	CTTTCCAGCT	GCTGACTTCC	GTCCGATAAA	180
20	CTGTTTCTGG	TGCGATCCCG	ACCTTGAAGC	TATCGGCCGT	GAACCTCCGT	ACCGTCAGGC	240
	AGATAACCAT	GTCATCAAGT	GAGTCACCGA	TGTGGCAATC	CGCCAGTATC	GGAGCCGCAAT	300
	CCTTGATAAG	GACTGACACA	CCGTGCGCGC	CTGCCTCGCT	GGCATCGTTC	TCCAAGTACT	360
	CAGCAACAGT	GCCAATGTGT	TCCACTATAC	CGGTAAACAT	CCTATCAACT	TCTATGGGCG	420
	ATATAGGCTT	CGGTATGCCA	TCTATGCATC	TTCTTTTCTG	CTACCGCGAG	CTTTTAAAC	480
	TCGTAAAGCA	AATTACTTAT	AATGGCGGTT	CGCCATGTAG	CTGACTAATA	AAACTAGAAG	540
25	ATACGACTAA	CTATCTGATT	ATACTTTAGG	ACTATCTCTC	CTTGCGCTGG	TCACAGAAAC	600
	ATCGTTGAGC	AAGTCGCGTC	TATCGGGAAA	ATCACTTGGT	TCCTTTGTCTG	TAGAGCTAAC	660
	TGCCTGAGAA	GCTGGAAGC	GCTCTTTTAA	AGTCTACTTC	GAATGGTGGT	GTACGTCTGG	720
	GTGCTGGC						

1462RP

	GATCTTAATT	TAAAATTTTA	ATTAACATTT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAATAAAAT	TAGTAAATA	120
	AATAGAAAAC	CATAAGTTAA	TTGATTCTAT	AAGAAAAATG	GAATTATTTG	TGGCATCTTA	180
	ATTTTTATTA	TTTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATAAA	240
35	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAATTTAA	TTTAAATATT	300
	AAATATACCA	TTTTTATTAA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
	ATTTAATTTA	TATAAATTAT	TTAATTTACT	TCATTGATAT	ATATAATTAT	TAAATGTACC	420
	TTTCATAATA	TTTATTTTTA	TTAGTCTAGT	AATATTTCTA	TTTAATAGTC	TACCCTTTAA	480
	TTGGATATTA	CTACCTACTA	AATATTTACC	TAATAATATA	TTATTAAGAA	TACTTAAATC	540
	TAATAATTTA	TTATCTAAAG	TATATAAATT	AATTAACCTT	TTTTATTATT	ATTTAAATTA	600
40	TTATTAATTA	GTAAATTATA	TTTATTTATT	TTATTAACAT	AATTTTTTGG	ATAATAATAT	660
	ATCATTATTA	AATGGTAATT	TATTAATAAT	TATCTTAATG	A		

1462UP

45	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTAAATAATA	AATCTATTAA	TTATATAAAA	60
	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCATTCAT	TTAATACTCC	TCTAATTCAA	180
	TCTTAAAATA	TTCTTAATTA	TTAAATTATA	TAATAAAAGT	TAGTGGATAT	AGTTTAATTG	240
	GTAAACATA	TGTTTTAGGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATTAT	300
	ATCATTAATA	TAATAACTCT	TTAATTAGAG	TGGTACCACA	AGAATGCTGA	AAGCATTAGG	360
50	GGTGTGTACC	TTAGCTCTCT	AATTAAAGTT	ATAAAATTAT	CTTAACCTAA	AAAAATAATT	420
	AATTAAATAA	ATAAATAATT	AATTAAATTT	AAAAATGTTA	AAAAAAGAAA	TAAATAATAT	480
	GTTATATTTA	AATAGATCAA	AATTTCAACA	ATTTCCATTT	CATTTAGTAC	TACCATCACC	540
	ATGACCAATT	GTTACATCAT	TTAGTTTATT	AGGTTTACTA	TTAACTTTAG	CTTTTACTAT	600
	ACATGGTATT	ATTGGTAATA	TTTATCCTTT	ATTATTATCT	TTATTAGTAG	TTTTATTACT	660
55	AATAACTTTA	TGATTTAGAG	ATATGGTAGC	TGAACCTTACT	TATTTAGGTG	ATCATACTTT	720

AGCTGTAA

1463RP

	GATCCCTGAG	TCTGCTACCA	AGGAGGTCGA	GGAGGAGGAC	ATCGATATCG	AGCAATTGAA	60
	GCAGGAGATG	AAAGGCAACA	AGGAGGCCTC	TGCTTTGTAA	GCTTGCTGTT	TGCCGCTTGT	120
5	GCTAGCCAAT	CGTTGCTGAG	ACTATCTAAC	TTGTATACAT	GCCGCTATCG	CGGCACGCCA	180
	AGCGAACACT	ATAATGTATA	TGTCAAAGTTA	AATACATCAT	ATATTATCTT	GTGCCTCAAG	240
	GGTCTTAAAG	ATGTCATAGG	ACAGTCGCGT	GCTCAGACAC	ACGAATATAA	TCATAATAAT	300
	AAATATATGG	CGGTCAGCTT	CATGACCACG	TCAAGCCTTG	ATACCAGAAG	ACACTTCTAG	360
	GAATTTCTCA	ACGGGAGAGA	AAACACTAGG	GTGTAGGTCG	TCATTTCGTC	AGGACATCTG	420
	CTCCTCGGTC	CACAAGTTGG	CCTCTGGTAC	ATAGTCTGGT	TCACCGACAC	CCAATAAGCC	480
10	ACCGTGCGCA	GCCCAATCGC	TGACACGTGG	AAGCTGTAGT	GTCTTCCAGA	CGTCATCCAT	540
	GGCGTCCAAT	AGGACATCCG	ACAGGTCGTT	CGTGTGGCCT	GGAGTAGGAA	TGATACGGAG	600
	TCTCTCGGTC	CCGCGTGGAA	CGGTAGGAGT	TGAAGGGCCT	GTACGTAGAT	GCGATGCTCT	660
	CCATCAAAAT	GTCGGAAGCA	CGCTTGGC				

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1463UP

	GATCAAACAG	TAGAAGTATT	AGAGCTGCTT	GCAAAGGGCG	TCATAAACAA	GAGAGCTGTA	60
	ATGTCGACAA	ATTAAACAGA	AAAATATCAT	TATTAGTGGA	TAAATAACCA	ACTTGCACTG	120
	AGAGTATAGT	TCTACATGTT	TATTCCGTAA	CAGAATTTCT	ATCCAAATAG	TTTAATTCCG	180
20	TTTTACTTAT	TACCGGAGTA	GCAGTGCAAG	AACCTTGAT	CCCAAAATGC	TAGAGGGACA	240
	TGCAGATGTA	CTAGAAAGCA	ACGTCTGTTT	CTTTGGATTT	AGCAGCGTCA	GGCGAACAAA	300
	AAAAATAGAA	AGTCAACAGG	GATTGGGAAG	TTATGAGAGT	TGATATGTTT	GTCCATTAGT	360
	AAGTCATTCA	GTTGATATGA	GGTGCTTAAA	TGTTTGTAA	AAGCAAGAAC	GAAGAGAGAT	420
	ACAAAATGTG	CAGTTGTGAA	TCGTGAAATT	GACACCAGAG	GACGTCACCT	CCCGTTGCCA	480
	CTGTTTGCCA	ATTGCTTCTC	GAGCTGCTCA	ACCTTGCGCT	GTAAATCTCT	ATTGACTTTC	540
25	TTTAGTAGTT	CCAATTCAAT	ATGCGTTTCC	TTTCGATCTT	CATAGCTGAG	CAGTTTCGCC	600
	ATCTCCTGGT	TCTCTTTTGT	CAACATTTCC	AGTCGGACAA	TCATCTTGTG	AGCGAGGGCT	660
	TCTTCGTCAT	AACGGCCGAA	TCGGGTAACG	GAATTAGAGG	GATT		

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1464RP

	GATCGAAATA	ACTTCCGCTG	AAAACGCAGC	AGAGGCAGCC	AATGGTCAAA	TGGAGCGAGA	60
	ATATCCACGA	TATTTCTAGG	GTACTGTTGC	TTGCCAGTTG	GTGCTCGGAA	ACATAACCCT	120
	CAATGGCGCC	CAGTGTGTTG	TACATACCCC	ACACCGGAAA	CAGACCCATG	AATGACCCGA	180
	AAACCACCAG	CCACGCGCGT	AAGCCGCCAT	CCGGGTATTC	GTTGGAGTTA	TCGAGATATG	240
	CGCGTTCTTC	TTCTCTTACC	TTTTCGTCCG	TGAGAGGGAC	AGTCTGCTGA	GCGCACGTGG	300
35	TCGTGGGGCC	ATCGCCAAAA	AGCTCTTTGT	CGCCACAGC	TGTGGCTCTG	CCGCTGTGAG	360
	GACGCTAGG	GCTACGGGCT	CATCGCCATG	CCGTACTTGA	ACGCTGTCTT	420	
	TGTCGATGAC	CACCATCGTT	CCTAGCACGT	ATGGGAGATG	CTCCGAACCG	CGTCAGCGCC	480
	ACCACAGACC	ATCTATCTAC	TTAAATACCT	AATTATCTGG	TGTCCAGCTA	AAAATCCGAG	540
	TATCAGTCAT	CCTGTGGCGG	CCTTATCACC	CATTAGGGTC	CGCTTTGCGG	TAGTGCATTA	600
40	CCGTCGGCGG	GATTCATCCT	CCAAAATGTC	TCAAGCGATG	CCTTGATTCC	GAGTGTACAA	660
	GGGCCAGATT	CCAACGGGCC	AGGAGGCAAC	TAATAGAGG			

1464UP

45	GATCTTGCGC	TTTTTCTTCA	GACCGCGGTG	GGTGTAGTAT	TGTTCTCCTT	TAATGTTGGA	60
	GTTGAGGCGG	GACGAAGAGG	GCGCAGAGGG	GTCTGGCGAG	GCACCGGTGG	AAAGGGGCCT	120
	GTCGGCGCGT	TGCAGGGGCA	GCGCGCGGTC	GTCGTGGTCG	TAGTCGTGAT	GTTGGGGCGC	180
	GGGCGGCGCC	GACTGTGCGT	CCAGCGGGTG	GCCGTTCGGAC	GCGAGCGCCG	AGAACTCGGC	240
	GTCGCGGAAC	TCGTACTCCT	TCTGCGGGTC	CTCGCGGCGG	CGCTTGCGCC	GCGGGTCCAC	300
	GGCACGGCGC	GGGACCTTGA	GCCCGTTGGA	GATAATGAAC	TTGTGTTTCA	CCGAGCCCTT	360
50	CGGATGCTTC	TTTCCGCCAT	TGCGTTTGGG	CGCCGGCGTC	TGCGCGTCCG	GCACGGGCGC	420
	GGCCGGGCGG	GCATGCAATT	CGTCTCGTTC	TGGCGAGACT	GGGGGGGGAT	AAACTCGCCC	480
	AGGATCGCGT	CCACGTTAGT	GAGGTGCGGG	TTGCCGTCTT	CTGCGGCTGC	GTGGTGGTGG	540
	TTGGCGCGGT	GAGCCGCGTG	CACCGCGTCC	TCCTCGTGGG	GCTTGGGCTC	CTGCTCGGGC	600
	ATGCCCCGTT	CGGCTGCATG	CCTCCAATCG	ACTTCGACGT	CGTACGATCC	CATCCAACGA	660
	ACCCCGTAAC	TTATCTCGAA	GTATGCCCTG	ATACCTATAC	TGGTCGTTCA		

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1465RP

	GATCCACTTC	TTTGGCGACA	AGACATTGCA	GGCGGCAAC	GA CTGGGAAA	TCTACAACGA	60
	CCCGCGCACC	ATCGGCCACA	GCGTCCGCTC	CCCCGAGGAC	ACCGTGAGGA	TCCTCAGAGA	120
5	GCTGTTTCGAC	CTGTAGGCGC	CGCCGCTAGC	TAGTTCTTTG	TAATTGCTCG	ACATTTACAA	180
	TGCATATTCC	TATATACACC	GCGCGCAGCG	CTCAGCTGAG	CAGCCGTACG	TACGCCAGCA	240
	CGAGCGCAAA	CGTACCCGTG	CACACGCCGA	TCAGCCACTG	CATGACCTGC	GTCTTGACCG	300
	AGTCGATTTG	CATCTTCATA	TTACTGACCT	CCTGGTCAAT	TCGCGTGTCA	ATCTCCTTGA	360
	TCTGCAGATT	GTGGTTGCTG	GA CTCTCCC	GGATGCGTCC	CTTTTCCAAC	GAGAGATCCA	420
	GCTTGAACCC	TGCGTTGCGC	TTCTGTGATC	CCTCTCGGAG	CCGGTTCCGC	AGCTGCTCTA	480
10	GGTCGTTTCG	AATCCGCTCC	TGTTGCTTCT	GGATGGAGTG	GATCTCGCTG	CGGTCCGCCG	540
	TCAGCAGTTG	GTCCCGCAGT	TTTGCAAAAT	CCACCCGCTG	CTGGTACGTC	AGCTTCGTAA	600
	GCTTCTCGCG	GGACGCTAGG	TCCTGCGAGA	CATGCGTCAC	GCCCCGCGC	AGTGCGTCCG	660
	ACATGATATC	CACGATCGCA	TTGCGCTGCT	GGCTTGCTGA	AGT		

1465UP

	GATCCCGCAA	TAGCTTGATT	CGATCGTCTG	GTGCGGTACC	TGCTCGACTT	CTCTTGCTCT	60
	TCTCTATGTT	CGTTGCTCAC	GGCCGGAAAA	CCACTACAGC	ACAAAAAATT	CACAAGGTCC	120
	GCCCGCACCAG	CCTTTTAAAT	TAGCGCAATG	GCAGCGAGTC	CTGGTATATA	AGGCAAAAGA	180
20	CGGGAGGCGG	ACAGCTACTA	CAGGCTCATC	GAGGCATGGT	ATGTTGCGCG	ACAGTGCGCG	240
	CAGGGGGCAG	GA CTAACTTT	GATGTTGAT	AGAATGCGTT	GTACAACCAC	GCGGTGAAAC	300
	AGAAAAAGTT	GCTGGAGCAG	GAGCTGAATC	GATTTGAGCT	CGGGGTGGCG	GCGCCGGTGG	360
	GGCTGCAGGG	TTCCATATCG	ACGGCACTGG	TGGGACTGGA	GCGCACAATT	GAGCAGTATC	420
	AGGCGCAGGT	GGCGCAAACG	GGCAGCGGCG	CGGAAGCCGG	CAAGCATGCG	CAGCGCGTGG	480
	GCGAACTGAC	GGAGTGCGCA	ACGAACGCGC	GGCGGCGGTT	CGAGGGGCTG	CGGGCCGCGA	540
25	GCATGCAGCC	GGTGGCGTTC	CAGAGCGGGG	CGGCAGCGCC	GGAGGGCGCC	GTGAACCAGC	600
	CGGCGGCGGG	GGCGCGCAC					

1466RP

	GATCTCTTAC	TTTTCTTACT	CACCAATGTC	TTTAACAGAC	ACCCAGAGTC	ACGGCCGGCA	60
	GCCTATCTGC	CGTGCTGGCG	CCATGCCCCG	CCCCTGGTAC	TGGCCCGCTC	GTGCTCGCGG	120
	TAGTCTCACA	GCAACGGAGC	TTGCTCCAAT	TGGGCTGCAT	TCTCCCGACC	ACAGTCTGTT	180
	TGTCACGTGA	CTCTCAGCCG	TCCCGAATGT	ACATTTCTAT	TTATCTACTT	CTTGCCGCCCT	240
	TGCCGCCACC	ACATCCGGTG	CCGGGCAGCA	CACCGACCGC	GCATCGCGGC	CCTCGCGTTC	300
	GTAGAACTGC	GCACAGCAGC	TGTACAGTGC	CTCCACTGCC	GCCGCGCAAC	GGCCCTCCCT	360
35	GTACCTCTGC	CGTTTTAGAG	ATGCCTGGAT	CGCACATGCC	TGGGCTTTGC	ATGGGGGCTG	420
	TCCCTCTGCG	CTGCGCCGCC	TATTGTCCAT	GTTTTGTGTT	CTATCTGTTG	GCCGGTACCA	480
	CGTTGTTGTA	CCAGAGTACA	TTGTGCGGGT	GACCCCGTGT	AATGTCACCC	CGTGGGCCAC	540
	AGATGACCCT	GCCACATGCC	TCATTTCTTT	GACCGCACCG	TGCCGCGAGA	CCGCCCACAT	600
	GGGCGGTGCG	CAC TCCGACG	ACACCCACGG	GGCGGCACTG	CAAGGGTCGC	AGGTGCGGAT	660
40	GAGTCAAAAC	AAACCAGGTG	TGGCGCTGGG	CGGGTGAAAA	TCGACTCATA	GAGAC	

1466UP

	GATCTTATTA	ATTTTGTATG	TGCTATATTC	TAAATTCAAG	TAATGATAGC	GCGTGATGCG	60
	GTACGTACCT	ATACATATAA	CGCACAGTTC	ACCATCGTCT	ATGCGTGTAT	GAAAATCACT	120
	CCAGCCGTGC	GACACGCCAC	GTGTAATCTA	GTGAGTTTCA	AGTTCTTCCT	CCTCATCGGC	180
	AGAAAGTTTC	CCCGCGGCGG	TGAGGTTCTT	GAGCCGCTCC	TTGAGCTGCG	CGATAAGGCT	240
	ATTCTCCCTT	TGAGCATGCA	TGCGGATACC	CTCTAGAGAC	ATATGAGCCG	AATCTGCACC	300
	ATCTAAACCA	TGTTTCGCTG	TGCTGCCAGT	GGCAGCTGCC	AGTTTGGGAC	TGGACAGACC	360
	TGTCTGTCCA	TC TTTGTAAG	AATCCTCGGT	CGTTGCCGAG	TTGGAATTCA	TGGTTCCCAT	420
	AGTGTGCAAG	ATTTTCTCCT	CTTCTGTTAG	TTCCAGATGG	GTACCTGTCA	GATTGATCAA	480
50	GGACCTGCCG	CTTTTACGGC	GCGAGAGCTT	GGGCAGAAGA	GAGTGCCCGG	TTGGCGTCCG	540
	TTACCAAGAG	TTTGTAATGG	AGGTGTGAGA	TCTCGGAGTC	CTTGGTAGTC	TCAGACACGA	600
	AGCACGGGCA	TCATGTATCC	ACTTCGCAAC	AAGCGAAGTC	CAGCCACACT	GGTGTGATGC	660
	GCCCAAGCCC	CTACCAGTGT	CACCATCGAA	GTAT			

1467RP

	GATCGCAGAC	TCCGCCGGAG	AGACTTTCGC	ACCTCGGGCA	CAGGTCTTGA	AAGAGAGCTC	60
	CGGCCGTTCC	GTGCCAGACT	CTTGTATTATC	ATGTCCGTAA	GAGCAGCGTT	CGTGCCAGGT	120
5	ACGCCCTTCT	TGTTCTGTGT	TCCACCAATT	GATGGAATTT	GAGACGTGAA	CCTCTGCGGA	180
	TTCRRKCTAT	TGAGCACACC	ATTGGCACCA	CTTGAGCCCC	TTCTGCTCTGC	CATCCCTAAT	240
	CGTCCTATCC	TACGGCCGGC	TAATAAGTTA	CTACCAGACT	CTGGCCCTCA	TCTGGGACTG	300
	ATGTTATCGT	CTGCAGCCAG	ATCCTGTTTG	TGACCCGATC	GAAATCATCG	AGTACGAATA	360
	ACCACGTGAC	CATTATTTCAC	GTGATGAATT	TGGCGGTCCC	TGTTGCCGAC	TCTTACTCCA	420
	GGTTAACCAT	GACTAGATGG	GCATACCTCA	GATACGTTAT	TCATGGGATC	CGGAGTTGCC	480
10	GCGTCGGCCG	AACCGCCCGG	TGAATCTGTG	CTGACGACCT	AAAAAATAGT	GTGCGCAAGC	540
	TTCCTTAATC	TGTGAGATGC	ACACTGACAA	ACTTGAAGGC	TGAACCATCA	AAGCGATACG	600
	CCTCATGCAC	GTGCTCAATA	AGGTCCAGGA	AGTCTCGCAA	TGGGGCAAGC	AGACGGTAGA	660
	TTGCAAGACA	CAGACGATTG	GGTTGTGCCA				

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1467UP

	GATCGTCCGA	GTGCAAATCC	ATACCAAAAA	TGTGGACCCA	GGTACGGGAT	TCGAACCTCT	60
	CGAAGAAAAA	TAGCCTCAGT	GAAGTGCCCA	ATTGCCCTTAT	AGTCGTTTTG	CAGAGCATAT	120
	AGAAATGTGG	GACAAGGCGG	TGGGGGGGCT	TGTCGGACGC	GACGGAAGAA	GGGATCTGGG	180
20	CGGGAATTAC	GGCGGTGAGA	GGCAGGGGTG	CGGAAGAGAA	AAAGGTGAAG	CGAGTTGTTG	240
	CCATGAGCGA	GATGCAGCAG	CCAATACCTA	TCCCAATGGT	AAACGAGGCG	GTCCAGATGG	300
	CCCAATGGCG	GAGGGCAACA	GGGCCCCGCT	CCTTTTTTCG	CGGTCTGCGG	TGCTGTTTTCT	360
	TGGACTTGAC	GGTCAGCTCG	GTTTCATAGC	CGGACTCGGA	CTCGTTGCAA	AGGTTGTGCA	420
	GGTGCTTGAG	CAGGCGGTGC	TTCTCGTGGT	GGTTGGACAT	GATTATAGGG	CTGCAGTATA	480
	CTCGGATGCA	TTTGCGTGCG	GTGTAGCGCT	TCAGGAGAGC	CGCCAGCGTG	CTCTTCTGGC	540
25	CCTTCTGGGA	CACGGGAATC	ACGGTGGGGC	AGGGCGCCTT	CTCGCACAGG	CCGTCCAAGA	600
	GCTCTGGCGC	CTGCGCTATG	TCGTGGAAGA	CCACCATAAC	CGCGAGGTAC	CGCTGGCCCA	660
	CGTCCCAGCG	CGTGACCATG	CCGAGGTTCT	TCACGTCAAA			

1468RP

	GATCTCGTCG	CTCATTTGTCG	ACCTGCAAAA	AGTGTTTCAGA	AGGAAGGCAA	CATGTGTTTT	60
	TAACTCTACG	GCCGTGGCCT	CAGAGATTGT	TCACTCAATG	TCGTTTCATCA	TTATGAATGG	120
	GTCGCCGGCG	CCTGCCGGCC	TCGAACCCGC	GCCACACGGC	CTCCGCCGCG	CGCTGCCCCG	180
	CTGGGCCACG	CAGGGTCCAA	AACCCACCCA	AACTCACCGC	GCCCACCCGG	CTACACCGCC	240
35	GCCAGCACGT	CACGTGCGGT	TACCCGCCCT	GCCGGCACTG	AAAATTTTTT	GCCGCCAACA	300
	CTATCGCGCC	CGAAAAAGCA	ATTTGCCGGC	CAACCACACA	ACGATCTGTT	ACCGAACAGG	360
	ACAGGACTCA	TGCCCCGTTT	CCTTCTTTAT	TTATTTACTA	GCTCCACATA	GATATTTTTG	420
	ATATTTATAT	GGTGTGTTTT	CCTCCGCACG	CCGCAACCCA	GCACTTAGCA	GACCACGGGG	480
	GCAGGGACTG	ACACCCAGCC	AGAACAGAAC	AACAACAGGC	GACCTTACAA	TGAGCATGGA	540
	AACGCCCCCT	GTAGATATCG	ACAACATCAT	CGACCGCTTG	CTGGAGGTGC	GGGGCTCGAA	600
40	GCCGGGGCAG	CAGGTGGACC	TCGAAGAGCA	CGAGATCCGC	TACCTGTGCT	CCAAGGGCCG	660
	CAGCATCTTT	ATCAAGCAGC	CCATTCTTC				

1468UP

	GATCTCAGAA	TTATCGGCTA	GCAATTGATA	TTAGCATACT	TAATTCGTGC	TAAATACTTT	60
45	GGCATCGCAT	CTAGACATAG	GAAGTAACCT	CAAAAAAGCT	ACGCAGATAG	TAAACCTGGA	120
	AGAGAGATTG	CGCAACAACA	ACGGCCAGTT	GGAAAAAGTA	CCACCACTTG	ACCCTGTCAT	180
	TTGTAGATCT	AGCAGTGTTT	CTGTGTGTGC	GTTCGCGAAT	CTCGATGTAC	TGTTGCTCGT	240
	TCATTACTTC	CATTGTGAGC	ATGGAGAGCT	TGCGCACCCG	ACCCTCTAGC	GTCTCCGAGC	300
	TGGAATCAGC	GGCATCGGGG	GAGAGAACAC	CGTAGGTATT	AAACGTGACA	TCCTTAGTCA	360
50	GGTAGCCCGA	ATTGTCTGTT	GCAAAGCAGT	ACTGGTATTT	GCCATCTGTA	GGCGCCTTCA	420
	AGGTCAACTC	ACCGTGCAGC	GACGCACGCT	CGCGATCCAG	CACGTACCGT	CCGTCAATCC	480
	CGTACACCAG	CAGGTCTCCA	GACAGCTGTT	GATGTGATTG	TGGGTCTCTG	TCGCCGAATT	540
	GATAAGTGAT	TGTCAGCAGC	TCCCCGCCCT	TCAACTGCTC	AAAGAAACAG	CGCCGCCCGT	600
	AGGGGGGAAG	AAGTACATTG					

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1469RP

	GATCAACTAC	ATCTGCGAGC	AGCAGCCGAA	TTGTAAGGTG	GCCATCATAG	CATATGACAA	60
	GTGGCTGCGT	TTCTTCAACC	TGCGCCCGGA	GTCGAGCCAG	GCACAGGAGC	TGATTGTGTC	120
5	CGAGCTCAGA	GAAGTCTTCC	TGCCGCTGTA	CAGCGGCCTC	TTCGTGAGGC	CTGCGGAGGC	180
	AATGCATGTC	ATACAGGACA	CGTTGGTCAA	GCTCGAGTCG	TTTATCCAGG	ACGACAAGCT	240
	CTCGCACGGC	GCCGAGGCGT	GCTTCGGGTC	GGCGCTCGAG	GCCGCGCTGC	TGGCGCTGGA	300
	CACTGCCACC	AATGGTAATG	GCGGCAAGAT	CATTGCGACT	CTGAACACGC	TGCCACCCGT	360
	GGGCAACGGC	AATCTGACGC	TGCGGCGCGA	CGACGGCCTC	AAGAAGAGCC	TGAAGTGCGA	420
	CAACAGCTTC	TACACCGCGC	TGGCGGACAG	GATGCTGAAG	GCGTACGTCG	GCCTGGACCT	480
10	CTTCTGCACA	GGCAGCGCCT	TCATGGACTT	TGCCACGCTC	GGCCACCCCG	TGCTGGCCAC	540
	CTCCGGGACG	TTCCGCCACT	ACTCGAACTT	CCAGCTCGAC	GCGACGAGTT	CCCGCTGGGT	600
	CAACGACATG	CTGCACGCCG	TCAGCAGCAC	CGTCGGCTAC	CAGGCGCAGC	TCAAGGTGCG	660
	CTGCTCCTCG	GGGCTGTCGT	CAGTCG				

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1469UP

	GATCGGGCGA	GCAGGACTAG	AGATGAGCAG	CAATGACAGT	GATTATCTCC	TGGTTACCTT	60
	CAAACTCTTC	ACTCTCCTCA	AGAAGTTGTT	ACCTGATGAC	TCCTTCTTAT	TGTCTGTGTC	120
	ACGCGCGCCC	GTGTAGGCGT	CTTCGTGCTC	CTCCTTCTCG	TCCTCAAGAT	AGCCAGAGTG	180
20	GGTCTTAGTG	AGCTTCAGGT	TGCCGTTCCT	GGGGTCGGGG	CCAATCGCCG	ACGCGGACGG	240
	AGGGCTTTTC	GCTCAGCTGT	GGCTCAGAGA	CTTCTTCTTG	CCCACCGTGC	TCTGCTTCAT	300
	CGCCTCTATA	GCGACAGGGG	CCGCCGGCGC	GCCGTGCGAG	AACGTGCTGG	AGCCAAGCCC	360
	CTGTGTCACG	GGCCCATGCA	CAAGGTCCGC	GGTTACCTTG	GCGTCGAACT	GCGTCACCTC	420
	CGAATGGTTC	TTGATAGCGT	TCACCGTCGA	CGACGAGCGC	TCGCCGACGT	CGCGGCGCGA	480
	ATACAGGTAC	GAGTCGTCGT	CCTCGTCGAT	GCCGAAGACC	TCGTTTCATCG	CAGACTTGTG	540
25	TGCGGTGGCC	CCGACAACGT	CGAGTTCGGC	CG			

1470RP

	GATCTTGCTG	CTATCCAGAA	ATGGGAAGTT	CTTAGACRAC	GGGGAATTAA	GCCCCTTTTT	60
30	CAATATTTTG	AGCGTCGTTT	CATAGCTCGG	AAGACGCAGC	AGAAGCCCCC	CCAGTAGTGT	120
	CTGTTCATGT	TCGCTCATGA	AAGGTGTCTC	TATCAAATCT	AGCTCCATCA	TCGCAGAGTA	180
	GTTATTATCT	TTCTTCCAAG	ACAGACGCAC	ATGCCGCAAC	TTGTCAGGA	TTACAGTAA	240
	ATAATGGTAG	AACCGCGGAC	TCACAGAATC	GACGACCGCT	CGAAATGAAG	TCGGCCCGTA	300
	GAAGATCGTG	CGGCCCTGCT	TCTCTATCAC	AAGATGGAAC	TGCGAAAGTC	TGTTACAGGG	360
	GGACACCGTG	CCCATAACGT	GCTTCTGCAT	GAACAGCTGC	GGTACCATCT	CGCTCTTCAT	420
35	CCGCGCGAGC	TCAGTCTCAA	GCTCGTCGAT	CCGTGCGAGC	AGCTCCACAT	TGGGCGTTTC	480
	AGCTGAACAG	CTCCCGTGAG	TTACAGTCGT	GCGTAAATCT	AGACAGGTAC	ACACACTCGG	540
	GCAGGCCCTT	CCCAATACAT	TTAGAGCACT	TCGGCCGCGC	CTTGTTGCAC	TTGACGCGCC	600
	GCTTGCGGCA	GAACACGCAC	GACTTGCTGA	CCTTCCGCCT	GGTTTTTACA	ATCTTGCCAT	660
	CGGACTCTGC	CATCCCGCCA	GCTTCAGCAA	AATGAGTAG			

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1470UP

	GATCGCGGAC	GTGGAACACT	GGCCGGAGAT	GCGCGCGGCC	ATCCTGGTGG	TTTCTGCGGA	60
	CCGCAAGGAC	ACGCCATCGA	CGAGCGGTAT	GCAGCAGACG	GTGCACACGT	CGGACCTCTT	120
45	CAAGGAGCGC	GTGCGGACGG	TGGTGCCGCG	GCGGTACGGA	GAGATGGCGG	CGGCGATCCG	180
	CGCGCGCGAC	TTGCGGACGT	TTGCGCGCCT	GACGATGCAG	GACTCGAACT	CGTTTCACGC	240
	CACCTGCCGT	GACTCATTTT	CGCCGATCTT	CTACATGAAC	GACACTTCGC	GCCGGATTGT	300
	CAAGCTGTGT	CATCTGATCA	ACGAGTTCTA	CAACGAGACC	ATCGTGCGGT	ACACGTTTGA	360
	CGCGGGTCCG	AACGCGGTGC	TCTATTACTT	GGCGGAGAAC	GAGGCGCGGC	TCTGCGGCTT	420
	CCTCTCTGCC	GTCTTTGGCG	CCAACGACGG	CTGGGAGACC	ACGTTCTCGA	CGGAGCAGCG	480
50	CGCCACTTCG	CCGCGCAGTT	CGACGAGTGC	GTGCGCGGCA	AGCTTGCGAC	GGACCTGGAC	540
	GACGAGTTGC	ACAGAGAGT	TGCCCGCCTC	ATCTTCACGA	AGGTCGGGCA	GGGCCCCAAG	600
	ACACTAAATC	CTCGCTCATC	GACCCCGAGA	CGGGCCTGCC	CCGCTGACGC	TATT	

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1471RP

	GATCAATTAA	CTATCTAGAT	GAGTCTAATT	AATTAATATA	CTTAAAAGTC	CCGTTAATAT	60
	CATTAGCTAC	CCTATCGGAA	CAGACCGTCT	GCTACTAGGC	CGAAAGGGTA	AAGCAGTTGT	120
5	CAGTCAGTAC	TTGCTGTGTC	TTATGGAATG	CCTGTCATAT	GCCGGCAGCT	TGTTTGTAC	180
	TGGAGTACGG	CGCGTGCCGC	CTTGACAGAG	GTACCCATGA	TTCTGAACGC	CAAGGTACCA	240
	CACCTTCCTG	CCACATCTCC	TCGACCTCTT	CCAAAGTCAA	ACCCTTTGTC	TCGGGGACAA	300
	AGAAGAAGAT	GTAGAAGAAC	GCAAAGATCA	AACAACCCAT	GAACACGTAG	CCGTAGTAAA	360
	ACCTGATCGC	ATTGGTAATG	TATGGTGTA	AGAAGGCGAT	CAAAAAGCCC	CATATCCAAT	420
	TCGCGGCTGT	GGCGATAGCC	ATGCCCTTGG	CTTTGACTCT	TAATGGGAAA	GTCTCCGAAA	480
10	CAATGACATA	CGCAATTGGG	GCCCAGGTAG	TTGCAAAGAA	GAAAAATGTA	GAGGCAGGTA	540
	AAAACAATCA	TAGCATTGCC	TGCCGGTCTG	GAAGAAGGCT	GATCGGGTCC	ATTGGGCCAT	600
	AGTCTTGTC	CACCAACGGA	GGCAAAAATA	ACCATACAAA	CGGCCATTGC	CGCGGCACCG	660
	TAGAAGCAAA	CATTTCTCTC	TGCCAAATCT	ATCGACAGTG	TTACATTG		

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1471UP

	GATCTTCGCC	TTCTTCTACA	TGTTCTTCTT	TGTCCCAGAG	ACAAAGGGTT	TGACTTTGGA	60
	AGAGGTCGAG	GAGATGTGGC	AGGAGGGTGT	CGTCCCATGG	AAGTCCGAGT	CCTGGACTCC	120
	TTCTTACAAG	AGAAATGCTT	ACGAGACTGA	GGAGGTGAAG	CCAGAGAAGA	CCTGGGCTTA	180
20	AAAACTTTAA	ACTACAAACT	TTTTTGTCTT	GCTAATCATC	GGGTAAAAAC	CTAAACCTAA	240
	TCATATGTTCA	TTAATATTGT	TATGACGTTT	ACGAGATAGC	ATATGTAAAT	TACTATTAAA	300
	AATATGCGAT	TAATCTGTAT	TTATTAGTTG	TAATTGCAAT	GCCATATGAT	ACTGCAAAGC	360
	AATACATGCC	GAGATAACCA	ACGCCACTGA	GGCGGGACTG	GGCCCTTCT	CCGGCCCGGC	420
	GAACATGCCT	GTCGTTGGTG	GGCCGCGTGC	CCGTGCGCGG	CCAGCCGCAT	GCCCCTCGTC	480
	GGTCATCGCC	CCACTTTCAA	ACTTTGTAAT	CGAGCAGGAA	ATTAAGATT	GTTATAAATG	540
25	ATATCAAATT	TTTCGTCGTT	TCTTTTCAGT	GAGTAATATT	GTCCCGGCAC	CGCACGCCGA	600
	TGATGCCGCT	ACATCGCACA	GGGCCAAAGC	ACAGGTGCTA	AACATTGCT	TAGTTGGCGT	660
	CGTTGAGCTC	GTTTATGCTT	AGTGGAATAT	CTGCAGCATA	TTCAATATCA	AGTCTGAA	

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1472RP

	GATCTATCTC	CCAGCTTAGA	GAGACCGTCC	GGATGTAAGT	GATACCCAGA	CAGCCAATGA	60
	TACTGGTCAA	GTTTTGTAGT	TTTATAAGAA	AACATATATT	AAACGGCTAA	AGACAGAAGG	120
	CGAAAAGCCC	GACTTTTATG	GGCGTAGAAG	TCGTGAAAAA	GGCGAAAAAC	TATATTTCCA	180
	CTTAGGGCTC	CTCCTTCCTC	ACGTAAACGC	GCATCATCAT	ACGCCTTCTG	TGAGTCAAGA	240
	GCACTACGAC	ACGCCGTGCA	TTCCCTCATA	CAACCTTGCC	AACACATGAT	CATGTCCAAG	300
35	GATATTGCTA	CGACCCCA	ACTGTCCGAA	CCAGACAAGT	ACTTCGTTGA	GCAGCGCGAT	360
	TTGCTGCTAC	AAGAAATCAC	CTCCACGTTA	GACTCCATCC	TGAACAACCT	AAATGGCCCTG	420
	AATATTTCCC	TGGAGAACTC	CATCGCAGTA	GGCAAAGAGT	TTGAGAGCGT	GTCCGAGCTT	480
	TGGAAGGTCT	TTTACGACGG	ACTCGCGAAC	GGAGCGGCTC	CTGGAGTTGC	CGCAGCCAA	540
	CCGTGCTCTC	AGGACCTGCC	CACGTAGCCC	GTCGCCGCGC	ACCAGAATGC	TGCAGCGGGC	600
40	AATAGTGACG	CACCAGCGCC	ATCGCAGTAG	CGTTTGCAT	CTGCCCTGGC	TTTACACCCG	660
	TGCACCCACA	TTGCGCTCTA	CTTTTATGTG	TCATC			

1472UP

	GATCTCGATT	GAATGCCAAT	GAAGGTTTAT	GGCCGTCACG	GGAGGTATAA	CAGACTTGTA	60
	ACGACTTTTG	GTAAGACCCA	CGGTGAGGAA	GATAGCTGGT	TTAGCAGCGA	CGATGAGAAC	120
	CACGGCAGAC	CAGTTAGCGA	CGACACAACC	AAACTCAGCC	TGAGCCAAGA	TCGATGCAGC	180
	GAATTACCGG	AGGAGACGAT	AGGTGCGAAT	AGAAAACGTC	CGGCGGAGCG	AACGCAGACG	240
	GATCCGGTGT	GGGAGTTTCT	GGAACGGCCG	GCATCGGGGC	AGAAAGCGGAG	AAGACGAGCA	300
	ACATGCGATT	CTACAGAATA	TAGAGAGAGT	GCCAGTCAAG	AGTTTCTAAA	CGCTGTGAAC	360
	GTTGTGTCAGG	GCATAGTGTC	TTCTCTCAAG	CCTGCAAAAG	AGGTAGTTGA	GCACTGGGCG	420
50	GAGCTTGAGG	ATGTGCCAGA	GGATCGGGGC	AATAACGGGC	AGGCGGTCTA	TGGCAAAACA	480
	AGAACATGCT	TGCAAAAGCG	GAAGAGGATT	CTGACACCGA	AGCTGCTGCA	CATGAGTCTG	540
	ACGAACCGCT	GCACAGGGCG	ACGAAGCACT	ATCGCGGCAC	TTTAATGAGC	TGCGTACGAT	600
	GGGCGAGACT	CTTAAGTACA	GCGAAGATCT	GGACTTTATA	TTGTCCGACA	ACTCCATGAC	660
	GACACCGGAA	CATAGACGCA	CCACATGCTG	CGCTTGTTGT	TGGATATGAT	GAACAACGA	

55

1473RP

	GATCGCATCA	TCCTGTACAC	CAAGCGCGAC	GTCTGCGCCG	CGCCCACCCC	CGCCGCGCTC	60
	CACCGCTGGC	ACGCCGAGAC	CGGCGACGAC	TACATGCTCC	TCGACGCCCC	CAGCGCCGCG	120
5	GACGCGCGCG	CGCTGCTCGC	CGCCGTGCGC	GCACGCTACG	ACGCCGCGCG	TGCCGCGCCC	180
	GGCGCGCTCC	CCCTCGGCTA	CCGCCGTGCTC	GTTGCGGGCA	TGCCCAACGT	CGGCAAGTCC	240
	ACGCTGGTCA	ACCGCCTCCG	CGCCTCCGGC	ACCGCGCGCC	GCGCCAAGGT	CGCCGCCACC	300
	GGCGCCACC	CCGGCGTCAC	GCGCGCTACC	AGTGAGTGCG	TGCGCATCGC	CGATCACCGC	360
	GCCGCGCTCT	TCATGCACGA	CACCCCCGGC	GTCGCCCTGC	CCGCCGCGCG	CTCCTCCGTG	420
	CGCCGGATGC	TCGCCCTTGC	TCTCGCCGGC	TGCGTCGGCC	CCGCCGTCTG	CGACCCCGTC	480
10	ATCCAGGCCG	ACTACTGCTC	TACCTCCTCA	ACCTTCAGGG	CCTGGCCCCC	TCCTACGCCG	540
	CCTACAGCCC	CCCCACCAAC	GACATCGCCG	CCCTGCTCGC	CGCCGTGTGC	ACCCGCCACC	600
	GCCTACGCTC	CGAGACCGCA	GCCGCCCTGC	ACTGGCTTGC	CATCCGGGCC	CCGGGCTCT	660
	GCCTGGAACC	GGAAG					

1473UP

	GATCTAGACG	GAGTTATTAT	GCCGCGGCAC	CTCCAGCGAC	TGATACTCAA	GAATGTGCGC	60
	TCCGTGCGGT	GGTGGAGGTT	CCGAGAGATC	CACGAAATTA	CGCTAGATCC	TAATACGTTT	120
	ACCAAGAAAC	AGGGCTTTGT	GGGAACATA	CACGGGCCAG	ATCAGGATCG	GGTGGAAAGTG	180
20	CGGCAGATAA	ACAGGGCTGT	CATGAGTCAG	GACACATACT	TCCACTTTGA	TAGTCTTTTG	240
	AGGGCCAGGT	TCCAGAACCT	CAACTACATC	AGTCTGCACA	ACGTTTCCGA	GGAAATTACT	300
	GGCATCATAG	TGCCTCACCG	ACTGTATTGC	AATGGCCGCA	TCAGCATTGC	AGGCTGCGTC	360
	GTGAAGGGGG	TTGTAATGAT	CTAAACTTGC	CCGGATATCC	CTATTGAGAA	ATAAACACAT	420
	GGGTGAAGTT	ATACATAGGC	GCGGAAGAAG	CCGCTTGAAT	ATTGATAGAC	CGAATAGTGC	480
	GATCAATGTA	ATTAAATAGA	TAGGTTACAG	CCCTACCGGG	CTGGCATTTG	GTCCGAGATT	540
25	GGTCTGCCTC	TACCAAGTCA	GCCAGTTACC	GGAGGGTGAA	GTAGTAGGAC	ATCATAACTC	600
	ATAAAAAACG	TTACATTCTG	TGTGCTTGTC	GGGAAATCAG	TAATCATGCA	GGTGCCTCGT	660
	GAAACCGAAG	GAAACGTAAT	GGCGTGGAAT	AAGTAAAAGA	TGC		

1474RP

	GATCGTTTCAG	TTTAATCAC	TGGGACGCAC	TGCCTTGCGG	TTCCAGCACT	GCCTGAAACT	60
	TGGCCAGGCG	TTGCATCACG	GCATTAAGCT	CCTGTACATC	GCGCTCGTGC	TGGGCCTCCA	120
	GCTGCAAGCG	CAGTTCAGCG	CTGATATGCT	TCCCGCCCGG	TGTAGACATC	TGCGGCAAGC	180
	TAGGGTAGCT	GCCCGACCGC	CGCAGCGGCG	AGCTGCGCGC	GCCCTTGTC	GCCGCTTCT	240
35	GTGCCCCCAT	TAGTGGCCGT	ATCATCGTCT	CGATCCCGCC	GTTTGCCATC	ATCGGTATGG	300
	GTGTGTTGTA	ATCGTCAATT	ACCGCACTCC	AGTCTCTGTC	CAGGTCCGTA	AAATACTTGT	360
	CTTTTTTGCC	GCCAGCGTGG	TTAGACCCGC	CCGTGGTGTT	GCTCCGAAGC	GGGCTCAAGT	420
	GCACGCCGCG	GTGGCTGCTG	CTGTGGCTCG	ACAGGGACGC	TGCATAGTCT	GCGACCTCCT	480
	GATGGCGCTA	ATATTCCCAT	CGCTATCTGC	AGGCTCCAGC	GATGGCGACG	CCAGCTGATT	540
	CGACTTCGCC	GATGACGGCG	TCTTCCACGA	CTTGATCAGC	GAGCCCAACA	GCGACGAAGA	600
40	TGATGAATTT	GACTTTTGGT	ACATTTCTTT	GGACCCATT	CCATTATGGG	GAACCGTCTT	660
	GATAGCCATC	ACAATGTATA	GCTCGCTACT	CTGAACCGCG	TGGCAACCAC	TGCAAC	

1474UP

	GATCGAATTC	TCACAGGCCA	GTACCTGCGT	ATTACAGGTT	TGCCATAGTA	TGATTAGAAC	60
	CGTAAAGCCC	AAGAATGCCA	GGGCCAAGAG	AGCTCTGGAG	AAAAAAGAGC	CGAAATTGAC	120
	GGAGAACGTG	AAGCAAGCGC	TTTTAATTCC	TGGCCAAACT	TCGAATAAGC	TCTTGACGGA	180
	TGTTATGGTG	GACCTTGGTG	GACTCAAGAA	GCCTGATGTG	AAGCGCTTCA	CGCGGAAGAA	240
	CGAGCTTCGT	CCGTTTGAGG	ATGCGTCGGG	TGTCGAATTT	CTCAGCGAGA	AGAATGACAG	300
	CTCGTTGGTG	GTGGTCTGCT	CCAACCTGAA	GAAGCGGCGC	AACAACCTGA	CATTCTAAG	360
50	GACGTTTGGG	TACAAGGTTT	ACGACATGAT	GGAGCTGCAG	ATTGCAGAGA	ACTACAAATT	420
	GCTAGCGGAC	TTCCGGAAGC	AGACGTTTGC	AGTGGGGTTG	AAACCGATGT	TTTCTTCCA	480
	AGGTGCGGCA	TTGCACTCTC	ACCCAGTATA	CAAGCACGTC	AAGTCTTTGT	TCCTCGACTT	540
	CTTCCGCGGT	GAGGTGACCA	AGCTGCAAGA	CGTTGCAGGG	CTTCAGCATG	TGATAGCAAT	600
	GACGATCCAG	AGGATGGCGA	GCCATTGCC	AACGTCCTTT	TCCGCGTCTA		660
	CAGGCTTAAG	ACGTACAGAA	GCAGCCAAGG	TGGTAAGAA			

1475RP

	GATCCGACCA	ACGAGCGCAT	CTGCAGCCAC	ATCGTTGATA	ACGTCACCAT	GATCGACGAA	60
	ACCGAGGAGG	ACCAGGGCGC	AAAGAAGGGC	GCCTTTGCTG	TTTGAAGCCG	GATCCTGCGG	120
5	CGTTCAACCG	TAAATAGTCT	TATAGCCAGC	ACGCCAGGCG	CCGGCCGGTT	CCTATGTAGT	180
	CCTGCAATCG	CTCGCTTGCT	AGCCGCACGA	TCACAGAATA	CAGCTACTTT	ATCCTAAATC	240
	CACTCCTATC	AAAATATCCA	GCCGCGACAT	TTGTTCTCTG	TCTCGTGGGA	TGTGGCGGTC	300
	GCCATTGTGG	AGTAGGGCCG	CAACTCGGAC	AGCGACCACA	GGTCGCCATC	ACAGCTGCCG	360
	GTCCCGTGTC	CGTCCCTGGA	ATCCTGCTCC	AAGCCCTTCT	GGTCAAAGCC	AGCCAAGCTC	420
	CCCTGTCTGA	TGGCGTCCCT	GACCGCTGCG	TCCAGCAAGT	CCTGGTATGG	ATCTGCGCCG	480
10	ACGCTTCTGG	GGGCCGCGAG	CGTTGTGTGA	AGCCAGTCGC	ACAGAGAGGG	TGTCGCTGTT	540
	AGCGCAACAG	ACGAGGCGCC	TGTGCCGGCC	GCATGGGCGG	CCGTGCCGAA	TGCGTGCGGG	600
	TTCATGTAAT	TGCTGCCCTG	GTCCGATGTG	TATTGTGTCT	GCGAACGGGA	AATCGGGGAC	660
	GCAGGAACGT	TCGCCTCGCC	GCCATCGTTC	TCGCAGCTCT	TCGGTTGCGG	CACCAAAGCC	720
	TCCTTCTGCA	GCATCCGCCC	TGAGCCGTT				

15

1475UP

	GATCTTCCGT	CCCGAGTACG	GTCGTCTCTT	CGAGATATNA	GCACGCAGCG	CAACTGTATC	60
	AAGCTAACCA	ACACAGTKCG	CACGCTTTTC	GAGCCGAGCT	CAGGCGCGAG	GTGAACCAGC	120
20	TCTGAGACAG	ACAGACGCCC	CTTGTTTACA	AGTAGCTCAA	TAACACGTCC	GGCTCGCTCG	180
	CCGAGGTGCG	ACCGCGCTAC	CTCTGTGTAC	AGGAAGGTTT	CAGGACTCAA	TGTCCTCATC	240
	TCCAGTGTGC	ATACCGGCAC	CTCCGCAGCA	CGCTCGTTTT	CGACTTGTCC	ACCTGCAGCA	300
	CCCATAGATC	CGTTTATTAT	GCACTACGAC	CTCGCCCTCA	CTCAAGCCCA	GGGCCGTCTG	360
	GAACGCAATA	CTCGCTAGTG	CTAGTTCCCA	CCTAATATCT	ATCTCATCGC	CCATCGAGCA	420
	GCGGGCCAGC	TAAAAAATCA	CCACTGCGCG	CTCACCACGC	ACGGTTCACT	AAATACGAAA	480
25	CAGTTGTTTC	TCACGTGTTG	CTCACGTGAT	TTTACCCGGC	CCGTATAATA	TCGGGTTCTC	540
	AGCGCGCCGA	GCCAAGGACA	CTTCTGTAT	CATAACAAAC	CAGCACAGGC	GGTAGGAGCT	600
	ATCGGCAGAG	TCCCAATACC	CTTGCTACTG	TTGACATTAG	GTGGTTCAAA	TGAGTGTCTG	660
	TTTAGTGGTT	ACCAAGAGTG	TGGCGACAGC	CACATTGGGG	ATCTACACCG	GGATGGTGGT	720
	AACGCGGCAG	TTGGTCTCTC					

30

1476RP

	GATCGTATCG	CTAACTGTAA	TATCGAAAGA	AGCACAGACA	TCCCGGAAAA	ATGACATCTC	60
	AGTGACACTC	TTCAACAAAT	CATAAGAAGA	AAAGTATGTG	ACTAATGCTT	GCAGAAAAAT	120
35	AAATTGCTCG	CTACCAGTAA	GCGATGTTAG	TAGCGTGCCA	TGGCATTCAA	TAAATCGTAA	180
	GAGATACGTG	GGTGGTATCT	CGATGCTTTT	GAGGTACGCA	AAAATTGGGC	CATATAAATC	240
	GATCTTGAAT	GGTAGCCTTT	TGCATATCGA	TTCTTCAAGA	AGTCTGTMTA	TAAAGTTCTTT	300
	ATCAGAAATG	TGCATAGACT	GATGCAGGAG	AGCACTTAGC	ACATGCCCTT	TATTCCTAGG	360
	ATAGAGCAAA	TATTCCTTGA	ACGAAGCTGG	GTCTTTCCGG	AAGTCAGGCT	TCATACCATA	420
	AAGGTACATG	TATACATTCC	TTGCGACATC	CATATCCTCA	ATACTGCTTT	CAAGCATCGC	480
40	AAGGTAAAAT	TCGTAGGAAA	ATTCGGGTAC	CCAGGAATGC	TGTTGAAATT	GCGTCCAGAG	540
	TTTGTATGCT	GTCCTTGGGT	GGTTCCTTGC	GACGGCCAAC	AGGAAGTTGG	GACAGAACCA	600
	GCGTCTGACA	GGGAATCAAG	ACCATCTGTT	GAGCGAATTT	GCGTGAGAAG	GCGATCAAGC	660
	AGCTTCACAG	CAACTTCCAG	GGAATCTAAG	CTGACAAGCC	CAGCTAC		

45

1476UP

	GATCTGAAAC	TAACAACAGC	AGTGCGTGAA	CCAAGAGGCA	TTGGAGGCGT	ATGACGGCGT	60
	GTCGCAAGGC	AAGTACACTA	TCGGCTTGGG	CCAGACCAAC	ATGAGCTTTG	TGAACGACCG	120
	CGAGGACATC	TACTCGATGT	GTTTGACCGC	GTGCTCGAAC	TTGATGAAGA	ACTACGATAT	180
50	CAAGCCGGAA	AGCATCGGCC	GCCTCGAGGT	GGGTACGGAG	ACGTTGCTTG	ACAAGTCCGA	240
	GTCGGTGAAG	TCTATTTTGA	TGCAGTTGTT	CGGCGAGAAC	ACCGACTTGG	AGGGTGTCTGA	300
	TACCGTGAAC	GCCTGCTATG	GCGGTACTAA	CGCGTTGTTT	AACTCCTTGA	ACTGGATTGA	360
	GTCCAGTTTC	TGGGACGGTC	GTGACGCAAT	CGTTGTTTGT	GGTGACATCG	CAATCTACGA	420
	CAAGGGTGCC	GCCCCGCCCA	CTGGCGGTGC	GGGAACGTGC	GCTCTCCTGA	TCGGTCCAGA	480
	CGCCCCAAT	GCTTTTGAAT	CTGTGCGTGG	CTCGTACATG	GAGCACGTCT	ACGACTTCTA	540
55	CAAGCCTGAC	TTCCGCAGTG	AGTATCCATA	CGTGGACGGC	CACCTTCTAC	TAACATGCTA	600
	CGTCAAGGGC	CGTCGACCAG	GCTTACCGCG	CCTTA			

1477RP

	GATCTTTGCG	AGGGACCACT	CTGCAATCCA	AGAAGACTAG	AGGAGTTGTC	TAGGACAACA	60
	AAGTTTATAA	GGAGACTTCT	GGTGTTTTAC	CGTCCTTTTC	GATACCGATT	CTCGACAGTA	120
5	TATTCAAAGG	CCAATAACGC	CAAACAATAC	GTTAAAGTTG	GCTGCCAGTT	TTTCAACACA	180
	CTACTACAAC	ATTATGAGGG	CATAAAGGTG	CTTCTAGATG	ATAGCAAAAT	CATTCCCTCAG	240
	CTCGCCAGTA	CTCTCTATAA	GGCTATGGAA	GGGCATATTT	TACCCAGTAA	GCTCTTCTCC	300
	TCTTGGGCTC	TCCAGAATAC	GTTATGTGGC	TCCTACTTCA	AATTCTCTCG	ATTGCTAATG	360
	AAATCTAAGG	AAGGAATCAA	TATATTAGAA	AAATGGAACA	TGTTCACTGT	CATCTATAAA	420
	ATGTTTCAGC	CATCACCCCT	AGCGGAAGAA	TATTTGTGTAC	TCATGCTTCC	AGAGTTGGAC	480
10	CTCTCTCACA	GCATACATTG	TAGGATTATT	TTTAGCAAAG	CGCTAGTCGA	CAGTAGAGAA	540
	GTCATAAGGA	TCAATGCTAC	CAGGGTTTTA	GGCGAAATGA	TCAGCAGCGT	CAAATTATCT	600
	GATCCCACTC	TGGAAGAGTT	CATGTTAAAC	CTGTTGGTCG	CTCAGTTGTA	CGATTTATCG	660
	AGTGAAGTGG	TAGCAGTGCG	CGACCAGATA	CTGTACCATT	ACTGTTTAA	TCAAAGTAT	

1477UP

	GATCCGAATG	TCCTTAGTCT	GTGGGAAGGA	ACCGATGGTG	GTGGTTGGGA	ATAGCGGGAG	60
	CTTGAAAATT	GGCTGCTGCT	CCTTGAGACG	CTCCCCGAAT	GGTGCGGCTC	TCGTGGATAG	120
	CTTCTCGTTC	AAACCAGCAA	CACGTCCTGG	ACAGCAGGAT	CGTTGGTGAT	CGCAGAGGCG	180
20	GCACGCGCAG	CAATCGAGTC	TGCATTGGCC	TTCAACTCAG	AGGAAAAGTC	TTCCGCCAGAA	240
	CGGTTCTTAG	CGAGGACAAC	AACCTCATGC	AGCTTCTGGG	TTGCCAAAAGA	GAACCAAGTCC	300
	TTGATCTCTG	GCTCCAAGGC	AGACTCGTTT	TCCAAGTCAA	CTGGAGTGTG	CAACAAGGAA	360
	GAGGACGTGG	CAACAATAAC	GCGGTCCCCT	CCTAGTTTCT	CAATTGCCTT	AGAAATAGTG	420
	GCAGCCGACT	TCGCGAAGTC	ATTCTTCCAG	ATGTTTCTAC	CGTCAACAAC	ACCTACAGAC	480
	AACGACTGGT	TTTCGCCAAC	GATCGCTAGA	ACGTCGTCCA	ACTGCTCTGG	GTTTCTCACC	540
25	AAGTCGAAAT	GTAGGCCAGC	CACCTGGAAG	TCCACAAGCG	CCTTCAAGTT	CGGAACGACT	600
	GTCCCGAAGT	AGGTGGTCAA	CACAATGTCT	AGAGACTTTT	CCGCACCTAT	ATGTTTCATA	660
	GCGGTCTTAA	ACGCAGACTG	TACGTCTCT	GCAAGATCTA	AGACCAACAC	AGGCTCATCC	720
	AGCTGA						

1478RP

	GATCATTATG	CATTTTATGA	TATACACTGC	TATCAAAGAC	GACCAGTCGG	TAGTGAATAC	60
	ACACCGGCTG	GCAGACACAA	CCAATGCCGA	GGATGAGGCT	AGTGAGGACG	AGTTAGAGGA	120
	GCTCGTTAGT	AGCACTGCAC	ACAGCGGCGA	TGCTACTAGC	GAGTGAAGAG	GTATTTTACC	180
35	TGAGCTTTGG	AATATATAGG	TAGGTGATGA	GCTTTACAAT	ACGTATTTCG	TAACAATGAA	240
	ATGCAGGAAC	TCTCAAGCT	CTTTAAGTTC	TGTAAAACG	GTATCAAAAA	CCGTTTTTCC	300
	AGCGCTGTCT	GCGTAAATGA	CCTGGATTAT	CGCATTGCAA	TAGTTGCTGC	TCCTCAAGGT	360
	CAGATCTATG	ACGCCTTTTG	CGCCGAGGCT	GGTACGCAGT	TCGCTGCGTG	GCATGCGGAG	420
	GATCTTGTCA	AATAGGCCTA	TCTGTTTGTT	TAGGCTAGCG	ATGTTTCGCCT	CACGAGCATG	480
	GAGCGTATCG	GGCTCGCTTC	GTTGTGGAAG	CAGCTCGATG	GACGAACCAG	GAACAATGTT	540
40	CAAGACGCAC	TCCGTAACAA	CTCTTTTAAC	CACCTGTAAG	TAGTTTCTAT	GCCTTATTCT	600
	ACCCAAAACA	GGTCTTAATA	GGAGAAGGTC	ACCATCAGCT	CTATATTTAT	GCTTGAAGT	660
	TGCTGGCTTG	AGGCC					

1478UP

	GATCTGAGTA	TCAAGATACC	ATGAGCGATT	CTTGCTCACT	CTTGACGGG	ACTGCCCCGC	60
	TTATCCAAGT	GCAGACAAGA	TGCAACATGC	ATACTGGCAG	ACCAGGCCCT	CTCGATCATC	120
	GAGTTGCTTT	AAGCAACATA	GTAGGAGGCT	TCGAAGGAGG	AGTTCTTCGG	CTACCTATGT	180
	AAGAGATGCA	GCGGATGGTT	ACTGCTGGTC	ACGTGCTAGA	ATCATATACC	ACGGAAAAGT	240
	GGATATGTTG	CTTGCCCTTT	AGATATGGCA	GTTTGTCCAC	CCTACTTGAC	ACAGCTGTAA	300
50	CAACGTTGAC	TAAGGATAAA	CAAGAGCTAC	TGTCAACGGG	CTATCCATAC	AATGACATCT	360
	GATCTAATGG	AGGTGGAATC	GGCCCATACA	CCGGATGTTT	ATAGCGCAAG	CAAGGACAAC	420
	GTTGACAAGT	TTGTGATCT	GCTTCGCCAG	GTCTCCAAGA	CTACTATAAC	ATTGGACTCC	480
	CGCTATGTGT	GGAAGTCTCT	TCCGCGAGCT	ATGTCTTTGC	GCAAGGAGCT	GCAGCAGCAG	540
	ACCTTCACCA	TCCTTATCAC	GCTCCTATAT	CCGGACGACT	CGGCATTCAA	GGTGCCATTG	600
	CTTCGTGTGG	TGAACAGAG	CTCAAAAGCA	GCCTCGAGGA	TGCGGAGGCA	TTCCAGGGCA	660
55	AGTACCCCGC	AGACTTTATC	AGCTGACTGC	TGACGGCAAG	ATTGAC		

1479RP

	GATCCGCTTA	CAGTAGCATT	GTCTCCGCAG	GTTCCTGCCC	TCAATTTTAT	CCCGGCCCTC	60
	GAAGAACTCC	AACTCGAAGA	GGAAAGTTCGT	GCGGCACTGG	CATAAATTGT	CTATGCCAG	120
5	CCCCGTGTTGG	CAGAACGCAT	GCTTGCACTC	TGCAAACTGC	TGCACCTCGA	ATTCCGCGAT	180
	CAAGAGCTGT	AGCTCCACGA	GCGCATCCTT	GGTAAGCCTG	CTGCCTCCGG	AGCGGTGCGG	240
	GCACCGTTTG	TCGATGCATT	CGTTGATCTC	CTCTGTTAGG	TTGCCGTCTG	TCGTCCGCCA	300
	ATTCTCGAAA	AGCGTCGGGC	GCACTATCTC	CCTGCCTGAA	GGCACCTTGT	TCTCCTTGTT	360
	CCGCTCGTCG	TTTTCGTAGG	GCGAGGTGAC	TGATGATGAA	TCATTTCATA	AGCTGTTTTT	420
	ATTCCGGAGG	CTGCGCTTGC	GCTGCACGTT	CACGTCAAAT	TGTTTCAACG	CCCTCTTATA	480
10	AGGTCTTTTC	TCCATTATTA	TAGCACTATG	CCAAGATCCA	GATGTGGCAA	TCTGGGATTA	540
	CTAGACCTGT	TGCGCCAGCA	TCGAGTTCTC	TTATATACAC	TGGCAGTTTG	TGTCTGACAC	600
	AAAGACGTAA	AATTGGGACT	ACGAAAAGGG	AGTCGCCAAA	CAAGTGGCAA	ACGTTGTAAA	660
	AGGATAGTGT	ATATTTATAC	TATTAGTAAT	TATGT			

1479UP

	GATCCGGGCA	TTACGGTGCC	CATCTACGAG	GAGGACATTG	TCGGGGACCA	GGGCGGGACG	60
	GACGTAGACG	GGCAGCCGCA	GAAGCTGGGT	TCGTACCGGG	CGCGGGCCGG	GCGCTTCTCG	120
	AACACGCTGT	CCAACCTGCT	TCCCAGTATC	AGCGCGAAGC	TGCACCACAA	CCGGAAGGGC	180
20	GGGACGGGGA	AAGTCGCGCC	GTCTGCTGCG	GACGCGGACG	CGGGAGCCGG	GTCTACCGTG	240
	GTTGCGGGAG	AGATGGCGGG	CAGCATCAGC	CCTCCGCAGG	ACCTACATAA	CGTGGTCAGC	300
	TTCCCGGAGC	CATACGGGCT	TGCACAGCCA	CGCACTTCGA	GCGAATCGTA	TACGTATGGT	360
	TCTGGATACA	GTGGCCACCT	GCAGCCACCA	GTCTCCAACC	CTGCTACGCG	GACTCGGAAT	420
	AATACTGTAT	CTTCGCAGAT	TACTTCGCTT	TCAAGCATGG	GCCAGCTGGG	AACCCCCAGC	480
	ACGAGCAACA	TCTGGACCAA	CAATGGCTCA	AGCCCGGCAG	ATCCAATCAG	CAACATGCTC	540
25	ACGACGCAGT	TCAACCCGAT	CCCCCTCCCC	GACTTTGGCC	AGTCGAACTA	CTACGACGTA	600
	ATCACGCAGC	AGCAGCCTCC	GCAGTCGACG	AACTCACTGA	ATGTGCCCTC	CGGGGGTAAT	660
	ATTTCTGGGA	AAAACGTACT	CGTTCTCAAT	CTAATGCTTC	TAGCATATAC	GCAGAT	

1480RP

	GATCCTCTGA	GGCGAGCCCT	ATCCCAAGTT	TATTCCAAC	TCTTGCCGAA	AGGTAACAAA	60
	CCGTTTATTT	ACATGAGTTT	ACACATAACA	CCGGAGAATG	TTGATGTTAA	TGTGCATCCT	120
	ACAAAGCGTG	AAGTACGATT	TTTGATGAA	GAAGAGCTAA	TAGAGCGCAT	TGGTAATTTG	180
	CTCCATGAGC	GGTTATCTCA	GCTGGATACT	TCGCGAACTT	TTAAACCCGG	CTCTTTTGACA	240
	CCTGGGAAAC	ATAGTTCAAC	TGTGTCTCTC	GCATTCCGGC	AATCAGCGAC	CCCCGCAAGT	300
35	ACACAACCAA	AGGCAAAACG	TGCAGAAAAC	ATGCTTGTCA	GGACTGATGG	TAGCCAAGCT	360
	AAAATTACTA	ATTATGTCTAG	AGCAAGTCAA	AGCTCTACCA	GCTCATCCTT	TTCCACTTCT	420
	TTAAGAAAGA	AATCACATGC	GGCAGCAAAGT	GATGAACTTG	GCAGCATTTG	CGAGGACTCC	480
	CAAGATACAG	CAACATCGAT	GACAACCTCT	ACACAAGAGC	CTAATCATAC	CAAGTCTAGA	540
	GCCATTTTAA	CCTTATTGAA	TAATGAGTAT	GAAGTCGTAC	AGCGGGAAAG	AACGGAAGTA	600
	AATCTCACCA	GCATCAAAAC	TCTAAAGCAG	GAAGTAGACG	AAGATATGCA	TAAGGGAATT	660
40	AACAAGTGTC	TTTGCAGATA	TGACCTATGT	TGGTGTCTGT	GATGCAACAA	GGCGACTTGC	720
	ATCTATACAG	CATGGTTTAA	AGTTATTT				

1480UP

	GATCGCGTCA	TGGGATACAT	AAACCACGGA	ATCAATGAAA	AGCTCGCTTA	CGAACAGTTT	60
	GGATCTGTAC	CGGAGAAGGG	CTACTATATT	CCTCCACAA	TATTTCTGGA	CGTTCCTCAG	120
	AGCTCGAGAC	TCTGCCGTGA	AGAGATATTC	GGCCCTGTGG	CCGTAGTTGC	GAAATTCAG	180
	GACTACGATG	AAGCTATTCT	TTACGCTAAT	GACACTAACT	ATGGGCTGGC	ATCCTGCGTT	240
	TTCATGAAA	ACATACGCGT	TGCGCACCGC	TTTGTCCTGT	ATGTCCAACT	TGGCACTGTG	300
	TGGGTAAATT	CCTCTAATGA	TGAGGAGGTG	GGAGTGCCCT	TTGGCGGGTT	CAAGATGAGC	360
50	GGTATCGGAA	GGGAGCTGGG	GAAGGCAGGC	CTGCAAACTT	ACCTCCAGAC	TAAAGCAGTA	420
	CACCTGAACT	TTGCTTAGAT	AGAGCAACTC	ATATATTAGA	ATCACTTCAT	ACATCAACTA	480
	TATATCATTA	TGTATATGAC	TATGCCAGAG	GTGTAGTGGA	ACCACTATTT	ATCACGTGAT	540
	AGGCGTTGCG	CGGTCAATCC	GCCAGTACCT	CGGTGTCAGA	ACGCGGGCGA	CACATTGAGC	600
	AGGTGCTATA	TACAGTTGTC	GAGGACAGTA	TGGCACGCAG	TACCATTATA	GCAAGTAAGC	660
55	CGTGTGCTGT	TTGCATAAAG	CGTAAGGTCA	AGTGCGACCG	GCTGGTTCCC	TGCACGAACT	720

GTGTCAA

1482RP

	GATCCATTCTG	TTAATATGGA	TTGTCTACAG	TGAGAGCAAA	GAGGGCGGGG	GATTTAAAGC	60
	ATGGTGGGGC	GACGCCTATT	TTAAATGGGG	GTGTGTTGCA	ACGGTMTTGG	CCGGGCTTCT	120
5	TGTCCTGCAT	AGTGAAAAGT	TCATTCGCCA	AAGAACGTAC	GAATTCCTTC	TGATACTGCA	180
	CAAGCTCTTC	AACATTGTCT	TTATTTGTATG	CATGTATATG	CACATCAAAA	CGCTGGGATG	240
	GCACGGCTGG	GTCTGGTCGA	TGGTTGCCAT	CTACTGCTTC	GAGCGTGTGG	CCCGGATAGC	300
	TCGCATTGTA	CTTGCTGGAG	GCATCAAGAA	GGCCACATTA	ACAGATGTTG	GGGATCGCGT	360
	GCTCAAGATG	ACAGTGGAGA	AGCCAAAGCA	TTTCAAATAT	TACCCGGGGG	CTTATGTTTT	420
	CGTTTATTTT	ATTAGTGGGA	AGGATGCTTG	GTTCTATCCA	TTCCAGTCGC	ACCCGTTTAC	480
10	CGTCCTTAAT	ACACCCAAGA	TCGATGGCGA	CAACCTGGTG	ATTTATTTCA	AAGTGCACAA	540
	GGGCGTGACG	CAGCAGCTGC	TAAACAGGAT	CTTCTATCC	GGGAAAGAGT	CCATCGAATA	600
	CAAGGTGCTT	CTAGAAGGGC	CCTATGGAAA	CACCATTCGG	CGGCTTGCTG	CTCCTGACCG	660
	GCGCTACGTG	GGCGCCAGCG	CAGGTCCTGG	CGTA			

1482UP

	GATCGCGCGG	TTCGGCGCGG	TGGCGCCAAA	GCTGAACCGG	TCCGCGCCGA	AGGATGCGAT	60
	GTGGCGGCTG	CGGAATTACT	CGATGAAGTG	CAATGAGGCC	AACGATGTGT	ATCTGCTGCT	120
	GAACGGGTCC	AGCCACGTAG	CCTGCGACGT	GAGCGACACA	CTTCTCGATT	GGTTGGCCAG	180
20	CACCGAGGAT	GAGCCGGTGA	TGGAGCTGGT	GCTGCGAGAG	TGGCTCGACG	TGAACCCGGC	240
	GCTGGAGTTC	CGCGTGTTCG	TACGAGGTGG	GGAGGTCTTG	GGCGCGTGCC	AGCGGGACCT	300
	GAACTACTAT	GACTACCTGA	AGCCGCTGGA	GGAGAAGCTG	AGGACGGCCA	TTGAAGACTT	360
	CGTGCACGAC	GTGATGCTGC	AGCGGCTCCC	GGACGACACC	TTTGTTCGGG	ACGTGTACAT	420
	CCCGCGGCCG	TTCAAAAAGG	TCTGGCTGAT	CGACGTGAAC	CCGTTCGCGC	GGGAGACGGA	480
	CCCGCTGCTG	TTTTTCATGA	ACGAGCTGTG	CACCTGAAGC	CCAACGCCGA	AGGGCACCGG	540
	AGCTGCGCCT	GGTTGCGGAA	AACTACATCG	GTGCTTCGCG	GGAAAACAAC	ATCGGTGCGT	600
25	TCGCAGCGAA	AGGAGCACTC	GGAACACCAG	GTACCTCTGG	ACGTGGTCTG	GGCAGGGCTC	660
	AATCCGCAAA	GCATGCAGAA	GCTGGTTGAG	A			

1483RP

	GATCCAAAAA	ACCTCTWAAG	GTACAGTCTC	TAATTGCTTC	CATSTCTTTT	TGAACATACA	60
5	TGGACCATGC	ATCCTCGTTC	TTGTTACGGA	CAGAATCCTG	YAATGCAGCA	ATGGCACTTG	120
	GCTCGTTGAC	GTGCTTATAA	CCACCATCCC	TCCAATGGTA	TTCCGCGGCT	TCAGGCAAGT	180
	TGACAGATCT	CTTAATCKTA	AACCTCGATG	GATAMCCCG	CTCGTGCAAT	GAAAAGGCGT	240
	CTTGSAGCAAT	GTATTCAAAG	GTAACACCCT	TAATTCTAGA	AGCGGTTCGG	GCAAAACACA	300
	AATCAATCAC	TGAGTTATCA	ATACCTAAAG	CTTCAAATAT	CTGCGCTCCC	TTGTAAGATG	360
	CCAGAGTAGA	GATACCCATC	TTCGACATGA	CTTTTAGTAT	ACCGCCGTCA	ATTGCTTCCT	420
10	TGTAATTATG	CAACAGTTGC	TCATCTGTAA	TATCAGAGTA	GTCATCGTTA	ACATTCCGAA	480
	CTAAACCTTC	GTTATTCAAT	CTGACCAGGG	TTTCCATCGC	TAAGTAAGGG	AAAATACCGT	540
	CACACCCATA	GCCAAGAAGA	ACACAGAACT	GGTGAAC TTC	G		

1483UP

15	GATCATCAGC	CCCGCTGCTC	CGCCGCAGTA	ACGGCTCCAC	GTCGTAGTCT	GGCGTCCCTG	60
	CTAGTCCGTG	GCTCATCGAG	AGGTCTCTTT	CCTCAGGCTC	GGAGTTGGCC	ACGGAGGCAC	120
	TTGAAAGACT	CTGTCTTCGA	TTCAATCCCC	CCGCCCCGTA	TTCCCTCGCCC	TCGTGGCGTG	180
	GCTTGGTGAG	GCCCTCCCGC	TGCAGATCTT	CAACGTCATC	CTTCAGCTCC	TGGAAGTTGG	240
20	CAAGAATTCC	GGTTTCCTGA	GAGACATAGA	ATTTGTCAAT	TCCGCTCAGC	TCCTTATCCA	300
	GCGCCGCAAT	GAATCTTTCG	ATGTAGCTCT	GTGCAAGCGG	CACCCGCTCG	GGGTCTCTGT	360
	CAAACGTCTC	ATGCTGGTAC	AGCTTGCTTT	TCTGCAAGTG	GTACACGAGC	TTCTTCAACT	420
	GCGAGTACGC	GATATACTTC	GACGAACACT	CAGGGACCGC	GTTGAATTGC	AGCGAATGTG	480
	AGAACTTCAT	CTTGGCTTCT	ATCGCCTAAC	GGCCCTGGTC	CGTCGCGATA	CAGGTCTGTC	540
	TCATTGAAAG	TACGCAGCGC	AGGCATAGGT	TTAATTCCAG	GCTCCCAGGA	GATTTTCGTG	600
25	CAAGAGGACG	TTTTAATTCT	CATTATATCA	CGTGCCCTGG	CTATATTTAT	AAAGTTGCCT	660
	CTAACGGG						

1484RP

30	GATCCTCTTC	TATAACTCAA	TTAACAATGT	TTCTCTCTGT	GGAGTCGTTT	CTGCATCTTC	60
	CGTAACCCTT	TCATTCTGAG	GTGTAGCCAT	TTTTATCTTC	TGCGCTGGAA	CACTCGGGAA	120
	TTCAAATTGA	GTTATTGGCA	CCTGTGCCTC	CTTCTCCTTG	TCCGGTATAC	TTTCTTCAGG	180
	AGGATAAAGA	GGCTCCGATG	GTGATGATAG	CAGTGTTTTC	TTAATATCCG	GTTCTGAGAC	240
	CTGCGGCTCA	AAGCCAGTTA	CTGATTGCGA	CTGGCGATTG	TCCATCGGCG	AACCTTGTGT	300
	GGTATGTAGG	ATTGCTGGAG	TGAGTTCTGC	AGCGTTGGAA	GAGCTCCTGG	CATAGCTACG	360
35	ATATGTTGGC	TCAGGTTGCG	TCCTCTCGTA	CGGAACAGTG	TTGGCTGGAG	AGGACTCTGG	420
	TTGTCCGTGC	ATTTGATAAG	TGTATGGATC	AGAAGGTAAG	TGTGGCATGG	AATATTGTGT	480
	CGAAAGATTA	ATATTCTCTA	ATTGTCTCTC	TAACATGGTG	TCATAAATGC	TCATTATATC	540
	CGAAATTTTG	GCATTCAATG	CTACCAAGGT	ATTATATTTG	TGAAACGTAT	CGTTAAGGGA	600
	ATGGTTTAAAC	CGAGGCCGAG	TTCCAAGGAC	CTTCTGGTAT	AGCATCTGCA	GCTGTGTATC	660
40	CTCTAACACG	GCATTCAATTG	GCTGACCCCT	CCTCTTCTTC	CACTAGG		

1484UP

45	GATCTCGGAG	AACGTGCTAC	AACACTCGTG	CCGGGTCAAG	CCGGACCCGA	AGCTGATCGA	60
	CCAGCAGCCG	GAGATGAACC	CCCAGCACAC	GCGGACTGCG	ATCGTGAACT	TTGCGTTCGA	120
	GCTGGCGCAG	AAGACGCGGG	TGACGAACGG	GATCTTTTTT	CACGCGGTGC	GGTTGTACGA	180
	CCGTTACTGC	TCGAAGCGCG	TGGTGCTACG	GGACCAGGCG	AAGCTGGTGA	TTGCGACCTG	240
	CCTGTGGCTG	GCGGCGAAAA	CGTGGGGGGG	GTGCAACCAC	ATCATCAACA	ACGTGACGGT	300
	GCTTACGGGT	GGGCGCTTCT	ACGGGCCCAA	CCCGCGGGCG	CGCATCCCGC	GTCTGTCCGA	360
	GCTGGTGAC	TACTGCGGGG	GGTCGAACGT	GTTTGACGAG	TCGATGTTCA	CGCAGATGGA	420
50	GCGCCACATC	CTGGACACGC	TGAGCTGGGA	CGTGACGAG	CCGATGGTGA	ACGACTACGT	480
	GCTCAACGTG	GACGAGAACT	GTTTGATACA	GTACGAGCTA	TACAAAAGGC	AGCTGGAGCA	540
	CAATCGGCAG	TACGCCAACA	AGCGCAACTC	GCAGGACAGC	AACGCGACCG	AGGAGGACGT	600
	GTCCGAGGAG	GACGAGGACC	TGGATAACAA	GATCCAGTTA	ATCAACATCA	AGAAGTTTCT	660
	GATAGACCTG	GCCGTCTGGC	AGTACGACCT	CTTGAAGTAT	GAGGTATTCC	GAGCTA	

1485RP

	GATCCCCGCG	TTATTAGCAC	GGTGCCTTAA	CCAACTGGGC	CAAGGAACCA	ATTACACTTA	60
5	AGATGCTATT	TGCAGATATT	TGTAGTCCAC	TCAAGTCAAC	ACGGGCATAT	TTTACTTTCT	120
	AATTCCTAAA	TTCTTAACTC	TAAGCCAAATC	TAAGTAGTTT	ATCCTATCAT	CACTTGATCC	180
	TTGCGTTTGT	TTGGTCTATA	ACCTTTAATT	GGGTAGTGCT	TATGGAAATA	TATATAATGA	240
	GATATTACAT	GGGTCCCATATA	TAACTTCCGT	ATGAGAGTTT	GGCCGAGTGG	TTTAAGGCGT	300
	CAGATTTAGG	TTATTCTCCT	AAAATCTCTG	ATATCTACGG	ATTCGCGGGT	TCGAATCCCG	360
	TAGCTCTCAT	TATTTTTTGT	ATATTGTCTT	TCTCAGGCAT	GTGACATTTT	GCATCATAAT	420
10	CATACCGAAG	ATATGGCTCC	CACCGTGACC	TGATACATTC	TCGCATCTGA	AGGCATGCAA	480
	TTTAATGCAA	CTGTGGCTGC	AGATGCTCTA	GGTAGGAACT	AGCACAACAT	CTAACAACATA	540
	GCCTGCCATA	TACAGCGCAA	TGACAGCGTC	TGAGTCGTTG	TGGCACCGAT	CATAAGCCAA	600
	TTCTGATTGT	CTGAAGACAG	GCTATGAGTC	TCCCACAGTC	CTCCTTGCTG	TCCCATACGC	660
	ATATAAATAC	CCTTAAAACT	CAATTAGCCG	GTATTTTATT	TGAGCTGCAG	AAGGTATCTT	720
	AACTCAGGTA	TAATATACTG	TAATGGGG				

1485UP

	GATCGGAGGT	AGTGTTTTTCG	GTGGGCACGG	AGCTGTAGCA	CGCGGGGTCC	AAGAGCGGCA	60
20	TTGTGCTGTG	TATGTTGGTG	ATGACCTCGA	TGAGCTGCTT	GCGGAGGTGC	TCCACGTAAAT	120
	CTTCGGTGCG	GAGCCACAT	TCCTTCGGGT	CGCGGAAAT	GGTTGCCAAG	TACTCGAGCT	180
	GCTGCGAGAC	CTTCTTGAT	TCTAGCTCGC	GGTTCAAGCA	GACGATGGCG	TTGCGCTGAA	240
	GGATCGTGAG	CTCGTCGAGC	ACGTCAACGA	GGTCGTCGAA	TTGTGGCACC	GCGCTCAGCG	300
	CGCCGTCGAT	CGCCTTAACA	AAGGCGCGCC	GGGCCCTTCAG	GGCCTGTCCA	CTAAAGAGAT	360
	CACTGCGCTC	GAAAATGCTG	ATTGCCTCGC	GCATGTACGG	CACAAGCTGG	CGCGACACGA	420
25	ACAGATAGCT	CATGTGCCGG	GAGTTCGACG	TCACGCTAAC	TGCCGAGTGC	TTGGTTGAGT	480
	GGCTGAAGGG	CCTACTGCCC	CGGTAGGGCG	ACCCGAGAAA	TGCGTCATCA	CCTCGTCTTC	540
	ATCTGGCTTG	AGATACAAAT	CCGAAAGCGG	CACGTTGCCT	GTCATCGCAG	AGTTGTTTGA	600
	CAAGAGCAGC	TCGTCTAGTC	GCTGCTGGAG	CTGGCCCACT	TTGCTTTTGA	GTAGTTCCAC	660
	TTCACTGCCC	TTTTTCGGATA	GCATGAGCTG	CAAGTGGCAG	TTCTCGTTTT	GCAACGCCAG	720
	CACCTCATCG	GGCGCGGTAC	CGCTGCTCTT	GCAGA			

1486RP

	GATCCTTCTT	GTACATTTCT	GATTTTAAACA	ATGTCTTCAT	AGCGTATATT	TTACCGGTAT	60
35	CTTTCTTCTG	CACCAGACGG	ACCTCACCGA	ATGCACCCTT	TCCTATGACT	TTAACAGTGT	120
	GGAAATCTTC	CAGGGATAGC	CGTGTCTTAC	GCAAGCGCAG	AAACTGCGAC	TCCTTTTAC	180
	CCAGTGAAGA	AAGCTGTCTG	TTCTTTCTCT	CTTCAGACCA	GCCATGAGAT	AATAGCTGGG	240
	ATTCAAGTTC	CACGCGTCTT	TGGTTGCGCT	CAATGGCATG	ATTGACAGAT	GATTGGTAGA	300
	AATTCTCGAC	TTTCAGCTTC	ACTGCAGCCG	CTTTTCTTGT	TGTGGATTGT	CTCAGTAGCT	360
	CTGGACGTCT	CTCGAAGTAC	ATATAGTTCC	CCACTCCCGA	GGTTTGCCGT	TGGCCCCAT	420
40	TGGGCGATTG	TGGAAC TGAA	GAGCACTGCA	GGGACTGACG	GGATAGCATA	GCGCCCTGCG	480
	AGCTCTGGTT	TCCCAC TAGC	GTCTGATCGC	CAAGGCTTCC	GTCTAGTAGT	CCAGGTAGAG	540
	CTGCAGGCTG	TAAAGGGGAC	TCCGACCCCC	CAAAC TGTTT	ATACGCAGAG	GAAGCAGGCT	600
	GCTGCCCACT	GTAGTCCGAG	CTGTTGGAGT	AGTGTCTTGG	TGAAGAATGG	CCGGGGGCAA	660
	GAGTAGTGTC	GTTACAGTTC	CGTAAAAGAG	TTGTTGTTCT	GGCTGTAAAT	GCTGGTCGCC	720
	GTAGGCGGG						

1486UP

	GATCAAAACA	GCATGTCTAA	GTCTGTTGCG	CGCTGCCCCG	AGTGCCACAC	GGAACTGCGT	60
50	AAGTGCCCTCA	TACAGCAGAA	CTACAGCATC	GTGATTTGCC	CGAACGAGCA	GTGCATGTAT	120
	CCGTTCAATG	AGGCCGAGGT	GATCCAGCAC	CTGGTGACAG	CAAGTGACAA	GGAAATCCTG	180
	GAGGTGCAA	AGGTGCGGCT	GAAAAACGAT	AATATCACAG	GCAGCGGAGG	CGCGCTCATG	240
	GAATAAGGAA	CCAACCGTGT	GCTATATACG	TGTACTGTCT	ATGTTAAGTA	GGTCTCGTGC	300
	GCCGCGAGCC	CTGCGTGGCT	AAAGCTTTAG	ATTGGAGTTG	TACATGATGT	CGCCATCGAC	360
	GCTGATGCTG	ACACTGAACT	CAAGGTCTTC	GTCGGTGGAT	ATGTCCCACG	TTTTATATAT	420
	CATCATCAAC	GCGAACACAT	TGCAAAATGCT	GCCGATGAAC	AACCCGTCGA	GGTAGTGCTT	480
55	GACGCCCTCG	CAGATCTCGT	ACGAGATGGT	ATACATCAAC	ACCTGCCCCAG	TAGTTATAAA	540
	AATGACACCC	AAAATGGTCTG	ACCCTGTCAAT	CCAGAAGTTG	GAGAGCACGA	AGATGGAGAC	600

CACGAGCTGG CACACCGAGT ACATTAGGAA CGCGAGGCCA TTGAGGCCGT ACATTACAAC
GAAAAGGCCG TCGTGTTTGT TTTCATGTCT GGGTGGTGCT GAATCCAATT TGGTGAAGG

660

1487RP

GATCGAGCGC GAGCCCATCA ACAACGAGGA GTTTGCCTAC CAGCAGGAGC TGATACGAAA 60
GCGGGACGAG GAGATAGCCA ACATCGAGCG TGGTATCGTT GAACTCAACG AGGTCTTCCA 120
AGACTTGGGG TCCATCGTGC AGCAGCAGAG CGAGCTGGTA GACCACATAG AAAACAACAT 180
ATACACTGCG GTAACCAAGCA CGAACCATGC ATCTAACGAA CTGTGCGCG CACTGAGATA 240
CCAGCGGCGT TCCAACAGGT GGTGCCTATA TCTGCTTCTC GCTCTGCTGG CATTGCTCTT 300
CCTGATCGGG GTGACAGTGC TTTAGAACAT CTCAACTAGT CTACTATGTA ACGCTTTAAT 360
ATACTACTGG CTGACCTACT CCTCCCGCAG TTCCACACAG TTCACGCAGC CGTCATCGCC 420
GCCGGTCACC AAAAGAACGC GCCCGTCTAA CGCCAGCCAT TTCACCACAT TGATCTCGTA 480
GACCGTGTGC GCGCAATCTA CGCGGGCTAC CACTTCCCAC CGGCCAGCCT GTACCTCTTT 540
GTATACGCCC AACACACCAT CCGAGCCAAC GCTCGCGATA AGCCCGTCCG CGCTCCAAC 600
TACGCTGTAC ACAGCCCGCG TATGCACGGC CGGCAGGACC GTCTCTTGGA TCCACTCTTT 660
GTCGAAGACG TCGGCGTCGT CAGTGAGGCA CCGCCAGATG CGC

1487UP

GATCCCAATA CTGGGACTTT ACTAATACCA GCCATGCGGG CAGCTCTGCA GCAGCTGGTA 60
ATGACAAGGA GGACAAGAAG AACAAATACT GGAACGCAGA CGCCGAGTAT CTGATCGAAG 120
AGGTGAAGAA AAACAAAAAG AGTGTAGTAA ACTACCTTGA ATCGAAGACG AACGACGAAA 180
TGACCCGCAA GGGTCTGATC CGGAACCTGC AACGATTTGC AAAGACAATT CTAATGAAGG 240
AAGGGTTTGA AAACCTGGAG GATATCGTCA CGCTTTCTCA TTTGGAAAAT AGACTGCTGG 300
TAGCCCTAAA ACTTAACGAG ACAAAATGAAT TTACCAAATT ATTGAAAGTC TATTGCATCA 360
GCCTAGCAGA AATGGGCTTC AAAAAATAGAT TGGATGATGT GCTGAGCTGG CTGTATAACG 420
ATGGAGAATA CAAGGTGTGC ACAATAGCTA ACGAGAAGCG GGAGGAACTG CTGAAGCAGA 480
TATTGGTTGC ATGTGCTGAT ATCCGGCAGG TCCAAAGAGT GACAACCAGT TACGCATCTG 540
CTCTTGGTCT TCTTGATGTA TCTTTATAAT TATTGCTAGT CTATAGACAA AGTTGGGAAT 600
CTGAATATAA CT

1488RP

GATCAACAAA TGATTTTCCT ATTTTCCGCG CACCGATCAA CGAGATATCA TAGGAATCAA 60
TGTTGCAGGC AAATCCCTCA CCGAGTATGA AGCTCTGGTA TGCTGTTGGC GTTGTTCCTT 120
TCATTAACTG CCGGTCCCTG GGCAGTTCCC TTAAGTTTGG ATGATCGAGA TATCCACAAT 180
TTGGCTCATT CATCGTCTCC AATCCAATGA TGCAGTTTTC TTGGAACAAC TCAGGCGCGT 240
TGTCCTGAAT GTACTTGTAG AACGTCATTA CGGCTTTCAA GAAGTGCCCC TGGAGGTAGT 300
CTTGAATATT TCTACCATTA ATTACACATT TAGGGGCAAA TAACTTGCCG CTAATAAAGA 360
GAGTGAACAT AGTCTGGCAG GCTAGGCGGT AATAGTTTGT GGACCAAATC ATTTCTGGAT 420
ACTGTGCTTT TTCCGCCTGC GTCTCTGAAT CGATATAGTA GTTGTGCAAT ATGGCAGCCT 480
CAGTAGCTAG GAACCTCTTC GGCTGAAAGC CTGCGCAATG CAACGTCCAT AATGGCGCTC 540
CTGATCCCCC AGAAAAGCGA GACCACAGT CCTGGTGGGG GTCTAGGTAT ACGTACATGC 600
CGCCCGCCTC CTTGATCTTT TTAAGCACCA TCACCGTGTA CTTCATGTAT TCCTCATCGT 660
ATATCCCTGG GCCGCCATGC TCCAAGGCCT CCCAGGTGAA CAAATAACGG ATACA

1488UP

GATCTCGTTT AAGCTGCTGG TGAAGTTTGC GAAGGGGTAT GAGCTTTCAC GACGCGAAAC 60
AAACCAGCTG AAGCGGTCTA TGGGCGATGT CTTCGGTGTG GTGCCCTTTT CTGCCTTCCT 120
GATTATTCCG TTTGCAGAGT TGTTGCTGCC CTTCGCGCTT AAGCTTTTCC CCAACATGCT 180
GCCATCCACA TATGTTTCTG GGACGGAGAG ACAACAGAAG AGAGTTAAGC TAGAGGAGGT 240
GCGGCGCAAG ACGTCCAAC TTTTGCAGGA GACACTAGAG GAGTCCTCAT TGATCAATTA 300
TAACTCGGTA GAAGGTTTCA AGAAGCGCAA AAAGTTTCTG AGCTTCTTCC AGAAGGTGAA 360
CTCCCTAAG GATGGCAAGA CCAGTGTITT TACCCATGAA GAGATTTTGT CCATCTCCAA 420
AATGTTCAAG AACGACACTG TGCTAGACAA TCTCTCCAGG CCGCAATTGG TTGCCATGGC 480
GAAGTATATG TCCTTGCGGC CTTTTGGCAC TGACAACATG CTTAGGTACC AAATCCGTTA 540
TAAATTGAAG AGCATCGTGG AAGACGATAA GAAGATAGAC TACGAAGGTG TTGAGTCACT 600
GAGTACAGAG GAGCTCTATA GTGCCGCCG TTCGCGCGGG ATCAAAGCCT TCGGTGTTTC 660
TAGGGAAGAT TTGGTGGAAA AAAT

1489RP

	GATCACGCCG	GAGCACGTGC	AATCATTGAA	CGAAAGCCCC	GGGTTGCTTG	CTTTGGCGAT	60
	GGAGAGTCAC	AGGGACCCAA	TTACCGGTGA	GAGTACATTG	GTGCGTTTTC	CCTACGTTGT	120
5	TCCGGGCGGT	CGTTTTAATG	AACTTTACGG	CTGGGACTCA	TACCTAATGG	CTTTGGGTCT	180
	TCTAGACTGT	AACAAAGTGG	ACATAGCACG	TGGGATGGTT	GAGCATTTCA	TCTTTGAGAT	240
	AGAGCATTAC	GGTAAAATAT	TGAACGCCAA	TAGGAGCTAC	TACCTCTGTC	GGTCACAACC	300
	CCCGTTCCTA	ACCGACATGG	CTTTGAAGGT	CTTCGAAAAG	TTCGGTGGTG	ACCAAAATCC	360
	TACCGCTGTG	GATTTCTTGA	AAAGAGCATT	CATCGCAGCC	ATTAAGGAAT	ACAAGAGTGT	420
	ATGGATGGCA	GAACCGCGGT	ACGACAAAAC	CACGGGTCTT	TCAATTTATC	ATCCAGATGG	480
10	TATCGGTTTC	CCACCAGAAA	CCGAGCCTGA	CCACTTTGAC	GCAATTTGCC	GGAAATTTGC	540
	GGAAAAGCAC	AATGTAACGA	TTCCGGAGTT	CAGGTGCATG	TACGATGCCG	GCGAAGTACA	600
	CGAGCCCGAA	CTAGATGAGT	TCTTTTTGCA	TGATCGTGCT	GTACGTGAGA	GTGGACATGA	660
	CACCTCTTAC	CGTCTAGAGA	ACGTCTGTGC	TTACTTAGCG	ACGATTGATT	TGAATCGTTA	720
	CTATACAA						

1489UP

	GATCGTAACA	TTGCCCAATA	GCTTGTTTTAG	CTCGTCATCG	TTTCTGATGG	CTAGCTGTAG	60
	ATGTCCTGGG	ATGATTCTGG	TCTTCTTGTT	GTCTCTGGCG	GCGTTACCGG	CCAACCTCTAG	120
20	ATGTTCCGGC	GCCAAGTATT	CTAGCACAGC	GGTTAGGTAC	ACAGGCGCGC	CCGACCCGAT	180
	TCTCTGTGCG	TAGTTGCCCT	TTCTGAGCAA	TCTGTGGACT	CTACCGACAG	GGAAAGTCAA	240
	ACCGGCCTTA	GCCGATCTCG	ACTGCGAAGC	CTTGGCGGCA	GAACCAGCTT	TACCTCCTTT	300
	ACCAGACATT	ATTTGTGTTG	TGTGTGTGTG	TGTGTGTTTA	GTGTGAAC TG	CGTGTGCTAT	360
	GAGAAAACAC	TACGCTGAAA	CTGCTAAATA	ATCCAGACAG	GTCCCCCCAC	CGCAAAGGAT	420
	CCACGCTATA	CTTCTCTCTA	CATATTTATA	CTTGTCTTTT	TGCCCTTCTAA	TECTCGATCG	480
25	TACGCGTCTG	ACGCTTCAAC	AGACCTTCAC	TAGACGCTCG	ACCTGTGCGG	GCTGGTTTTT	540
	TCCGATGACA	TGTCCGTGCT	GGTTTTTTTC	CGCTGAAAAG	GAAAGCGCGT	GGCTCCCAGC	600
	ACCAGAGCCG	TACTAGCTCT	TTCCGCGTTG	TGTCCTATGT	GCACGCGAAA	TTTCATAC TG	660
	TAGAGTGTGC	CATCAGCTTC	ACAGAGTACA	ACGGTAGG			

1490RP

	GATGACCTTC	CGATACTATG	CGAGCGCTTC	ACGACATCCA	AACTGAAGTC	GTTCGAGGAC	60
	CTGAGCCGCA	TCCAAACGTA	CGGGTTCCGC	GGAGAGGCAC	TTGCCAGCAT	TTCTCACATT	120
	GCGCGACTAC	ATGTGGTGAC	GAAAACGAAA	GAGAATCAGT	GTGCATGGAA	GGCTGTCTAC	180
35	GAGAATGGGG	TAATGGTGGG	GGAGCCGAAG	CCGACGGCAG	GCAAGGATGG	GACGACAATC	240
	CTCGTACAGG	ACCTCTTCTA	CAATGTGCCG	TCCAGGCTGC	GGGCGCTGCG	ATCTCCAAGC	300
	GAAGAGTTTG	CGAAAATAGT	GGATGTGGTC	GGCAAGTACG	CAATCCATTG	GGATGGTGTG	360
	GGATTTTTCGT	GTAAGAAGTT	TGGCGAAACA	CAGTACGCGT	TAAATGTACG	TGGGACTTCT	420
	TCAAAATCAG	ACAAGATACG	GGCTGTATTT	GGTGTCTCCG	TCGTTGCCAA	TTTAGTTGAG	480
	GTAGATATTT	CTGCAGACCC	TGAGCAGCGT	CTTACATCCA	GTTCGGGGCA	GATTACAAC T	540
40	CCAGACTTTA	ACAACAAGAA	GTCTATACCT	GCTGTGTTTT	TCATTAATAA	CCGCCTTGTT	600
	TCCTGTGATC	CTCTGAGGCG	AGCCCTATCC	CAAGTTTATC	CAACTTCTTG	CCGAAAGGTA	660
	ACAAACCGTT	TATTTACATG	AGTTTACACA	TAACACCGGA	GAATGTTGAT	GTTAATGTGC	720
	ATCTAC						

1490UP

	GATCTCAAAG	ACCCAGTACG	ATCGCGTCAT	GGGATACATA	AACCACGGAA	TCAATGAAAA	60
	GCTCGCTTAC	GAACAGTTTG	GATCTGTACC	GGAGAAGGGC	TACTATATTG	CTCCCACAAT	120
	ATTTCTGGAC	GTTCTCTAGA	GCTCGAGACT	CTGCCGTGAA	GAGATATTCT	GCCCTGTGGC	180
	CGTAGTTGCG	AAATTCAAGG	ACTACGATGA	AGCTATTCTG	TACGCTAATG	ACACTAACTA	240
50	TGGGCTGGCA	TCCTGCGTTT	TCATGAAAA	CATACGCGTT	GCGCACCGCT	TTGTCCGTGA	300
	TGTTCAATCT	GGGACTGTGT	GGGTTAATTC	CTCTAATGAT	GAGGAGGTGG	GAGTGCCTTT	360
	TGGCGGGTTC	AAGATGAGCG	GTATCGGAAG	GGAGCTGGGG	AAGGCAGGCC	TGCAAACTTA	420
	CCTCCAGACT	AAAGCAGTAC	ACCTGAACTT	TGCTTAGATA	GAGCAACTCA	TATATTAGAA	480
	TCATCTCATA	CATCAACTAT	ATATCATTAT	GTATATGACT	ATGCCAGAGG	TGTAGTGGAA	540
	CCACTATTTA	TCACGTGATA	GGCGTTGCGC	GGTCATCCCG	CCAGTACCTG	CGTTGCAGAA	600
55	CGCGGGCGAC	ACATTTCAGCA	GGTGCTATAT	ACAGTTGTCT	AGGACAGTAT	GGCACGCAGT	660

ACCATTATAG CAAGTAAGCC GTGTGCTGTT TGCATAAAGC GTAAGGTCAA GTGCGACCGG
CTGGTTCC

720

1491RP

GATCATCTCC GAATAGGTCT CGGGCACGAC GGACACAAAG CGCGCGTCCG AGTCACTGCC 60
GTCCTGCTGG GCGGGTGCGA AGAAGGAGAA GATGAACGAC CCCGACTTCG ACTTGTGCTC 120
CGACGCCAGC TCCTGGACGA CCGTGTCCAC CTTGACCTGC ACCAGCGTGC CAGGACACGA 180
CAGAAAGTCG TCCTTATTCT CAGACAGCTT GTTCACAGCT GTAGGCTGGT AGTCCACCAG 240
CGCGTCCGCC GCCGGCGTGG CCCCCTCTGG TCCACCACGG ATGTGCTCTG TGTACACGAC 300
CGTCGCGTCC ATGTGCAGGA TCGAGCCGAC CGGCACTGGC GCGCGGAAGG TGGTGGAGTC 360
CAGCGATACG AACCGCGGCA GAGAGTGCGA GATCGATGAC GCCGCGCAGT ACGCCAGCTC 420
AAATGTCTGC CGCATCAGGT AACCGCCGAA GATCATGTAC GAGTGTCCGT TCCGGTATTG 480
CGGCTGCATG AACATCGTCG ACTTCAGGTT CGTGTCTCTG ATCGACACCA CGCCGCGCGG 540
ACGCGCTCG CGCGGCGTCG CGCGCGACGC GCGCCACAAC CCGTGGATCA TCCGCGACTC 600
CTCCGCGGTA GCGGGGTTCC TCTCTAGACT CTCGCTCTGC GCCTGTAGCT TCTTCGCGCT 660
GTTGTGGCTC TCCGCGCGCC GGAACCTCAC CCACTCCTGC TGGTCTTGCG GTAGCA

1491UP

GATCTTGAAC AAAAAGTAGT TTGTTATTCT CCAGCTGCGC AGTCTCTTCC AGGGTTTTAC 60
TTCCGATGCT TATTAATACT GGTTCCTTAG ATGGTTCCTG ACTTTGGCTA TAGGCCATG 120
GTTCCGCGGA CTTGTGAAGG TATGCATTGA GAGTCCTCTG GGTAGAACGT GTGGTCTCTC 180
CTGTAGTTTT AGCAGCGGGC TTGGCCGGGA CTGGTACATC AGGCTGAGGT AAAATCTCGG 240
CTGGCGTTGC AGGTTCTATT TCTGTGGGTG GCTCTACACT AGGATCCAAT ACTTGGGCGC 300
TACTAGTATC GCATTCGTCA ATATCATCTA TGGCCACGAT GACAGAACTT TCTTCTTCCA 360
TAGGCTGGGA GCATGCAGTA ATCTCGGAAC ATGTGGTAGT ATTATGTAGG TGATCGTCTT 420
CGAATGTCCC AATCAGCTCC TGGCTGGGAA CGAGTTTGCG CCTTTTGACC TTCAACTCGG 480
AGTCTTGATG TGGGACTGGC AGTGACGGTA AAGATTTAGG CAGCATGAGC TCCTGTTCTG 540
TAAAATGCCC GTCCAGTTTC TCTGCTAAAC TTTGGAGGAC ATACTCTTCA TTGTGAAGCA 600
ATACAGTCCCT CTTATCCGGA GTCACATTCA CGTCTACAAA CTGCGGGGAG AGCTCAAAAT 660
TTAGAATAAT GACGGGATAC TGGACGTTGT TGAAGCTTCG ATATATGTCA TTGCAACACT 720
TCAGGACTT

1492RP

GATCTACTTC TCCAACAACG ACCTCCTGTG GTCCAATGGC TACCCCGTGA ACCGCTTTGG 60
CCAGGGCGCG TTCCGCATGC TTATCGAGCG CCTGTACGGC GAGCTCAACG CCGGCTACAG 120
CCTGGCCCAT ACCACCTAGC GCAAGCCCAA CCGCATTGCC TACGACTATG CTGCCCGCGT 180
CCTGGGCGCC TGGTCCGGC TCCAGACCGC ACAGCCGCCC GCCACGGTAT ACATGGTTGG 240
CGACAACCCC CACAGCGACA TAATAGGCGC ATACAACCTAC GGCTGGCGCA GCTGCTTGGT 300
GCGTAGCGGC GTCTATCGCG ATGGAGACAC GTTACCATGC CAACCGACCC TCGTCTGTGA 360
CTCCGTCTTG GACGCCGTAA CCGCCGCTCT CCAGCACTCT TCACATTAACT TTCTATACTT 420
TTACGTCTTC TATATACCG GCTCGTCCGT CCGCAGATGC CTAGATCTGA ATCTTCGCCA 480
CCACAGTTTG CTCCTGAGCC AACTTGTCTG CGTTGCGCCG GCGCATATGC TCCTTGACAG 540
TGCGGAGCCC GCGGCACGTA TGGTTTTCCA TCAGCCGGTG GCGCGAACAG AACTGGCCGT 600
CACAGAACTG

1492UP

GATCATGTTG GTGGCCTCCT GCGTCGGCTG CGGCGTGAAG TTGGGGTTTG ATTCCGCGAC 60
GAGCGCCTGC GTGAGCCGGT TGATCTGCCG CACGTTCCGC TCGAGCGCCG AGGCCTTGTA 120
CTCGTCGGCC GACACGTCGT CGTCTAGGGA GAGCTGCTTC GAATTGGAGT TATACTGGAG 180
CATTTGGTGAT CTGCCTGTCC GCAAGAGTGG TGGAAAGACGT GTTCTTTGGC CTGTTCCGCTG 240
AACAAAGCAC TCCGTGTTTT TCATGACCGG CCGTGGTCCCA GGAGCGCAGA CCGGAGAAGC 300
GAGCGTCAGG GCCGCGCGGC AGGGACGCTAG GCGGCTGCTC CCCACTATGT AATGCTGGAT 360
ATGAAGAACA GAAATACTAG ATAATATATT TGTATTAGAC AGTCTGCGG ACCGGCAGAG 420
GGCGGCGTTC ACAAGTCCGC ATCGTCTCTA TCCGGCAACG GCAATGCCGT AGCGCGCTCC 480
AGTCTCTGCT GGTACTGCTG CATCAACTGC TCGTCCCCCT GCACCTCTGG AGGCGCCTAG 540
GCAGGCGAGC CAC

1493RP

	GATCGAATAA	AGTAGGTTTG	GCGCTGACCG	GCATCACCCG	CGGACGTAGC	GGGAACAAGT	60
	TCCCCGTGTA	AATGTTTTCG	TAGTCGATGA	AGGTATTAGT	ATTTCATCTC	TCCAGCAAAG	120
5	ACAATTCATA	CTGTTGGGCG	GGCCGCGAAG	AGTTACCACT	GTATTCTGCC	AACGCTGCGA	180
	CGCTTCGGCA	ACTAGATTTC	AGTGCCCTCT	GGAGCTCTGA	AACATTATCT	AGGATGTTGA	240
	ACGGATCGAA	AGCGGTGTTC	CGGGGCATAG	CGGACATGGC	AGTTCTCAGA	TTCTGCATAG	300
	AACCGGCATA	TAGAGCCAGT	GCCTCCTGAT	GCTTGCCCTC	CTCTTGGTAA	AGGGGAGCGA	360
	GCCCGCGGCC	TACAAGCTGC	GCACGGTAAA	ACACCTTGAC	AAGCTTCAGA	TATGCAGTGA	420
	GCTCATCGTC	TGAGTAGACA	CCGGGTAGAC	CCATAGCCTC	CTCTGCATGG	GTGATTATGT	480
10	TGTTGATGAC	GTGGTTCAGC	TGCTTGTAAT	TGCTGAAGCG	AGCGGTCTCT	CGGCCTTCTT	540
	GCCATTTCGAC	CCACAGAGGT	TGCAACAGCG	CAACATCGCG	GCCCATCGTC	GCGCACAAGT	600
	AGTTGAATTG	GAGGTATGTG	AGCAATATCT	GGTCGTCTCT	TCCCTCATAG	TGCACACCTT	660
	CCTCTGTGCT	GCGCTCCATT	GAATGCTCTT	GGGCATCAAT	TGCCGCGTTC	CACTTCAGT	

1493UP

	GATCATACTT	ATCCACCGGT	CAAGCCAGGT	CTCAATCTTG	ACGATGAGCC	AGCCGGGCGG	60
	CGTCGCCATC	TGGAGCCAGC	GCTCCCCGAA	GCCAATTAGG	TACCCTAGAC	CAAGCCCGAT	120
	TAGGTGGCCG	ACAAAGCTGG	AGCCGGGCAT	TAGCAGCGTG	ACAAGTACCA	GGAACACCAG	180
20	CGGATATAT	AGGGTCGGCA	TCCTTCAGACT	TGCGAGCTCG	TAGTGGGGGC	GGAAGCCCGC	240
	CTCCTGCACT	GCGAAGTAGC	CACACAGCGT	AAAGCACCAC	CCGCTCGCCC	CGCCTACGTA	300
	AACGTTTGGG	TACAACAACA	TGCCAACTAA	GCAGTACACG	ACGCCCGTCA	CAATGGCCAG	360
	GAGGTTGAGC	GTGATTCCCG	TAAACACCGT	CCCGTGTGAC	GCTTCGAACA	TCGACAGCGG	420
	CACAAACAGC	GACATCAGAT	TCAACAGCAA	ATGGAAGATT	GACAGGTGCG	CCAGTGGATA	480
	GAGGGAGAGC	CGCGTCAGCT	GCAGCTTCCT	AAGCGCCCCC	GGATCCAACA	GGATCTTCTC	540
25	GTTGATTGGG	AACACCCAAT	TCAGCACATA	CACAAGCGTA	AGGGAACACC	GACAAGCCTG	600
	CAGTAAGAGC	GCCCGGCTTA	TGGACCCCGG	TCCGTAACAT	CGACTTCCAA	TCCATCTTGC	660
	TCAATCAAAG	TGGCAGTTTG	CTTGGGCGTG	GCAGTGGACT	ATGCCTCGCC	AGTTGCCCAT	720
	CAAAAC						

1494RP

	GATCTTCGTT	CGTGAAAACC	TTGCACGTCT	TCATGAGCTC	AAGAATTGCC	TCTGCATCTA	60
	TTCTGTCCGG	TTGGATTCTG	CCTTCCTTAT	AGTCCTGAAT	CATGCGCGCA	AAAGCGCGCG	120
	GCGTCCAGTC	ATGACGGGAT	CGGCCCTTAT	AGGACTTCCC	TGCAAGCCCG	ATGAGGCTCC	180
	GCCAGCCATT	TTCTTCAATA	ATATTGACAA	GTCTTTCGTT	TTCCAACACG	ACCTTGTTTCG	240
35	CGAGACTGTG	GAACGTGTTT	ACGTCTATCT	GCTCAAGTAT	TTCTACCCTT	TCCTCAGCAG	300
	ACCATCGCAA	GTTGCAATCT	GCCTCTTGGA	ATGTCTCCAT	AAGCTTTTCA	TTGATGTTAT	360
	CCACTGCTTT	ATTTGTCAAG	GAGAGGATTA	GTATTTTATT	AGGAGCTACA	ATCCCTTCGT	420
	AAACCAGGTT	GTAGACTTTA	TGCAGTAGTG	TCACGGTCTT	GCCAGACCCA	GGTCCCGCTA	480
	CCACATTGAC	AGTTGTACAA	GGCTCATATG	GATGTGTTAC	TACTCGTGAT	TGGGACGTCG	540
	TCAGTGCTTT	CATTTCATGA	TGATACATGC	TCGAGCGTCG	GCGAAGGAAA	TAAATTTCGTG	600
40	AATTTCCGTT	TTAAGATACT	CAAAAGAGAT	GAGATAACCG	CCCGCAAGGC	GGAGTAGAAT	660
	TACAGCAGCT	ATTGAATATA	TTTAGTTTAT	TTATCTGGCT	AGCTTAACCA	CTAGTGT	

1494UP

	GATCCTTTAG	GCCATCCTCT	CCAAATTACC	CGTGCTTGCC	TTCACTAGCT	CAGTCGGAAG	60
	AGCGTCAGTC	TCATAATCTG	AAGGTCGAGA	GTTTCGAACCT	CCCCTGGAGC	AAGTTTTTTG	120
	CTCCGGGAAA	TAAGTATTTG	GAGCTGGACT	GAAGCGCCAA	CCTATGCAGC	TTTGCTGGTG	180
	CGAAGTGTTT	ATTTCATGCT	GCGGACTATG	TCTATATATC	TTGCGCGTCT	TGTTCTTCTG	240
	CTGGCGAAGA	GGAAATGGAT	TCTTGGGCGT	GGTCTGCAAG	CTCTGCTAGC	TTCTTGGCGG	300
50	GCAGAAGCTG	TTCAAACGCC	TCTTTCCAGT	CATGGTTGTC	AAAGTATCTG	AGCATATCTT	360
	GGATAACGTG	GGTGGTGGTC	AGCACCTTCC	TGCCGCATAG	CTTGATGTAC	TCTCTATTTG	420
	GTAGGCGACG	AGTAGGAATG	CCCAGTTCTT	TGGCCTTATT	GTAACAGAGA	GCTTTGTGGC	480
	GGTTCTTGTG	CACAATGCCG	CCCCTATAT	ACGTCGTACC	GGGTTCAGC	GTCTCCAGCG	540
	TCTCATCAGT	ATCTGCAGTA	AGGTAAACTG	CGTTTCGTAGT	TGGAAGGGGG	GATTCTGCTG	600
	TGAAAT						

1495RP

	GATCGAATTA	GCGGGTTTTTA	ATGAAACATA	AGGAACGAGG	TCTAAATGCG	CAACATCCTT	60
	GAATGCAGTG	CCAAGATGTA	TGCCGTTCTT	GGTAAAGAAA	ATTGTACCAT	CGACATAGTT	120
5	AATGCCACAT	CCGATCACGT	CGTCTCGACC	ATAGGGCTTC	GAGTACGACT	TGAACAAAGA	180
	GCCGTCATTT	ATGTAACCGT	CCGACCCGTT	GTAAATGTAG	ACATCCTTAC	CAGTGCTACT	240
	CTGTTGCGAA	GTTGGCCTGG	AACCCCTCAA	AGGCCCTCTT	AATATGTTGG	AAGTTTGCCG	300
	GTTCAAGGCA	GAAAATTAC	CCGGGTCCCT	CGAAGGTGGA	TCGCTAGTGT	TTGCTTCGCC	360
	AGCATTTGAC	GCGACTTTTG	ACCAGTCCTT	AAATCCAATA	TTGATATTGC	AGGTTTGCCG	420
	TGACTGCGCG	CTGGTCACCG	ATAGTACCTT	AAATTCATAG	TAAAAGATAG	CCACTTTCTT	480
10	ATGATTAATA	CAAGCATTCG	CCCAGGTGGA	AGCCCACTGC	TGCTTCTGGT	TATTAAGTGA	540
	AGTCCGTAGC	CTATTATTTA	CAATAGGGCT	GTTGTCTATG	CCAGAGTAGA	GCTGCCAGTT	600
	GCGGTTAGGC	CGCAAGTTTG	TGAAACCGTC	TGTTGAGACC	AAAACGAGT	TGTTGCACTG	660
	TGTGGTCCAG	AGGTGGGGCA	AAAGGATACC	TATCGAGGAG	TATACGTCTG	AGAAA	

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1495UP

	GATCAGCCAA	CAGCTGAGTT	CTGATTTCGAT	GAGAGCTATT	AGTAAACTTT	TTGTGTTTAC	60
	GGTGCTGGTC	CTGGGATCGT	TACAGTACTA	CTGTGGACGC	TACGGCGCGT	GCCCCGCGCA	120
	GATTGCAGTG	ATAAGCCATT	ATACGTGGCC	TTGCACGTAC	GCGCCGGCAG	TACGGGATAA	180
20	ATTAGGGAAG	GCCAGCGAGT	GGTACGGGGC	CAATGCGGCT	CCGCATGTGT	CGGTGGCGAG	240
	CGGGTGGATG	CAAGGGAAGG	TGATGCCGCA	CCTGACGAAA	GTATCCCAGT	GGACGGAGAA	300
	GCATGTACAA	CCGCGGATGC	GGCAGGCTGG	CGCGGACGCG	ATAGTAACAG	CGCGCGTGGC	360
	ATGGAATGTC	GTACAGCAGT	ACCAGCGGCG	GCATGTGGTG	CCTCTGACAG	GGCGACTGCT	420
	GGCGAAGTGT	CCGTGTCTCG	AGAGGTGGGC	CGAACAAGCT	GCGCGCGGCT	GGCAGTGGCT	480
	CTGCAAGCAT	GCTCGGGCGC	TACCACAGCA	GTACAGCAGC	AGTATCCTGC	GTTTGTGGCG	540
25	CATATGGGGG	GCATATGGGA	GCCTTTGCAC	GGCGCCTACA	ACCGGATCTA	TCTGGACTTG	600
	GGCCGCCAG	TGCAGGAGAA	GACGTCCGAG	GACSCAGTGC	GGCGCCCGGG	GGGACTCAKT	660
	ACATCACATC	CACTATCACA	ATGACCATGA	CTCGTCTCGAT	GAATC		

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1496RP

	GATCGTTTTT	TGTCAAACCG	CAGTCGGGTT	CAAGGAGTAC	GTTGAATTTA	GCTCTTGCA	60
	TCAACAAGTC	TTTCCCAGTT	TCCACAATGT	TGTCGATAAT	GAAGGGTTTA	AAGTCTAGAA	120
	GCTCTTCTTG	CGTGAAGCCG	TTCTGGTGAA	GAATCTTCAG	TTGTTGCAGT	ACGGTCGATT	180
	TCCCGCTCTC	GCCAGAACCC	AACAACAAAA	CCTTGAGCGC	GCGATTGCTG	GCACTCGGTT	240
	GCCCCATTGA	CCCTGGTCCA	GCCACTGCCG	TTGTCTGCTG	ACTCGTCCCG	GATACCAACG	300
35	AGCGTTTCCT	GCCGCCCGCT	GTAGCGCCGG	ACGTGCTATG	ACTGGGTGAC	GTCTCAGGTT	360
	TGACTTCTGC	ACCGTAATCT	ACCCTCTTTG	CTCCTGTTTC	TACCTTCTGA	GAAGCACCAT	420
	GTCGTCTCTG	ACGCCGCTTT	TCCGCGTGTG	TTGCTGATCC	CTTGCTCTTC	GACGCGCACA	480
	ACCCCATTTAT	GTCGGGCTCT	ATATCCACCA	GTACTTGGAG	CACCTAGCG	CCTGGCTTTC	540
	TTTGAAATAT	TACCGTCCGG	GCAAAAGCCA	CTTATAGCGC	CTGATCAATG	GATTCCACTG	600
	CTAGAGGCTA	ATTAGGCTGC	CGCTTGTAC	TTGCGGGGCC	ATCACATTAT	ATTTCATAGCA	660
40	AAGTAGGTGC	CAACAGAAAA	AATCAGCCCC	CCTCCTTTAT	TGATCACGTG	AAGAAATCCA	720
	CATGAACAA	CACGTGAACA	CACATTTGG				

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1496UP

	GATCGAAGTC	AATGCCAGAC	TATCTCGTTC	TTCTGCATTG	GCGTCCAAGG	CAACAGGATA	60
	CCCCCTTGCC	TATAC TGCCG	CTAAGATTGC	TCTTGGGTAT	ACATTACCAG	AGTTGCCTAA	120
	TCCTGTTACC	AAGTCGACGG	TCCGCAACTT	TGAACCCCTA	CTGGACTACA	TTGTGGCCAA	180
	GGTTCCAAGA	TGGGATCTCT	CCAAATTTCA	ACACGTGGAT	AAGACTATTG	GGTCTGCCAT	240
	GAAGTCCGTA	GGTGAAGTGA	TGGCGATCGG	CCGGAATTTT	GAGGAAGCTT	TCCAAAAGGC	300
	TTTCCGTCAG	GTTGATCCAT	CTCTACTAGG	TTTCCAGGGC	TCTGACGAAT	TCCGAGACCT	360
50	AGATGAAGCC	TTGCAATTTT	CTACAGATAG	AAGGTGGTTG	GCTGTGGGAG	AAGCGCTAAT	420
	GAACAGAGGT	TACTCTGTGG	AACGTGTACA	CGAGCTTACG	AAAATTGATA	GATTTTTCTT	480
	GCACAAGTGT	ATGAATATTG	TCCGAATGCA	GAAGCAATTA	GAGACCCCTAG	GATCAATAAA	540
	TCCGCTAGAC	GAGGTTCTGT	TGCGGAAGGC	TAAAAAGCTC	GGCTTCTGTG	ACAAGCAGAT	600
	TGCACGGGCT	ATTTCAAGATG	ACCTCTCTGA	ATTGGATATT	AGAGCGCTCA	GAAAAAGCTT	660
55	TGGCATTTTT	CCATTTGTTA	AACGTATCGA	CACCATGGCG	GCAGAAATTC	CTGCGGTAAC	720

CAACTACTTG TATGTTACCT ATAATGCGGT CAAA

1497RP

	GATCATTTTGG	TCCTCTTCGC	CTCTACAAAC	TGTGAATATC	ATACTAGACC	TGAAGTCAGG	60
	TAGGGAGCAA	CCCAACCCCT	CGGTTCGCAGT	AGAGGCTGGC	AAATCCATTA	AAAAGACCGA	120
5	TTCGAATGGG	AACCTCTAAA	TTGAAACTAA	GCAATTTTCAT	GAACCTCTCGA	CAGTTCCCTGG	180
	TCCTTTCCAGT	ATTGACTATT	ATAACCTTAA	GAGAAGGTAT	CGAACTTACA	AATCTCTGAA	240
	AAGGGCGACT	ATTGAAGATA	TATTACATGT	TGTTGTTCGAC	AGAGATCTGG	CGGAGCGCAT	300
	TGTTACTCAT	ATCCAAAGAG	AATCTGAGCT	GCAACAATAT	GAGGAGGATG	GGAGGAATGA	360
	GGTATGAAAT	GTTCCCCATT	TGGATTAAGG	TATCAGGTGG	TCACGATATC	CACTATATGG	420
	TGCTATTAAC	GGCATGCAAA	GTGTAGAATT	AACCTAAAGA	ATATGTTATA	TATATATATT	480
10	ATAAACTACA	AACTAACGGA	CGCAATGAAA	TCTAAGTGTG	GCAAGGTTAG	CCTTAATACC	540
	GGTACTTGGA	TAAATCTCC	TTTTTCAAAT	GATACAAGCG	TCCCATTTC	AACGCCATGC	600
	CAGAATCACT	GGCTGGATTG	ATCATGATTG	TGATTGCGGT	TGCCTCAGTC	GGAAATAAAT	660
	TAGCAATACT	CATTATACCC	TTCCGCGACCT	CCAGCCGCTT	CTCTTGGGTA	GGTTCAAATG	720
	AGGCAATTTG	CATACTCTTT					

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1497UP

	GATCCTGTCA	CAGCGGGCGA	CGCCGCAGGC	CGCGTACGGC	GACCTGCAGG	ACGAGGTGAA	60
	GGTAGGAGGG	TCCGAGGCGG	CCTTTGGCGA	TCGGGCGTTG	TTCTGGGGCGA	TGGGCGGGCG	120
20	CGCGCCGGAG	GATGGCGACG	AGGGCCCA	ACTTGGTGCC	GGGGTGGCGC	CCATGGTGAC	180
	GCCGCACCTT	CCGATGGAAC	CCTCGCAGCC	GCACGCGCTG	CCACAGCAGG	CCCCCACTCC	240
	GCACCAGCCA	CAGCAGCCGG	CCCAGAAGCG	AATGCACATG	CTCCAACAGC	TGCACGAAGA	300
	GCAGAAGAAC	TATTCTTACG	TGGACCGCCA	ACCGTCAATT	ATGCAACAGC	AGCCACACAT	360
	GATGCAGCAA	CTGCCGCAAC	AACGGCCTCG	GATGCAGCAA	CTGCCGTTGC	AGGGCCAGTC	420
	CGAGACGCCG	AAGCCCGCAG	GCAGTTCTCC	AATGGTGGTG	CCCGTCAACC	ATAGGCAGCT	480
25	GTTGCAGAAC	CTCGACCCCA	GCATCCAGAA	AAGAGTATCA	CAGGATCTGA	ACAGCAAGCA	540
	GTATGAACTA	TTTGTGAAGT	CTTTTCATGGA	ACATTGTAAG	CGGTGTAATA	TTCCGTTTAA	600
	CCCAACCCTG	AGATAGGCGG	GACGCGGGTG	AACTTATTCA	TTTTATACAT	GTTGGTACAA	660
	AGAATGGGCG	GGGCAGATAA	TATCAGGAGG	CTGCAGCAAT	GGCGCGGCTT	GGCAGAAAAA	720

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1499RP

5 GATCAGCTTC ATCGATTACC CAGAATTCCG CTTCAACAGC AACGAGGCCA CCGAGATGCC 60
 CTTCGGCTAC GTACTGGACG CTGCTGGCAG GCCCATTTCTG CCATCAGGCA TGCTAGAGCT 120
 CATCAAAAAG GACTCCGAAC AGAGTCTGGA TGACCTACTT TAGGCTCGTT GAACAACAGC 180
 TTATAGATGA TGTATATATG CGCGTCGTCC GCCAGAGACT GGCATCGGAA GCCACGCAAC 240
 CTAAAGTCGA TAGAACTCTG TCAACAGAAT CAGTTCTTTT CCTCCTTCAG CATCTCGCCA 300
 AGCAGCTGCT CGAAATCGAT ATCATCAGAA GTGGTTTTTG CAGGAGCAGC TACGGCGGGC 360
 TGCTGCGACG CACGTCCTCT AGCCTTTGTAC AATGACACAC CCCCGAACAG CGTGAATAGC 420
 10 GTGCCAAGCA CCAAACATG AGGCTGAACC GGCTTTCCAA AGATGTTGTA AGCTTGACCC 480
 ATCGCTAATC ACCGAATCCG CTGCAGATAT GGGGTCTGAT GGTCTGGTGT GTAGCGGTGT 540
 GCATTTGTGA GCTCCTATTG GCGGAGGAG CAAGTCGATC TAGAGGGCTA CAATGAGGTG 600
 TTCGGGTGTT TGTCAAGGTA CGGAGGAGGT AGCACGTGAT CGTTCAAATA TCTGTACCGC 660
 CCCATGAACA TCTATTCCGT GCATTGGGTT TGGAGCACGG GCGATCATTG GAGACTAACA 720
 CTCACGAATT TTGCCTGGCG GA

1499UP

20 GATCGCAATG GAGAAGGTAA CGCTGCTACC GAAGGTTATC AGTGTTTTGA ATAAGGCGAA 60
 CCTTGACAGAC ACAATTTTGG ACAATAATTT GCTACAGAGT GTGCGGATCT GGCTTGAGCC 120
 ACTGCCGGAT GGATCCCTAC CATCCTTCGA GATACAGAAG TCTCTCTTTG CCGCGATTGA 180
 GAACCTCCCC ATAAAAACAG AGCACCTCAA GGAGAGCGGA CTGGGGAAGG TGGTCATATT 240
 TTACACCAAG TCTAAGCGTG TAGAACACAA GCTGGCCCGG CTAGCTGACC GGCTGGTTGC 300
 AGAATGGACG CGCCCTATTA TCGGCGCTTC CGATAACTAC CGGGACAAGC GTGTCCTGAA 360
 GATGGACTTC GACGTGGAGA AGCACCGTAA GAAAGCGGCA CTTGATTCTG CCAAATCTAA 420
 25 GAAACGGAGA AAGGCTGCAG TGGACGAGGA GAAACACAAG TCACTCTACG AGCTTGCCGC 480
 TGCGAAGCGG AACAGAGCCG CAGCGCTGTC GCAGACAACC ACCGATTACA AATACGCACC 540
 AGTCAGCAAT ATCTCGAACG TACAGACCGG GATCCGCACG GCAGGCGTGG GCTCCACGCT 600
 CAACAACAAC GATCTGTACA AGAGACTCAA CTCGAGACTT GCCAAGTCTA AACGGTCCAA 660
 GTAACCGCTG TGTACTTCAG CTAATAGTAT TATAATAACG TTTAATGATA CTGAAA

1500RP

35 GATCAGCTAA TGGCTGCTTG TCAAAGACCA AATCCTTCAC CCCTAGAACT TTTCCTAGAG 60
 CATCCATTCC GATAACCTAG GTCGCTTTGT GTCCTTAAAG AATATTGGTT TAATTTGCTT 120
 TCGCGGACGG AGTAAAGCGT TATGTAGCAT TTTTCAAAAG AGGCTTAATG GACACATCCC 180
 AGGATAGTAT GAATGAGAAA GTCCAATTCC TGGCACCATT GTGCTAGTTC TTATATTTAC 240
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 TTCTAAGTCT TCAGCTGATG GATTTCGCGC AAGGCGCCGC AGAGCTGCAG GTAGGTACCC 360
 ACACCTTCCA AAATCCTCAT GTGCGTGAAT CCTATTCTT TAATCATCTC CAGCCGCAGG 420
 GGTTCCTTAA TCTCTGTCAA GTTCTTCATG ACACGGAAAC ATGTAGTGAT TATGTCCACC 480
 GCCGAGTACC TTTGCCCCAC AATTCGCGTA AGTAATTGAG CGACTCATCA AGAGTAGCAG 540
 40 ATAGCAGCAT TTTCTTGATG ACCAGGGGAT GCGGCGAGTC CACTATCTTA AAAACGTTGT 600
 CGCCGTTTAC TAACGTGAAG CCCGCCACGG TGCTCTGCAG ATTGTTGATG GCCTGCCGCA 660
 TGTACCTTC CGCAGTGAAT ATCAGCGCCT CCAGACCATC ATTGGTGTTC TGTACGTTT

1500UP

45 GATCGCGACC CCCC GCGTCA CGGCAAGGCC CGCCAACCGC GAGGAGGAGA TCAATGGCTT 60
 TGACCTCGAG GCGCCGCCCC AAAAGAAGAC CAAAATACTA TAGTAGTACG TACATTGTAA 120
 TACATGCGCA AGACTTGCCG CCAGTTAGCC GCCCGCCTCC CAGGTCTTCA CCAGCGCCGT 180
 GCCGTCCGCA GACGTGCTCA GCAGCTGGCG GCTACCCTCC TTGTAGACGG TGTCAATGAC 240
 50 TGCGCCCGCA TGCAGAGACG CCAGCTCGTC GGACACCACT ACCTCGCTGG TCACGTCCAC 300
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 GCGTCCGGTG TTCCGCGCAG GGAGGGCAAA TCCCCGCCCT AGACGCTGTC CGGCCTGCTG 420
 GCCGTAAAAG CTCACACTGT CATCGAAGCC CAGCGCACAC ACCTCCTCTC CATGCGCGGA 480
 AGTGACAGC GAGGTCACAC CACTCCGGTG GCGGCTCTGC GTCTTCCACA CTGCGTCCG 540
 GCTGCGCCGC TGCTCGTAGG CTCGTACCAC TGGCTCAATC CCCGACGTGT ATACCCGCCC 600
 55 GGCCGAGACC GGGCAGACGG CGGCTGATAG CAGCGGAAAG TCGGTGGCCA CAAAAGCCGC 660
 CGGG

1501RP

	GATCTATTTA	AATATAACAT	ATTATTTATT	TCTTTTTTTA	AACATTTTAA	ATTTAATTAA	60
	TTATTTATTT	ATTTAATTAA	TTATTTTAT	TAGTTAAGAT	AATTTTATAA	CTTTAATTAG	120
5	AGAGCTAAGG	TACACACCCC	TAATGCTTTC	AGCATTCTTG	TGGTACCACT	CTAATTAAAG	180
	AGTTATTATA	TTAATGATAT	AATATGTAGA	TATTCAGTTT	TGAACGGAAG	ATATATGTCC	240
	CTAAAACATA	TGTTTTTACCA	ATTAAACTAT	ATCCACTAAC	TTTTATTATA	TAATTTTAATA	300
	ATTAAGAATA	TTTTAAGATT	GAATTAGAGG	AGTATTAAAT	GAATGAATAA	GAGGTGGTGA	360
	ATTTAATATA	AACCTCAATAG	ATGATGATTT	AGTAGTATTC	ATTAAGAAAA	TATTTATTTGA	420
	TTCAATAAAA	TCAGGTAGTT	TTATATAATT	AATAGATTTA	TTATTAACCT	TATTAGTTAA	480
10	ACCATTTATT	AATTGATCAT	AAATAATATA	AAGGAAATAAC	ATTAATGATA	TAATAGTTAT	540
	TATAGAACCA	AATGAAGATA	CTAAATTTCA	ACCTAGGAAT	AGATCAGGAT	AATCAGGAAT	600
	TCTTCTTGGT	ATACCATTAA	TACCTAAGAA	ATGCATAGGG	AAGAAAAATA	TATTAAGACC	660
	TAAGAAAAAT	AATCAGAAAT	GAATTGTGAT	AATTTT			

1501UP

	GATCAAAATA	AAATAGAAAT	TAGCTTAATG	GTAGAGCATT	CGTTTTTACAC	ACGAATAAAT	60
	TGAGTTCGAT	TTCTCAAAATTT	CTAAATAATA	ATTAACAATA	ATTTAAATTTT	GGGTAAAAAT	120
	TAATAAATAT	TAACGTATAT	AATAATTATA	TACTTTTATA	AATTACTCAA	TGTTATTAAAT	180
20	AAATTTATTT	CTTATCATTA	ATAATGATGT	ACCTACTCCA	TATAATATAT	ATTTTCAAGA	240
	TTCACTACTA	CCTCATCAAG	AAGGTATTTT	AGAATTACAT	GATAATATTA	TATTTCTATAT	300
	GTTACTTGTT	TTAGGTTTAG	TTTCTTGAAT	AATAATTATT	ATTATTAAAG	ATTATAAAAA	360
	TAATCCTATT	CTTTATAAAT	ATATTAAACA	TGGTCAAATA	ATTGAAATTA	TTTGAACATAT	420
	TTTACCAGCT	ATTATTTTAT	TAATAATTGC	ATTTCCATCA	TTTATTTTAT	TATATTTTATG	480
	TGATGAAGTT	ATTTCAACCAG	CTATAACTAT	TAAAGTTATT	GGTTTACAAT	GATATTGAAA	540
25	ATATGAATAC	TCAGATTTTA	TTAATGATAA	TGGTGAAACT	ATTGAATATG	AATCTTATAT	600
	AATTCCTGAA	GAATTATTAG	AAGAAGGTCA	ATTAAGAATG	TTAGATACTG	ATACTAGTAT	660
	TGTTATTCCG	GTGATACTC	ATGTAAGATT	TATTGTTACA	GCTCTAGATG	TTATTCATGA	720
	TT						

1502RP

	GATCGCTCCC	AACCCCTGCT	TGATCTCCAT	ACTCATCTGG	TTTTTCAGGT	AGCGCGGGTG	60
	GTTGAATACG	GACTTGTCGA	AAACGAACAC	ATAAGAGAAT	GACGCCACGA	TCAGGTACAG	120
	CAGCCAGCCA	AACACTGTCTG	TCACCAAAAA	CAGAGACAAG	CTCTGCCGCA	ACAGGCTGTA	180
35	TCGCGGCAGC	ACCGACCCGA	AAGCATGCGG	GCTAACCTCG	AACATAAACG	GTGCATACCC	240
	ATATACCTCC	AGCGGCCTCT	CAAGCGACCT	CCCGAACACG	CGCGTCGCAT	TTACCATCTG	300
	CTCCTTAATC	ATCGCCTGCT	GCCAAGTCCC	GCCCATCTTC	GGCGACAGCG	ATGCTGGCAG	360
	CAGTGTGGCA	TACACATAGT	CGAAGAAGTA	CGAGTCGCAA	AACTCGAGCA	CTAAATCCAT	420
	GGTCGGAGAA	CGCTATAGAC	TAGGAGAAAC	AATTTTAGCT	CTAGGTTGCC	TGCCTTCTAG	480
	CGTGATAACA	GATCCTTGCTA	CAGCTACTAA	AGCCCATCTG	CCGCTCTCCT	CTGGCTTTTT	540
40	GCACTTTTAT	ATGGTCCATC	CCGGCACTGA	CCTAACGTAC	GCGGCTCTAT	ACGACGCTAA	600
	AAAATCAAGT	TACGAATGCA	CTATACGAAT	GCGTTGAGCA	AGGAACGAAT	CCCTTTTGGA	660
	ACGACGATAT	CACGTGAACG	AAGCCGCAAC	GTTCCGGGTGC	CGGGCGCCTA		

1502UP

	GATCAAAAAAT	ATTCGACGCA	TTTGCCGCTC	TTTAGTGTAC	TTCCGGTTCAT	TATGGAGATG	60
	GCCAATTTTAC	ATCGGTATTT	TCGCCTTACT	CATAAGAGTA	TACAGTGCCA	ATTTCCGTGA	120
	ATTGAGGCCT	ATAAACATCT	GGTATGTCTT	ATCTTCAGTT	CTCTCTGGGG	ATTCGCCCAT	180
	CACCTGGGATT	CCATTCAGTT	TCAGGCTGCC	AGGAGTTGGA	ACTAAAACGT	GGTTTTTGGA	240
	TTCTCTTGAGA	TCTCTTTGCG	CATCAAGCCG	AAGATAGGCA	GCGGTGCTTT	TGTATGAATA	300
50	TGCGGTTGAG	GATGTCTCAC	TCCAGGTTGG	AAACCTATAT	TATGGTGCAA	TATATATTAA	360
	TGATAAGAGC	TTTCTCTGAC	TAACAGCAGT	AACTCTTAAT	TGAAGTATTT	GTTATTTCCA	420
	ATCTTCATAC	AGTATGTCAC	CCTGTTGTAT	TATAGATTTT	GTTTACGAAT	TGGATCGTGC	480
	TTTCGTGGCT	GCGAGGTCAG	AAGATCGATA	TAATAATATA	TATATTATTA	AATTATGGTA	540
	GGTAGGGAAT	TGCTATTTGT	GTCTAGTACT	CGATGCCTTA	TCTACAACCT	CTAGTTGCAA	600
	CACATGATAT	GCTGTGGACC	AAAACGCTAC	GGCGTTATTG	ATTTTATTCA	AGGTCAAGAT	660
55	CATATATTAG	CGTAATATCT	GTGGAGGTTT	CT			

1503RP

	GATCTTCGTA	TACATGTGCG	AAAGCTCCTC	CAAAATCTTT	TCGTCTCCAT	CATGAGAGGC	60
	TGCTACAGCT	TTTGAGCCGA	TAGAATTGGA	AATACCATTG	GAGATTGCTA	TTAGTAGGAA	120
5	GACAATATAA	GTACCATCTG	TCGATGGGGC	AGAGGCTTTA	TCAAGAAGGT	CCATCAGCTT	180
	GTTCTTTGGAT	ACAGCAGTCT	CATTTAATAA	TAATGCCTGC	TCACCACTGG	GCAAAAATTC	240
	AGAAACATTG	AGCAGTTCAG	AGAGTGAGTT	CGACTCAAAG	TTTTCGGTCA	TTGTCTCTAA	300
	CAAGACAAAA	ACAACGTCCT	TCCTGCTCTC	ATGAACATCA	TAAGCCTTGA	AAACCTCGAG	360
	CAAAATAGTA	TTGTCTCTGA	TCACGTTCAA	AAATACCTCT	AGAATTAATG	CCTTCCTCCA	420
	CAATAAAGTG	TCAGATTTAG	GAGACAGAGT	GTGGATTAAAT	AATGATAAAA	TAACTTCCAA	480
10	TTCCAATTCC	AGCAATGTCA	AATACTGAAC	CTTTATGAGA	AGTGAATAC	ATCTGGCGCT	540
	ACGAACCACA	ATTGCAAAAT	TTTTGGATGA	GGAAATGTAC	CTCAATAGCA	GCGGCACCGC	600
	CTTTGTTTCG	AACAGAAATA	ACAGATCTCG	GTGTGTCAAA	AATAATAATT	CATAGTTCAA	660
	TAAAACCAGT	TCTAGGAGCT	CTAATCCATA	CTCCTCATTT	ATGCAATTGC	TATCCA	

1503UP

	GATCTGCGCG	CTTCGAAGGG	AAAGGCGGGC	CCCAATCCCC	AGTCTATGTT	CAAGAGGGCG	60
	AACAGCAGGC	CGTCATGGCA	TTCAATAAGC	GAATGGGCAC	TCGAGCGTTG	GCACATCATG	120
	TGCTGGATAG	CATCATATAC	TACACAGACA	AGGTGGTGTT	GAAGGGGCTT	GGAAATTTGT	180
20	CCGCGAGCTT	ACCTTCCAAG	ACCTCCTCGG	CGACAAGCGT	CAGGGGTCGT	GTAAGGAAAC	240
	GCAATTGGTCT	CGAAGGCGCA	AATGATGTCT	TTGTATACCG	CACAAAAGAC	CTGGTATTCT	300
	ATAGTGATGA	AGATATACCC	AGAACCTAAC	TACTTGTGTC	GATATTTCTC	ACACCGCCTG	360
	GTGCGGAACC	GGGGGCATAC	ATTCTGTTTT	CACAAGAGGG	GTTGATGCAT	AAAACGCGCT	420
	TTCAAAAAGTG	GCAAGCGAGA	GCTGCCGACT	GTCTGTGCTT	TTGGTGCGGC	GACTGTAGGC	480
	AATGTGCCAT	CCCGTGCGCC	TTCTTTTACG	CGAGATCCAG	TCTCGCAAGC	CTGGCTGTAA	540
25	CCAGAACACT	CGGCTGAAGC	CCGCGACAGG	TCCCTCGTGG	ACCAGGCAGG	CAGCCTTGCA	600
	TCTGATAGGC	CGGATACTGG	GTATCTGCCA	AGAGAGG			

1504RP

	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTAAATAATA	AATCTATTAA	TTATATAAAA	60
30	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCAATTCAT	TTAATACTCC	TCTAATTCAA	180
	TCTTAAATAA	TTCTTAATTA	TTAAATTATA	TAATAAAAGT	TAGTGGATAT	AGTTTAATTG	240
	GTAAACATAA	TGTTTTAGGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATWAT	300
	ATCATTAAATA	TAATAACTCT	TTAATTAGAG	TGGTACCACA	AGAATGCTGA	AAGCATTAGG	360
35	GGTGTGTACC	TTAGCTCTCT	AATTAAGTTT	ATAAAATTAT	CTTAATAAAT	AAAAATAATT	420
	AATTAATAAA	ATAAATAATT	AATTAATTTT	AAAAATGTTA	AAAAAAGAAA	TAAATAATAT	480
	GTGATATTTA	AATAGATCAA	AATTTCAACA	ATTTCCATTT	CATTTAGTAC	TACCATCACC	540
	ATGACCAATT	GTTACATCAT	TTAGTTTATT	AGGTTTACTA	TTAACTTTAG	CTTTTACTAT	600
	ACATGGTATT	ATTGGTAATA	TTTATCCCTT	ATTATTATCT	TTATTAGTAG	TTTTATTACK	660
	AATAACTTTA	TGATTTAGAG	ATATTGTAGC	TGAACTTACT	TATTTAGG		

1504UP

	GATCTTAATT	TAAAATTTTA	ATTAACATT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
45	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAATGAAAA	TTAGTAAAT	120
	AAATAGAAAA	CCATAAGTTA	ATTGATTCAT	AAAGAAAAAT	GGAATTATTT	GTGGCATCTT	180
	AATTTTTATT	ATTTAATTGA	TTATTATCTA	TTTAACATAA	AACATTTTAA	AATGTTATAA	240
	AATAAATAAG	AAATTACTTA	TAGAATATTT	ATTAAATAGT	ATTTAATTTA	ATTTTAATAT	300
	TAAATATACC	ATTTTTATTA	ATAAATAGAT	TATTAAGTTT	ATTAATATTA	AGTGATATAT	360
	AATTTAATTT	ATATAAATTA	TTTAATTTAC	TTCAATTGATA	TATATAATTA	TTAAATGTAC	420
50	CTTTTCATAAT	ATTTATTTTT	ATTAGTCTAG	TAATATTTCT	ATTTAATAGT	CTACCCTTTA	480
	ATTGGATATT	ACTACCTACT	AAATATTTAC	CTAATAATAT	ATTATTAAGA	ATACTTAAAT	540
	CTAATAATTT	ATTATCTAAA	GTATATAAAT	TAATTAATATC	TTTTTTATTA	TTATTTAAAT	600
	TATTATTAAT	TAGTAAATTA	TATTTATTTA	TTTTAATTAA	CATAATTTTT	GATAATAATA	660
	TACATTATTA	AATGGTAATT	TATTAATAAT	TATCTTTAAT	GATTTAATGA	T	

1505RP

	GATCATCTTT	ATACCATTGG	CTCCTGTTCC	GTGTGCACCA	ACGTAATCAA	AAGCGTGTGC	60
	CCCCTCGCTA	CGCAGGAAGC	ACTAGAACTA	GCTGAGTAAA	GCAACGGTGA	AAGTCGATCC	120
5	CTGATATATA	TACGAAAACCA	GAGATACCTT	CATCACAAGG	ATCTTGTTCC	TCGTGGCCCA	180
	ATGGTCAACGG	CGTCTGGCTA	CGATAGTAGT	TACTTCTGAA	ACCAGAAGAT	TCCAGGTTTCG	240
	AGTCCTGGCG	GGGAAGTCCT	TATTTTTTTT	GTTCCCTCTT	GTTTCAGCTT	TTTGTCTTAA	300
	AAGGAGCAGA	AAGATTATTT	TGCAGCTCTC	TTTTGGCGCC	AGCTGGCAAA	AGCGAACTGT	360
	TGATTGACAA	GCTTTTAACC	TGTTATTAAC	CACCAGCAAC	CTCTCGAATT	TATCATGTCT	420
	CCATCAAATA	AGGATATTGC	TGCCCTAATT	GTTGACTTCC	TAACACGTC	CGCCAAAAC	480
10	GTAGGAGAGG	ATTACGAAGA	TTCCCTCAAA	GTGGCAATTG	ATTGTATCAC	TGAAGCTTTC	540
	GAACTTGGAC	CAGGCGAAGC	TGACACATTA	GTTTCCGAAA	AGTGTGGCGG	AAGAAGCCTC	600
	TTCTAGTTGC	TCACCACTGG	CATGGCTCAC	ACCTCAGATG	CAGGCGAACC	GAAGGTAGCC	660
	GCCGAAGAGT	TGAAGAAGGA	AGCTGAGGCC	TTGAAACTGG	AAGGTAACAG		

1505UP

	GATCAAGCTG	GACAAAAACT	TCCGTAACCTA	TCTGAACCTA	CTGGAAATGG	TTTCAAGGGTA	60
	CGTGGAGCTT	AACATGTATG	AAGATGTCTG	GCGAAAGCTC	GTTCAATTAA	ATGGGAAAAA	120
	TGAGCCTGAT	AGAGTTCCAG	GATATTATAT	TACGAGGTCT	ATCTCACTGA	ACCAGCTTTC	180
20	CACCACTATA	TATCCTGAGG	AGTTGGATAA	GTTTAATCTA	TCTCCTGTCA	CCGAGATAGA	240
	AAAGAGGGTC	GTGCAAGCCA	CTGAGTGTTT	CTCGAAACTA	ACATTAAACAA	ATAGCCATCA	300
	TGAAGAGGCG	CGCATACTGA	TATCAACCTT	TCAAAAAATTG	ACAACGAAAA	CTTCTCAAGC	360
	TACTTTGGAT	CCAAATGATG	ACGCAGATAC	CTTACTGGGT	TTGATGGTTG	TTGTAGTTTG	420
	TCGCGCACAA	GTTAAAAACT	TGAAGAGTCA	TCTAGATTAT	CTTAGAGAAT	TTGCGCAGAA	480
	TTCGGATGAC	GTAAAGTTTG	GGCTCCTTGG	GTATTTCGCTA	TCGACGCTCG	AAGCGGTGGT	540
25	CGGATATTTT	GATATTGGCG	GCAGCTCAAT	TAAACTTGAA	AGATTGATCA	CACCATGTCC	600
	AAGGAATAAG	ATCTTCTGGA	ACTTGATAGA	GCAAGGAATT	CCAATAAATT	TAAAGGAACA	660
	TGAAGAAGTC	CTCATATCGC	GCCTCCGTC	CTGTGAATCA	TTTGTCTTTT	ATGTT	

1506RP

	GATCTACCGG	TTCCGGTATCC	CCCTTTGAAA	ATAAATTCTT	TGTCTTTTGC	ATGCAACTAA	60
	AATGGGATGA	AGATGCAAGG	GATGTTATTT	TTAAGTATCT	CCATCTTTTG	GAGCTTTCTT	120
	CACAGGCTGT	AACATTAAACA	AGGTCAAAAA	CTCTACAGGT	TATAGAAAGG	CTTTGTCACA	180
	GAAAATTAGC	GTATACGAAG	TCGGATGAGT	CTATTTTCAG	CAGCATTAGT	GATATTCCGA	240
	TTGATGGACA	TGACTTGTC	ACCGCTGAAA	CATCTTCCGA	AGAGCAGCCG	AAATCTCAAT	300
35	CTTTGTTTCA	GCTATTTGAG	GAGAAAATAT	ACAGCCTAAA	CACCGACGCT	CCTTATATGA	360
	CTCCAGATGA	CCACTTTCATC	CAATTTGTGG	CTCCTCAAA	TCAATTGAGC	ACTAAGGAAT	420
	CGCCCGGAAC	GTGTGTGCTT	GTTACTGCCC	CTTCGATGAA	ACTGAAAATT	ATAGACTTTCG	480
	ATTCAAATAC	TTCCGGACAAT	GAGTATWATG	AAAATGTCCT	TATGACGAGG	TACACTGTCAG	540
	CATTGATTCA	AGCAAATGTA	TTTATCTTCC	AAGAAAGTGA	CTATAAAGTC	TTTGAGAACT	600
	CATTGTTTAA	TCCCAAAGGC	TACGGTGCTA	AAAGTACAGA	AAATTGGCAA	CCTTGGCTAG	660
40	GACTGGAAC	ATGTTTTTGA	CCGGAGCCCT	TGCAAACTAA	TACGGTTATT	AAAGAAATTC	720

1506UP

	GATCTCCCCA	TAAGCTCAAC	ATTTTCGATA	TAAGATATTT	GCGTCCCCGC	CCAAAACACG	60
	ACGGTCCGGT	CCAAACTCAA	TGCCCCATTT	GCAACAAACG	GCAAAATCATG	ATTCCATCTG	120
	TCCCTCTCGT	CAATCACCAG	ACTTAACAGT	AGTTGACGCT	TTGTCACTTG	GACTAGATAG	180
	TTGTTGGTAA	CGAAGTAGTA	TATCGTGCGG	CCAGCCAAGT	CGCTAAGGAT	GCCATCAACT	240
	TCGTGCGATT	CCATGTCTTC	TTCCGGAAGAA	AAATAAAGTA	CAAACGCCCT	GGTTATGGTC	300
	GCCCCATCAG	AAACCAATAAC	CAAAATAACCT	TTATAGCGTC	TATCATCGCC	ACAAAGTCTT	360
50	GTATACACTT	CTTCGGCAAC	GGCATCCAGT	CCTATGCTCC	ATATGCTGTT	AAAACGCAGG	420
	AAATTCTCGCA	GTTTAAATAAT	GTTTAAATAAT	TGGGCTACAT	GACCATTAGT	TGATATGTTA	480
	GACAGCACGG	ATGATGAGCA	AGAACATAAC	TCTTCTCTGA	TTGTACCTGA	AATGGCAGGA	540
	GTTTTATCGC	GGAAAGAGAT	CAGCTCTTCC	GCGTATGCAA	AGCTGGTATC	CTTGGTGTGT	600
	CTTCTAAGAA	TATTTGACAT	AGACTCCACA	TAGGCTCTGT	CATCGAGGAT	TGCAATGCCA	660
55	AGAGAGATCT	AGCGTTATCT	CAAACTACCTT	CCAAAACCTTA	TAATCTGTAA	TTT	

1507RP

	GATCGGCTGC	GCTCCAAACGA	TGGCAGCATT	GCTCCTAACG	GGGCTGAAAT	ATATGTCGGA	60
	CTCATGGCTG	ACTTTAGCGT	CGGCGGGCCA	GACACGTCCA	ATGCGCCCGA	GGGCTGTGTG	120
5	CTGCGGATCC	ACCTCGAAGG	ATGGCGGTGC	CAGATGGTTC	TAGACGGGAT	CCATATCCCG	180
	AACGCTATCA	ATTGGAGTGC	AGATGGCTCG	CAATTCTATC	TGACTGACTC	GCTAGCATTT	240
	ACCATATGGG	CGTGCCCGGT	AGTGGACGGT	AGCCCACAAC	TCCTCAAGAG	AACCCCATTC	300
	TACTGTACCA	AAAATACTGG	CAATGACTCA	CACACTTCGC	CGGAACCGGA	TGGTGGATTT	360
	GTGGACTGCT	TTACTGGGCA	CACTTTCGTG	GCCGTGTGGT	CCACTGGCAA	AGTCCGAGAA	420
	CTCGACAACG	CAGGCAGACT	ATTCGCTGCA	TATACACTAC	CGACGCCACG	AGTCAGCAGC	480
10	TGTTGTGCGG	GCCCCGCAGG	CGAACTGCTC	CTGTCCACGG	CGCACGCAGG	CGATTTCAAG	540
	ACTGGCGCAC	ACTCTGACGG	CGTCGGAGGC	AGCATTTTCA	GAGTGGTAAT	CCCCGGCCGC	600
	CGCGTTATCC	CAAGCCGCAT	CCCCGCGTCT	TGCGGAAGCA	TCCTTTAAAT	AATATTTACT	660
	TCTACACCCT	CTCGTCCCCT	CTACCGCCCA	GCTCATTGAT	GGGCCGT		

1507UP

	GATCGTACCA	GTATAATACT	GGGAATTGAC	GCGCGCAGCC	AAGGCGTCGT	AATCATCGTG	60
	TTGATAATTA	TGTCCATAGC	CATCCATWAT	GGAATTAGCA	TCAGCTATTT	GCTTACGGTG	120
	CTGACGAGCG	ACTGTTAATC	TCCATAGAGA	ATTCTCCTCA	ATAATTTCTG	AGACWGTCTT	180
20	CTTTTTTAAA	ATCGGCTTTG	GCCCCGGACG	TTGAGGGGGG	CCAGTGCTAC	CACCAGACTT	240
	CTTCTTCGAA	ACCCGCTTGG	AATTTTTCGT	ATCGGAACCA	TAGACAAGCT	CTTCCATATC	300
	CGCTACGGCA	TTGCGTGTCA	ATGTCTGAGC	GTGACCGCTA	TCACGTAATA	TAGGCCCATATA	360
	CAGCCATGTG	ACGTCCGAGT	CCTTGGACCA	GTTGACAACC	TCTGGGCTCA	CGGTGCGTAG	420
	ATTATTCCGG	GCTTTGGCCC	ACCTCCTCCA	GGATGCGTTC	TCGAGCCGCG	CCGCGTTCAC	480
	GAGGTCTCTG	TCTCCCTTCT	GTCTCTTCTT	CAGGATGATG	TACTTCCAGG	ACTGAGAGAT	540
25	GTCTCACTCA	GCCCAGTCGT	GCGAAAGGTA				

1508RP

	GATCCACAGG	CAAAATTTAT	GCATATAGCT	TGCTTATATT	TATGCGGTGG	ATTCTATATG	60
30	TCGCACGCTA	AATACTAATA	GCCGCCGGTA	AAAAGTAGTC	CTCGGCAAAC	TCGGTAACGG	120
	CAAGGTTCGGA	ATTATAGAAA	CGGGACTCAG	AAAAACTAAT	CCAGAGTAAT	TAAGGGACTC	180
	GGAAAGCGGA	GCCGGTTCTT	ACCGAAAACC	TCAACGGAAG	TATATGAAAA	AATTTATCCT	240
	GCAGATTATA	CCCATGCCCTG	TTTTATCCAA	GGTAGCCCAA	ATATATACTA	CAGGAAATGA	300
	GTGACTTTTC	ACTTCGAGAG	CCCAAATAAC	AATAATTTTA	GTAAAAATTTT	AGCATTGCTG	360
	CTACTCCAAC	TTTCCAATGA	ACACTTCTGA	AAGCGTAAAT	ATATAGCTAT	GCGGTTTGCC	420
35	TCCCAGGCTC	TAAC TACAAA	TTCCACCTTA	TGTGTGTTAT	TCAGGAAATG	CAGGGGAATA	480
	GTTGAATCAA	CGAAATAGCG	TTAATTTGCA	ACCGCCTTGT	ACGTGTATAA	AACCCACCCC	540
	CCTCCGAAAA	AGATGACTAT	CGTTATAAAC	TAAAAAACAT	CATCAAAAAA	GAAC TAAGTT	600
	ACTGAAAAGA	AAATGGTTTA	CCGTCTAGCA	GTGAATTTCA	GCAACCAGCC	CACATGGGTA	660
	ACCAATTTCC	GAATCTATCG	TTGCAGAATA	CT			

1508UP

	GATCTGGTAA	CGACTAAATA	AGAATCCTTA	CGCAGCAACG	CCGGCCGCGT	CTCGGCAGTG	60
	TAGTGTCTCT	CAAGTGCGCG	TCTGGCACTA	GTTAGGTCTT	GCAGGTGACC	TTTGAACCAG	120
45	TGCGGCTCGG	TAAGCACC GA	GATGGCGGAA	ACTCCCGCCT	CCGCATATGC	AAGCGCCTGT	180
	TCTGTGCAAA	GCGCCTCGCT	AATATTGCCA	CGCGACGGAG	ACGCACGTTT	TATCTCGGCT	240
	ACCACAGCCA	GCCGCGGGGC	GTCCCGCGCC	AGCCGCTCAT	GGAAAGTCCAC	CACGCCCCGC	300
	AGAACCCCCA	ATCGAAAGCT	CGCCTCCAGG	TCCGCCATAC	CAGTTCCCGG	CATAGCCATC	360
	TGCGCTGCCA	CGTCTCTCTG	TCGTTGAGCG	TATATCTCGC	TCAGCACAGA	GCCCGCGCCT	420
	GCCCGCAGCT	GGAGCTTGTC	GTTCTCAGCC	CACGTACCGC	CTTCCAGCGC	TAGCATGTTG	480
	CGCACCATTA	GCTGCCCCGTG	GTCCGTCAGA	ATCGACTCCG	GGTGGAAC TG	CACACCCTCC	540
50	ACGGTGTA CT	TGCGGTGCCG	CACGCCCCATA	ACCACGCCTG	TCTCCGTGCG	CGCCGTCAAC	600
	TCCAGCTCCG	CCGGGAACGT	TGACGCCAGT	CCAGCCAGCG	AGTGGTACCG	TGTCACTGCC	660
	ACGGCTGGGG	TACCCCTGGA	AGAACC GCGC	CCGTGCTGAC	GCAGCTCCGA	CGTTCT	

1509RP

	GATCCAGTTT	CTCTCGCATT	TTCTGAACGA	TGAGATATGA	GTCTAAGTTG	GCTAGATTAC	60
	TATATAGCCA	GTTGTTTCGCT	CGACGGGCCA	AAACCGAGAC	CGGTTCCCTC	CTTTGACAAG	120
5	AAGAATAATC	GCCATCTACT	TTGTTTGAAT	TCTTTAAACC	GTCTAACTCT	TGCAGTACCG	180
	TTTTTGGTAC	TACTATGCGA	TAGCTGTATT	TTGGGGCAAG	CACTCGTAGT	TCTTCAAGGA	240
	TATCCAGATG	TGATAACACA	TAATTAGTAT	CAACGACCAG	TGCAATATTA	TGCAAGTCTT	300
	GCCGCACTTC	AACCTGCGGC	TGAATTACTT	TTGCGAAAGT	CTCTTCGCCC	GGAATATCGA	360
	CTCTCTTGTC	AGGAATAGTC	TTAATGTTGT	TAATTTTCATG	GCTGTGATAT	TCGTCTATAT	420
	CCATCATCGC	TTTCAGCTTCG	TGTTCCCTTA	TAATTTCTGC	TTCAACCAAT	GCATCCAATT	480
10	CTGCAATGCT	ATATTTCTTA	TTAGAGTGCT	TAGGGTTCCA	AGTATGCGGC	GAGCTTATGG	540
	TATGCGTCTT	ATTCTGATGC	CTACGCTTGC	TCTTCCTCCC	ATGGTCCCTA	GACATCTCCT	600
	GTGTAGCTTG	GTGCATAGAC	TGTATATGAT	TGGACTCCAT	CGGAAC TAGT	GGCACGTTTA	660
	AAAGACATTA	ATTAGGTATC	ACCTCCATTA	ACGTACCTTT	GATATTTATT	ATATGA	

1509UP

	GATCTCGAGT	TTTCATGACGA	GTGCATGGAA	GATGTGTTTC	TAAATGCAAC	TAAGGTCCGT	60
	AAGGTCAAGT	AGGTGCAGTC	CTTTATCACT	CTAAAATTCC	CCTCTTCCTT	TGATGATGAG	120
	AACGCCACTA	CATCGATGCC	AAC TACAAGT	CACCATCAAG	ACTTAACAAC	TCAAGACGTA	180
20	CTTGGTGGAT	TGGTCGATGC	TATGGATGAT	AGGCGCGACC	AAGAAGACGA	TATCGATTTCG	240
	CAACAACCCC	TGGATGTA CT	TCTTTTGATC	GGCTGCGACA	GTCCAGTTTC	CAACTTGCCG	300
	CGGATTACGG	GGGTTGCTCG	TTCCGAGGAT	GCAGACGAAT	GGGATCTTGG	ACAGAGCAGT	360
	ATTACTCCTA	ACAAACTAGA	AATCCATTCG	GTCCAGACGC	CTACCACACA	CCGTGTGCGT	420
	GTGCTAGAAG	AAGAACAATC	GCCTTTGATC	ATGCTGCAGA	AGCGCAGACT	AGCCAGGAAT	480
	GGGTCAAGAA	CATTAGCCAC	AGCTACAATC	AACCATGACC	AGGAAC TGCA	ACTAGAAGTG	540
25	CCAGATAGAG	AAGCCGCTTC	GCCTGCCATT	GAACACGAGC	AAGCCACCTC		

1510RP

	GATCAGAATT	GGAAGGGATG	TTTGCCGGAA	GAAGTTCGTG	ATATCGAGGA	GCCCACTATA	60
30	CCCGTCATTG	GCCGGAAGTT	TTTCAAGTAC	GAATCTCCTA	TAAAGCACTT	GCTACCCCCC	120
	AACGCCACTA	TAAACGACCC	CATTCCCTCAG	CCAAC TGAGG	GAGCGGTCAA	TGCTCCACCA	180
	TTGGTTGGCG	CCGTTTATCT	ACGCCCAAAA	ATTAAAAAGG	ACGACTTAGG	TGAATATTCC	240
	ACCTCCGATG	ATTGTCCCGA	GTACATTATC	AGGCCTGGTG	ACCCGCCTGA	GGTTGGTAGA	300
	ATCGACCCAG	AAACGGGAAC	CATCATTACC	AATTCACAGA	CCGCCAGTGT	ACTACCGAAA	360
	ATGAATATGT	CTACACACG	TCTGTGCTCT	TTGAACCGCA	ACGGTAGCTA	CTCGAATT TG	420
35	ATAGGCCGTT	CCGGTAGCCC	AATTAACATG	ACCAGGTCCA	CCCAATACTT	CGCACCAGTT	480
	CCTAACGGCG	ATCTGAGAAA	TCTGCCAATC	GTGCAACAAA	TACCGAATAG	CACTATCCCA	540
	TCTGCGCAGT	CGCTTGCAAA	AGGCGGCATA	CAGGGGGACC	ATGGGCGGTT	CAATTAACGG	600
	TACTACCCCT	GCATACCAAC	CCCCTTCCAT	TATTAATAAC	CTAGCCGCCC	AGGCTAAGAC	660
	AAACAATACC	GTTCTTTGAA	ATATCTTTGGT	CGATACGCCC	GGTGCCCTACG	TTCTCCTATA	720
40	TCT						

1510UP

	GATCGCCGCT	ACTGTTCTAC	GACCACGCGC	GGGGGCTGAA	CCTGGCGATG	GGGTTCAAGC	60
45	TGGAGGACCC	GCACGCGCGG	GGGAACGAGC	GGCGCTACTG	CCTGGTGCTT	ACGGTGGACC	120
	TGCGAGAACC	GGCGCCGGCA	ATGGAGATCG	TGTGCGAGCA	CTGGAAGTTC	ATCTCGGGCG	180
	CGTTTCGAAA	CATGATCGAG	TACATCAAGC	AGCAGCGGCG	CGCGGAGCTG	CTGCGGGTGA	240
	TGCAGCAGGG	GCAGGTGCAG	GGCACATCGA	ACTTTTCGTC	CATGGTCAGC	GGCACCTATC	300
	TGCGCGGGAA	CAACCTGAAG	ATACCGAAGA	ACATCACGGA	GCTGACCAAC	GATAGACTGC	360
	TGTTTCGTCAG	GATACACAA	TGGAATGCAT	TTTACTTGGA	TAGACTGGGA	GGGCGAGTGG	420
50	ACTGAACCCT	TGGGGCGGTT	GCTGCGCGGC	AACAGTTGGA	AGATAGAAGA	CAGAAACGCC	480
	CGGGAAGCCG	AGGCCGGAGG	TGGGAGGCGT	TACATAACTT	ACATTCTTAA	CTAGATAGTG	540
	TTGCGCTGTA	CATCAAGTTC	AGACGTTAAG	GTTGAACGCG	GCATCGGTGA	TGTGTTTCGCT	600
	GAAGGGGGCC	AATGCAGATT	TGACGTCCTT	GTTGATGAAC	TTCTCCACCT	GCTGTGGGGC	660
55	CCTGCCACACA	AACGTGGAGG	GGTCCAGCAG	GGA			

1511RP

	GATCGACCAG	CTGGTGATGG	ATAGGCGGCT	GGTGCCGCTG	GGGCGCTTCG	TGCGGGGGCC	60
	CGATTTTGGG	CTGTTGTCGT	GGGTGAGGTG	GACGCTGCAC	AAGGTGGTGG	ACCTGTTCGTG	120
5	GAGGAGCCGG	GTGCGGGAGA	ACGGACGGTA	CCTGCGGAAC	TGCGCATACG	TGAACATGGA	180
	CGTGCTGGCG	GCGCGGCACG	GCGCGGTGGA	GGGGGCGCTG	GAAGAAAAGG	TGGTGGCGCG	240
	GGCGACGCGA	TATACGGACC	TTGTGTTCTC	GCGGGAGGAG	TTCTACGGCG	TGGTGCGGGA	300
	GAGCCTACGG	GGACGCGGGG	AGTACGATGT	GGTGCTGGCG	GACCTGGACA	AGCACCGCAA	360
	GGCGATTCTA	GTGGACGGAG	ACGTTGTGAA	GGTGGTGAAT	CCGGCGGTGC	GCGCGCTGGT	420
	GCAGCCGTTT	GGGCCTGACC	GCGTGACCGC	AAACGACCGC	CACATCGCAG	AGTTCAAGGG	480
10	CTCGCTGCGA	TTGGTGGAGC	GGCAGGTCCA	AGCGATCCAC	GGGCACGTCG	AAGAGACAAC	540
	CCGGGCGCTG	CGTTGGCGCC	GTCCCAGCGG	GCGCCGCACC	CGATGTGCAG	CGGCGGTACC	600
	TGCGGATGAA	CAACTCGCGC	AGGCCAGCCT	GTCTCGCGCG	CTCAACCAGT	TTACGAACCT	660
	AATGGAGATC	AAGGAC					

1511UP

	GATCTTGCCC	CACGGCCCCGT	CGCTCAAGTT	CCCCCGTCC	GCCACAAACG	CCCGGAACAT	60
	GCCGTCAATC	ACGCTGGGCT	CGCTCCACGG	CGTCTCCCA	GTCAGCAGCA	CAAAACACAAG	120
	CACTCCCGCA	GACCAGATGT	CCGCCGTGTC	CGCGTGGTAC	GCCCCGCTCGC	CCACCACCTC	180
	CGGCGCCAGG	TACGGCAGCG	TCCCCCGCCG	GTCGCGCGCC	AGCCGCGCGG	TCCCGTCCGG	240
20	CCGCGGAAC	CGCGTCGCCA	GCCCGAAGTC	CGCCACCTTC	AGGTTCCTCC	CCCGGTCCAG	300
	CAGCATGTTT	TCCGGCTTGA	TGTCCCGGTG	CGCCACGCGC	CACGCTCGT	GCAGGTGTGT	360
	CAGCGCCCGC	ACCAGCTGCT	GGTAGTAGAA	CGCGCCACCT	CCGAGTCCAC	CCCCACGTCC	420
	GGCTCGATCT	TGTGGAAGAG	GTCGCCCCCG	TCCGCCAGCT	CCATCGCGAT	CCATAGGTAC	480
	TCACGTGACA	CATTGCAGTC	CAGCACCCTC	ACCACATGTC	GGTGCCCGCG	CACCGCGTCT	540
	GCAGCACACC	TCGCGCGTCA	GATCCTCGTC	CGTCATCCCT	CGCGCTTTGC	AGCGCTCGAA	600
25	GTGCACGAAC	TTCACAGCCA	CTATCGTCTG	CGGGTCTGCG	CGCAACGAAG	CGGTTTTGAA	660
	GAACGCAACG	TGCCCTGCCC	AATCGTCTCC	CGAAGCTCTA	ATTCTTTAAT	CTCCGGGAAG	720
	CA						

1512RP

	GATCTTGACT	GGAAGGATGA	GGAGCAAACC	CCCGACAGCG	GAGAAACTGC	TATTTGCGTG	60
	TCTACACCGG	GCTCTACTCG	CATCCAAGTT	TAGCTATACC	TGCACTATTA	CTAGATATCT	120
	AATGCCTACC	ATATGTTGTG	ATGACACTGA	CATTACGCCT	TTAACCACCT	CAGCTTATTA	180
	AAAGATTCCA	GACATACAGA	AAAAATCCGG	TGTTAAAAGT	TATACATATA	CACCATTTTA	240
35	CCATATATAC	TGTAGACGAG	TAGAGCTACT	AAGCAGCCCA	AGAAACACTA	CCATATTCAT	300
	AATGGCGAGC	CTAAGGACTT	TCGATGCGTT	CCGTATGTGC	CGAGGGTTAT	AGTGACACAA	360
	CGATGCAGTA	CTAACAGTCG	TAGCAAAAAC	CGACCAGCAG	CACGTCCGTC	GGTCATCTCG	420
	CGGGGGCATT	ATGTCCATAA	TGATGTACCT	GTTCTCTGTC	TTTATCGCGT	GGGGGGAATT	480
	TGGCAGCTAC	TTTGGGGGCT	ATTTGGACGA	ACAGTACATC	ATCGACCCCG	AACTGCGGCA	540
	GACAACGCAG	ATTAACATGG	ACGTGATGGT	GCAAATGCCG	TGCAAATACC	TCGACGTCAA	600
	GGCAACTGAT	ATTACCAGGG	ACATTAAACGA	CGTGTGGAAG	AGACTGGTGT	TCAAGAAAT	660
40	CCCTTCTTC	GTACCGTACG	GCACCACATT	TGACTCTGTT	AATGAGGGTC	CGCACCCCGG	720
	AC						

1512UP

	GATCGAATGG	CATCCCATTC	ATCCGATGAG	GACGCTATGT	TAAATAAATA	TTATCTATAT	60
	ACTCTAAATA	CTATATGGTT	TCATCCGTTG	TACCCGATT	TAGAGATGCG	CGTTCTCGTC	120
	TCCAAGCTTT	AACTCGTGTG	GCTGACGATT	CTACATAACG	TGTATTGACC	AGGCTGAGCA	180
	GTAACGTTAG	CAACTTGGAC	ACCAGTTATG	AGTACCGATT	TCGACAGAAT	TTATTATAAC	240
	CAGTCAAAGG	TGAGCGGTTC	CTTCCGTTTG	GGCGAAGGTG	GCCTGGGATG	GAAGGCTTCC	300
	GCCACTGGCG	GGTCCGCTGC	CATGCAAAAC	AACGAACCAA	TTCTCTTGAC	TGCGGACGAA	360
50	CTGGCTTCCG	TGCAATGGAG	TAGAGGGTGC	CGTGGCTACG	AACTAAAGAT	TAACACGAAG	420
	AACAAGGGCG	TGGTGCAGTT	GGACGGTTTC	TCGCAGGAAG	ATTTACATTT	GTAAAGAAG	480
	GATCTCCAGC	GCAGATTCAA	CGTGACGTTG	GAACACAAGG	ACCCTCGCT	TCGGGGATGG	540
	AATTGGGGTA	CTACCGATCT	GACAAGAAAC	GAGCTGATCT	TCTCCCTAAA	CGGGAAACCA	600
	ACTTTTCAAA	TACCATATTC	GCATATCAGT	AACACGAATT	TAACATCAAA	GAACGAAGTT	660

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GCGCTGGAAT TCGACTTGC

1513RP

	GATCAACTGT	TGCTCCAGTT	GCTCCTTGGA	CTTGGTTCTC	AATTCAAAAAG	CTTTAACACC	60
	GGCCTGAGAT	GAGATGTTAG	TACTCCGCGC	ACCTATCAAG	CTTGGAATGA	CATTGCTGGC	120
5	AACCTGCGGG	GCCGCATCTA	CCCCTCGGCT	ACCGCTCGCT	GGCTAACCCG	GTATGCGCTG	180
	CTGTGCGCA	CTTCTGTCCC	ACGGATTAA	GCCTCTAACG	GTCACCTCGA	TACCCAACGA	240
	AAAGCTGCAT	GCCATCATCC	CACGCTATAC	ACCGCTGAC	ACATACCATT	ATGATTGATT	300
	TTGCTGTATT	TTGCACTAAG	AGCCACTCCA	AATGAACTGC	CTCTTCTGTT	GAAGATGTTG	360
	GCCTGCTGTG	GAAACCGACT	GTGCTCCGCT	CGGTGTGCGC	GAGCGAGTCT	GTCCGACCGAC	420
	GCAGAATCTT	CAGCTATACA	ACCCACACAC	CTCCGAATGT	ACGGATGCAA	CAGTCAAACA	480
10	CAATTACAA	TCACGTGACC	TACAGGTGAA	ATTAAAGATT	TCGGCAGATC	GCAAAGTGAG	540
	CGCCAAAGGC	GCGACGGAAC	ACCGGAGCGG	GTACACGATG	GGTGGGACTT	CTTACACTAT	600
	ATATCGATGG	TAACAGTGCA	CGCACAAAAA	AAAGTAGTAT	ACTAGGGTCT	ACGAGACTTC	660
	GCTAGTTCAT	TTACAGCCTA	ACCTAAAGAT	TAATTATGCC	AAGACAGTGA	TTGGAAGGAG	720
	A						

1513UP

	GATCTTTAAA	ATTTGGCAAG	AACAGCCAAC	ACTCCCGTCA	AAATAAAGAG	CAAAGCGCCT	60
	CCACACCTCT	ACGAATCAGG	TCCGAAAGGC	GATCTTGCAA	TGACGAGCAA	GGTTACAAAG	120
20	AAAGTTAGAG	AGTCGCACAG	TGCATGTGAC	GACCAGCAGC	ATAGTTCTCG	GGCTCGCGGC	180
	ACTGCAGCAG	AGGGAGCGCC	TAGTAACGTG	GTTCAAACCGT	CCCTCGGTGA	TTTGAAGAAA	240
	CTCGCAGAA	ACACACTCTC	CACCCCTACG	TCGAACGAGT	GCATTAAATA	ACGGCTGCGG	300
	TCCACGAACG	TGCAGGAGGT	GAAGCTGGGG	GGACTGCACT	TTCTGTTTAA	CAAGACGCTA	360
	CTACTGTGTC	TTTACATGGC	ATATGCGTTC	TACCGATACT	TCCAATACCA	GTACAACAGG	420
	CTGCGTATCA	AACACTGAA	TCTGGCCTAC	TCGCCGTCCA	ATACCCCGCA	GCTGATCAGA	480
25	CAGGACGTGC	TAAAGTTGCA	GAAGTCCCT	AAGCGGCTGG	CAGCGATTTT	GGCATACAAG	540
	TCTGAAGGGG	AGGTGCGCGG	TGGCGTCCAC	GGCTTGATAA	ACGACGGAAG	CAACGTANTA	600
	TGCTGGACTG	TGCTGCGGGG	CATCAAGCAC	CTGTGCGTTT	ATGATCATGA	CGGGGTGCTC	660
	AAGGCCAACG	TGCACCAGTT	CCGCCAGGGC	GTGTACGATA	CCTGGCGCGC	TACTACGGCC	720
	CAACAA						

1514RP

	GATCTGCGTG	TATATTTGGA	TGTATATGGA	CTTCACACTT	TCGGAAGCAA	TGGAACTCGA	60
	AAGCTGGTTG	ACCACCTCTG	TGTATTCTCG	TAGTCTTTCT	GAAACGACGG	TAAGAAAATT	120
35	AACCTTGAGC	GGCGATAGGG	AAGATGCAAC	TTTAAATTTC	TCTACTTGGT	TACTCAAATA	180
	CTGATATAAT	AATGCAGCCT	CAAATATGCT	GTGGAAAACA	CCACTTTTCG	CGTTCCGGAAC	240
	ATTGGGTGGG	ATTTTCGATA	CCTGATTGGA	GATCGGGAAC	AAACTCGACG	TAGTAGCCAG	300
	TAACGTGTAG	GAAATATACT	TTAAACGTC	GGCCTCGGGC	ACCATGTTGC	TGTAGTATGG	360
	GTTAGACAGA	TATGCCAATG	GAGTATCGTG	CTGCTGCGGC	CGCTTGGGGA	CCGGGCGCGC	420
	GTATGCAGAG	GTTACCGCCG	ACCGGCGCTC	TGAAAGCCGC	TCCACATTCT	CGAACGACTC	480
40	TGCATAGACA	CTAACCGCCC	TGCACGGCGT	CATCAGCGAG	TTGTGCCGTT	GCAGCGTGGC	540
	GTTTCGTAAGA	TATCCAGACG	CGGTGCGCCT	GTGTCCGAAG	GGCGTGCTCT	CCTGCGGCAC	600
	GCTGTTTCAGC	ACCGTCAGGT	ACTTCAGCAC	CTGCTCCTTG	CTACCGAAAC	TCTCCAGCAC	660
	TTTCACGAAC	ATCTCGAACT	TCCCCCACTG	CTGCGTCTGC	TCCGGCGTCC	GCACCATCTC	720
	CGCCCGGTAC	ATGCTC					

1514UP

	GATCTCCACC	GCGTCCAGCA	CCACGATCCG	GTCACCGTCC	CACCGCGTCA	TCGCCACTGT	60
	CCGCGCGACG	CTTTCGAAAA	CCGCCCGTCC	CTCCGCCGTC	GCAGCCCCCTC	CCCCGCTGTC	120
50	GTGCGTCCGG	TGCTCGGCCCT	CCCGCGACCG	CAGCGTCGCC	ACCACCCGCT	CTATATTAC	180
	GCCCGCGGGC	CTCAGCGTGT	CGCGCTTGAT	GCCAGGGCTG	GTGGGTTTCT	CTCCCACCAC	240
	CTCCAGGCTC	TTGATAAACG	TCGTCTTAAT	CACCTTAAAG	CTCGCAGTAT	GGCCCTTGCG	300
	CCCACATAGT	AGCGTCAGCG	TATGGTTTCC	CGAATCGTAC	GCGTATATCT	TGCCCTGTGT	360
	TACACCGTCG	AGGACGTTGG	TCACCCGCAC	CTTGAATCCA	AGGATATGTT	CCAAGTTGAT	420
	GCTCATTCTG	CTCACTTCCA	AGCCCAACA	GCTATCCTGG	CCACCTTAGA	ATGCCACGCC	480
55	TGCTCCCCGT	CCACTGGCTG	ACTCCCAATC	GTTTCAGTTG	CGGTGTGGGT	ATTTTTTTGA	540
	AGTGCGCTC	TAGCGATGAA	GTAAGATTTT	CTATGTATTA	CTATGTGCA	CAAAGGTTAG	600

EP 0 866 129 A2

TTCCAATAGT GCTTGCAACT ATCAGGTGCT GTGGAGTCC CAAGCAGACG AGTTGCTGAT
AGTGGAGCCG ATAGAGAATC CGATAAAGAT TATTCCCGAA AATCTAAGGA CAGGTGG

660

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1515RP

	GATCCTTCGC	CGCGTGGTCA	AAGCCCGGAT	AGGATATCAC	AGGGCACTGT	GCAAAGGTAT	60
	CGCATATTGT	TTCCATGAGC	GTTTCGCCCT	TCGGTCTCTT	CGCCGGCTTC	CACTTGCACG	120
5	TGGCCGCCAG	GAGCTTACAG	AGCTGCAGAT	AGTTATTACT	GTCAAACGTC	CAGGGTGCCC	180
	CGCGCCGTTT	GTGCGCCGCA	GCAGCATCCG	CGAAGTGGTC	CAGGTGCGCC	CGCGACAGAT	240
	GGAACCCGTC	CATGGGCACC	ACCTCAGCTA	TATTGACCGA	TGACGCTGGA	TCCAGGGCTT	300
	CGCTCGCGAT	GCGCACCGAA	TTGGGGAGCC	CGCCGCGCCC	GAAGATAACT	GCGGTCCCAT	360
	CCCCATCGTA	GAACCTTGTGT	GGCTTGAACC	CCGGGTCTCT	CACGTGCGCG	AAGAACCCCC	420
	GTGCGCGCTC	CTCGACCAGG	GCGCCTGACG	CAACCGGCAC	AGTCTCGTCC	AGGCTTTCCG	480
10	CAGCAATGCC	CGCGGAAATC	CTCAATCCAC	CCCTTCGTGC	CTTCAGGTGA	CTCTGGAATT	540
	CCTGGTTTCAG	GTCCCGCTTA	AGCCTCTGCG	CCATCGTAGA	CTTGCCGGAC	CCAGGATGCC	600
	CCACCACCAC	TACAGCCACC	CGATAGTTGC	TCTCGATATT	CTGAGCAAGG	AGATCCCACA	660
	CTCGCTTCTT	TAAGTCTTCG	TAGTCCATGC	CGCTTGCTGT	GTATGCCTGC	TGGT	

1515UP

	GATCTAACGC	CGGCTGTCTC	CTCCAAGCGT	GTTCCCTGCCT	CTCTTATATC	TGTATCTGGT	60
	AGCTTCAGCA	TTAAAAAACC	GTCCAGAGAA	TTGGCTTTTCG	GCCATGCTCG	AAAGCTCACT	120
	AGTCGGAGCG	CAGCATCTAG	GACACCAGTA	GGATGCAGAC	AGTGTTTAGG	CCATTGAGAA	180
20	GGTGTATTCT	GACGCCCGCT	CGAGGCCCTGG	CGCGGTCCAG	CAGGCTGCAG	TCGGGACACA	240
	ACAAGTGGTC	GACGATCAAG	CACGATAAAG	CGAAGAACGA	TGCTGAGCGG	AACAGGCTTT	300
	TCACGCGGAT	GGCCAACCAG	ATATCGGTGG	CAGTCAAGCA	GGGCGGGTCT	GCCGACCCGA	360
	CGTGAACTT	GCGACTGGCG	GCGGCGATAG	AAGCGGCGTC	CAAGGCCAAT	GTGACCAAGA	420
	AAAGTATCGA	AAACGCAATC	CGCAAGGGCG	TCGGGCGAGG	TGGGGCGCGC	GACAACGCCG	480
	AGGCATGCAT	GTACGAGGCG	ATACGGCCCG	GTGGCGTGCC	GTTTGTGCTG	GAGGCCTCAC	540
25	CGACAACAAG	AATCGGACCG	TGACCTGGTA	CGCGCCGCGT	TCAACAAGCA	TGGCGGCAAC	600
	ATGTCGCCCG	CTCAGTACTT	CTTCGAGCGC	CGCGGGTACG	TGGCAATCCA	GCCACCGGCC	660
	TCGTGCGAGA	GTTACAACGC	GGTGTTTGAG	GTTGTGTCCG	AGGTGAGGGG	CGTAGAAGAA	720
	CTGGA						

1516RP

	GATCCGACCT	TTGGTGGCTT	GGCTCGAGTC	TTTCTTCAAT	TTAAACCCCT	GTTCAACAGC	60
	AGATGAAATT	GTTAGTCTAT	CGAGTCCACG	TAAAAGACAA	TTTTCGACGC	TTGAGATGAA	120
	GGGTACGGCC	TCTCCCGACA	AGCGGCATCG	CCTGCACCGA	AAAGTATCCG	GTCACTCCTT	180
35	CATCATACGG	TACCTTCACT	ATCTCTTTCC	GCCGGAAACT	AAATACAGAA	ACATACCTTT	240
	AACATCCTTA	TTCTGTATTAT	CCTTTCTTGA	TTTCGACTGG	AATGTAGCGG	CGAAAGGGAT	300
	CTGTTTCAAA	AATTGGAAAC	GCTTACCACC	TCACCAACAC	ACCAGGACTT	TATTTCTGTAG	360
	AAACAGGGCA	TCGGCCTGAA	CAACAGTCAC	TAGAAACGGT	GCACCAAGGC	AGCTTGGCAA	420
	CGAGGAGGCA	CCCTAGGGCT	CAATGCGTTG	ATAGTAAAGC	ATGTACACGA	GCTTTGTCTC	480
	CGAGAGAAGG	AACGACGTCT	TGCACTCCGA	CACGTACGAA	TCTGAGATAC	ACCACCACGG	540
	GTGCGTAGTG	GTGCGACGTA	AAGCCTTCAG	TTTGCGGGGA	CGGCCTGGGG	ACGGGGGAGT	600
40	ACTTCGTGGC	AGCCGAAGAT	ACGCCGATGA	GCTCGCAGAG	CTGGCTCCGG	AGCTGTCTCTG	660
	CTCGGCTGAC	GCGTCCGGCT	TGGAGAC				

1516UP

45	GATCATTAAC	GAAATTCTTG	TGGTTGATTA	CGATGTTTCA	TGGGAAGATA	TAGCTGGTCT	60
	TACAATAGCA	AAGAAGTGTT	TGAAGGAAAC	AGTTGTTTAC	CCATTTTTCG	GGCCAGACCT	120
	TTTTTCGGGGT	CTCCGGGAAC	CTATCTCCGG	GATGTTGTTA	TTTGGACCTC	CAGGAACAGG	180
	TAAAACGATG	ATTGCCAGGG	CCGTTGCGAC	TGAATCGAAT	TCAACTTTCT	TTTGCATCAG	240
	TGCTTCTCTT	TTGTATTCGA	AATACTTGGG	TGAGTCGGAA	AAACTTGTCA	AGGCCTTATT	300
50	TTACCTAGCC	AAACGGCTTT	CCCCCTCAAT	TATATTCAAT	GACGAAATCG	ACTCTCTACT	360
	AACTAGCCGT	TCAGATAATG	AGAACGAATC	ATCCAGAAGG	ATTAAGACGG	AGCTCTTGGT	420
	CCAATGGTCC	TCCCTAACGA	GCGCCACGGC	TAAGGAAACA	AGAGAAGGCG	AAGAGGCCAG	480
	ACGCGTTCTT	GTCTTGCCCG	CAACCAACTT	ACCGTGGGCG	ATAGATGATG	CTGCTATTAG	540
	ACGTTTTTCA	CGGCGTCTAT	ACATTCCATT	CCCGGAATAC	GAAACAAGAC	TGTATCATTT	600
	GAAGAAGCTT	ATGGCCCTTC	AAAAGAATGA	ACTTTCTGAA	TCTGACTTTC	AACTCATTGC	660
55	TCGCATGACT	GAGGGCTACT	CGGGATCTGA	CATAACTGCT	CTTGCCAAAA	GAAGCAGCTA	720

TGGA

1517RP

	GATCAATGAA	AAACATGCAT	ACGATTTCAT	GAAGCAAAAT	TTGGCTTGGA	ATATTGCCAA	60
	CTCTATTTCAC	AAAACAGAAA	TACTAAAGGA	AGAGAACTTC	ACGTTATTAT	CCAAAGCCCA	120
5	AAGAGATGAC	GTGAAAGGAA	GAGAAAGCGA	GTTATTACTT	CCAAGCGAAT	TAAATCAATT	180
	AAAGATGGTC	AATGAGCGTG	AGCTGAACGG	CCATGCAAGA	AAAATAAGAC	TACTATCCAT	240
	GTGGGAAGTC	TTCAAAATGC	TTTAGGTTCT	GCATTATTAT	ATACACATTG	TAGATACAAC	300
	TCGAAACTAA	TGCATTTTCAC	GTCAGCAGTC	TAAAAGTGGT	CATGCAGTAA	CTTCACACCT	360
	TCTTTATTCC	AAGGACAAAG	GTATATTCCC	AGCTGTGTCT	TAGACAGTGT	CCCCAGCTTG	420
	AAACATGTGT	TACTCAAATG	GTTGGCAGTA	ACCTTACATT	GCCCAGAATG	GGTGATGCGG	480
10	TTAGAAGTGG	TATAATCCAA	CTGCTTCCAA	ACATCAGCGT	TATTAGGTGT	AAAGAAAGCG	540
	GATCTCTGCC	ACAGAATTTT	AGATGGAGCG	CGCAAATTCA	GTGCTCTGGA	AATCTCATCC	600
	ATGACAAGTG	GAACATCTTT	GTATTTGTCC	GACAGGATGC	CTTTTAATGG	TAGGTTAGCT	660
	AAATCTTTCA	TCAAAATTGA	AAGTGGTCCA	CCTTGTTCCT	CATGAGACAA		

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1517UP

	GATCCTCAAA	ACTACAGAGC	GAAGTTGAAA	AAGATCATAT	TTTGATAGAG	CGTAAGCAGT	60
	GGGATGAAGC	ATACGCTCTT	CTCAAAGGTG	TTGTGGATAG	ACATCCACAT	CTATATGATG	120
	CACATTTCAGC	ATTCCGGTTGG	TGTCAGCTGC	AGTTGGGCGA	CACTGAAAGC	GCTTTAGAAA	180
20	CATTCCAGCT	TATTATTAAT	AATGTGAAGA	GCAGCGACGG	CACGTCGTCT	CAGTTCATTA	240
	GCTCAGTACA	CTGGCGAACC	GCACAAGCAC	TTATTACTAA	GCAGCAGCAT	GAAGATCCTT	300
	CAGGTAATGA	GTTTATAAAG	ATTGCTTTCC	AGCATCTGGT	ACAATCCCCTG	AAGATAACCG	360
	ATCTTTTTGC	TCCAGGTTAT	TCCCTTCTTG	GACACATTTA	CGAAGTGTAT	TTTCAAGACC	420
	TGACTCGCGC	ATTTAGGTGT	TACGTTAAAG	CCTTTGAGCT	AGATGCCCGC	GACCTCGTCG	480
	CTGCTAAATA	CATGGTGGAA	TACTATAGTG	ACCTGTGCAA	TTGGCAGGCG	GCGGGCAACA	540
25	TCTGTGACCG	TGTAATCAAG	AATGATATGC	ATCTCAATTC	CGTCAACTGG	CCGTACAGAG	600
	TTCTGGGTGT	TTATTATTTG	GAGCTTCAAC	AGGAGGCTGA	ATCGATCGAA	TGGTTCCAAT	660
	CC						

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1519RP

	GATCAGACTG	AACCCATATA	TCAGCGAGGT	ATGGTACGAT	TTGGGCACTT	TGTATGAGAC	60
5	ATGCAACAAT	CAGCTCAGCG	ATGCCCTGGA	TGCATATAAA	CAAGCTGTTC	GCTTAGATCC	120
	GAATAACGTC	CACATAAGGG	AGAGACTAGA	GGCTTTGACT	GCCCAGCTAG	CCAACCCAGG	180
	GGCCCAGCAG	CCTCAGCAGC	AGCCTCAACA	GCAACAGATG	CAACAGCCTA	GAGGGCCAGC	240
	ACCCATTATG	TTGCAGCCAA	CATTGCAGCA	GCAAGACCAA	ACAAATCCGT	TGAATAACAA	300
	ACCTGCGTTC	TACCGGTCTT	CTCCCCACGG	AGTTGCGGTT	GCCGGAACAG	AGTCCGCAGG	360
	CCACACACCA	ATGTCAGGAC	GGCCTCAGCC	GTTGCAGCAG	TTGAACAATA	ACGGAAGTAT	420
10	CCTGGAACCG	TCATTGTTGC	CGCAAAAGAG	GCCTATGGAG	GGTGGAATGG	ATACATTGGT	480
	AAATGCCATT	TCGCAGCAGG	AGTTGCAGCA	ACATCAGAAG	AAACATATGC	CTTCTCAGAA	540
	CCATCCTAGT	TTGGCCCTGG	CTACAGGACA	GCCGCAGCAG	TTACCACCCG	ATGCCGCTCC	600
	CATAATACCG	CCCGAAAAGA	AAGGTGCGCC	TCTCCCCCAG	TTTCAGAAAA	CTGAACCAGA	660
	GCATGCGGCA	AAAAGACTGA	AGCCCCAGCA	GAATAACGT			

1519UP

	GATCAGGTAT	CGGCCAACAT	ATCGCGTCTG	TCGATAGCGT	CGAAGATTAT	CGTGATAGAT	60
	ATAGACTATG	AAGTGACGGA	CGGCAAGGTG	ATCGATGTTA	AGCTGGTGTG	GGCAAGCAAC	120
20	TTTCGACAAGT	TTGACTACTT	CAATGGCGAG	GCCAAACATCC	TGCACCGGTC	ACTTACCACG	180
	TATAGCGACC	TGCACGAGTT	CCACCACAAC	CTGAAGTTCT	TAACCCCTACT	CGACGCGTGC	240
	TCAAGCATCG	ATATCGAGTC	CAATGTGTG	CAATTTCGATT	TGTTTCGAGTA	TTACTTCGATG	300
	CTGCCGCAGT	ACATGCAGAG	CTACCTGGAC	GACAATGGCG	CGCAGCTCAC	GGTGCAGACG	360
	AACCTGAACG	ACCGTPTTGG	GATCTACTTG	CTCGACCATT	CCGAAAAGAA	GGTCGCCAAG	420
	CTGACATTTG	CCGCTACGCA	GGACCCGAAC	CAGCGGTATT	ACGAATACAA	ATACTCGAGC	480
	GAAACGAAGG	AGTGATCAAA	CCAGTCGGCC	GAGTCCTATA	CGACCCGGCAT	CACGCTGGTG	540
25	TTCGAACTTC	TCCGTGACCC	TCCGACGTAC	CTGCCCTAAGG	ATAGTTTGCC	GCCAGAACAC	600
	CCTGATGAGG	GCTTCACGAG	TGCTTCTGCG	TCCGAGCTGC	AGCGCCGCTT	TGCATTCAAG	660
	TGTCAAAATC	CACGAGTCAC	CCTCGTAAAT	GACTTC			

1520RP

	GATCTTCTGG	ACGCTTTCCCT	TGAGTTTCGTT	CATCTTGCCA	AGCACGTCTGA	CGTTGGGGTT	60
	GCCCCGAAAA	GAGTTGAGCA	TCGGCCCCAAG	GCGGCCCTGCA	ATGGCGCCAA	ACTTGCTCTAG	120
	CACCTTCGTG	AGCGTAGTTG	GGAGCTGCAA	AAAGCGCAAC	GTATGGCCCCG	TGGGCGCGGT	180
	GTCAAAGATC	ACCGTGTGGA	AGTGCTCGCC	GTCGCCCTGCG	TCCTGCTTCT	TGATGTGTTT	240
35	CATCACCTCC	ATGAACGAAA	GCGCCTCGTC	GATGCCCGGA	ATCGACCCCG	TGAGATCTGC	300
	GAGTGCGCCG	CCCTGTAGCA	AGCCCCGAGAG	CCCCGTCACTA	TCCGCCGCCGT	TCCGCGATCGC	360
	CATGTCTGTT	ACGTCTCTCA	ACGCCGCCGA	AGGGTCGATT	TCCATACACG	ACAAGTTGTC	420
	CATGCCCGTG	ACCTTGCGCG	CGTCCCTTCCC	AAACTTCTCG	TTGAACGCAAT	CGCTAAGGTT	480
	ATGCGCAGGA	TCCGTGCGAG	TCAAAAGAAA	CTGCTTAGTG	GGCTGCGCAA	GCGCCATCTG	540
	GATGGCAATG	GAGCACGAAG	ACGTGGTCTT	GCCCCACCCG	CCCTTCCCGC	CGACGAAAAT	600
40	CCACTTGTGT	GTTGTAGAGT	TGATCAACGA	GCGCAAAGAG	GCCTCTGGTG	TAATATCAGT	660
	CATGGTTGGT	GTACCGCGTG	AATCTGAGAG	TGCAGGCGAT	CTGAGATCTT		

1520UP

45	GATCAAACAG	TAATGACTTT	GTAAACGGTT	TTGAAGTACT	GCACGAGCTG	CGACTCTCTCA	60
	CTGCCCTGTG	GCGCCACAAG	CGCCGAAATC	ACAGCAACTT	CGCTTTTCAA	CTGAATGGCC	120
	TCCTGCATGT	TCCGTGGGAA	CCCAAGTAGC	ACGACGCTGT	CCCCAGCCTG	GCACACCTCC	180
	TTCAGATAGC	GGCCCATCAA	CGCAACCAGC	GCACCCCTTG	GCAGGTGCGC	CGAGTAGTCA	240
	TCGCCATGCA	CAGCATGCAA	CTCCTCTAAT	AGCGCGTGGT	ATTTGTCTGT	CTCGTCCGGT	300
	CGGAACCGCT	CCAGCGCCTG	CTGCACGCGT	ACGGCGCGGG	CCCCCGCTGG	CGCCCGGATC	360
50	TTCTCTACGG	GCACATCGGC	AAGCACCGCC	AGCACCTCCA	GCTCATCTGG	CTTGAACACC	420
	GTCACCCGCC	GCCTCAGGCC	GGAGCGGACC	TTCTCGAACT	CCGCTTCGCT	GAACTCTGTG	480
	TGCGGCTTGC	TCCGGTCAAT	CGACTTCGCG	GCCTGCACGA	AGATGAGCGT	GCTGACCACC	540
	GCAACGCCAA	CCATCTTCCA	CGCGCTAGGT	AGATCTTCCG	AACCAGGGGC	CTTGCTGGCG	600
	TATGGCCGCA	AAAGTCCCTG	CTGACGCCGC	AGAAGGAACA	ATCTAGGCTT	ACAAGTCTGC	660
55	GAAACATTTG	TCCTGCGAGT	TAGCC				

1521RP

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GATCGAATCT	KGTCTGAGGS	TCTTCCACGA	WTTGCAATGC	AATCTCCGGA	TATCCGGCCT	60
TCTGTAGATA	CGAGATGATG	TTCTGGCCCA	CAAGGTTGGA	CGTACGAATG	AGACGCAAGA	120
CTTCAGGGAA	GTTCTTGTTT	ACCAAAGCTT	TCTTAAAGCG	GTACTCGGTT	GGGTCAATGG	180
TCAATATCTC	AATATCGCCG	TCTCTGTTCA	AAGCATATAT	ATGCTTGCCA	TGAGCTTTGG	240
TAATGTATAG	GGTCTTGCTC	AAAGTTTTTA	TGATCCCGCT	GTCACCATTG	AATAGGCAGT	300
ACTWAATATG	GTTCAAAGTA	GACAAGAGCA	GAACACCAGT	TTCATCCCAC	GCCGCTGACT	360
TGATCCTGAT	CGTCTCATGG	TTAGACGTAG	TAATCTCCAA	CTTCCTAGTA	GCAATGGTCA	420
GCGTGTGTTT	ACTCATTAAA	GCAACGTATT	GCCCATCTGG	GGACCAGACT	GCATATTTAA	480
CCATCTTCAG	AGCTACCTCC	GCCAATTTTT	TCCCCTGCTG	CACGTGGAAC	AAGACTACCG	540
CCTTTGGTTT	CAAGATGAGT	ACCGCACCAG	GGCCTCCATA	GACAATGTCT	TTAACAGTTC	600
CTTCTATCTT	GATCGATTTG	GTTACCTTGT	TGTCCAACCC	ACGTACTTCA	AGAGATTCCG	660
ACGCAGAGTT	GTAGACAGCG	TTACCTATGC	CGAGCGACAA	AAGTCGCAAA	GCTTCCCTTA	720
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1521UP

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GATCCACTTC	CCAGATTACA	TGATAACATC	GAAGCCGAAG	GTCGCAAGGG	AAATGTTGGA	60
GCAGTATGAC	TTTATWCATA	GCGGCTTCAT	CAGCGTAGAC	GGCAAAATCAG	AAAGCCTCAT	120
CTTGGGCATG	CCGAAGAAGA	CCACCGGCAG	TTTGATCAGC	TCATCGAAAG	TTTTCTTATA	180
TGGCAGAGCA	CCCGTCACCA	TGAAGACAAG	CAGAGGCCCA	GGCGTCATCA	CCGCAATTGT	240
ATTCAATGTC	TCTACCCAGG	ACGAGATAGA	CTACGAGTTC	GTGGGGAGCG	AGCTCCATAC	300
TGTCCAGACG	AACTACTACT	ACCAGGGCGA	GCTCAACCAC	TCGAGAAATG	GCCGCCATTG	360
GCTACCCTCC	AACAGCCACG	AGGAGTACCA	CATATACGAG	GTTGACTGGG	ATGCCGAACG	420
CATCCACTGG	ATGGTCGACG	GCGAGATAGT	GCGCACCTTG	TTCAAGCGCG	ACACCTGGGA	480
CCCGGTCCAC	AAAATATACA	AGTATCCACA	AACGCCCATG	ATGCTCCAGA	TTTCCCTCTG	540
GCCCGCGGGC	ACCCCCGATG	CGCCGCAGGG	CACCATC			

1522RP

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GATCAAAAGC	GAACAGCGCA	CTTATGTCTT	GCCCAACCGA	CGCGTGCTCC	TGAATACCCA	60
ACGAGCACTC	CCTGGCCTGC	TATCTGCGCG	TATTCTGTCA	GAACGATCGC	CGCTAGAAAG	120
TTACCAAGCG	CGTCACACCT	GTATTCCCTG	GCTTCTCTCT	CGGCCTTCGA	TGTGCTGGCA	180
AGTAGTTCTC	CACGTTCTGC	AGCTGCCACT	GGAAACGTGC	AAACCAAAAC	AAACCTGACA	240
CCACTTCTGT	CTCTCGATCG	CGTCCAGCCT	CCAGAACTCC	CAGCGCACAG	ATTTTGTACTA	300
TAGCAACCCC	CGCGACTAGC	ACTCAAGAAC	TTTCAATTTT	CGCTTGAGCC	CGACCTTGTT	360
TTTCGAAGAT	TCTGACCTAT	CCTCCTATCG	ACGTCAGGGA	CACAAATCAC	ACTATAGTAC	420
CTCGAACAAC	AGTACAGAAA	AGAAAACCAG	CTGCTCCAGC	CAAAATTCAC	AAGTCCCGTT	480
AGCTGCTAAG	GCCAAATGGT	GATACTCAGT	CTTTAATCTT	TACCCAATTG	GGAAACTTCA	540
CCAAGGAGAG	TCTTGCGTCT	TAAGGTTTGG	CAGTTTGGTT	TAAAAATTTT	CTTGCACGAA	600
ATGTCAGAAAT	GTCGTGGGTC	CCCTTGTCGG	TCACGTGGGT	GTCGGTACAG	TGGGTGCTAA	660
TCACGTGACA	CGTGGATGAC	GACTGAGGCG	GAAAATTTGC	AGGTT		

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GATCGACAAT	ATTCCCCCAC	CAGGCGCAAG	AATCGAGTGC	ACACAGGCCA	CGCGCGCATC	60
CGGGCTCGGA	TCGGCGGGCC	TGGGCTGCAG	TGGGCGGCTG	GGGGCGGAAG	CACACTACCA	120
CAGTGTGCTG	TGGTGCGGCG	GGGACGCCAC	GCCGCGCAGC	TGCGGGCTGC	ATTCCAGCCA	180
CGCATGCACG	AAGAGCCGGG	TGACACTGCC	ACCGCTGGCG	TCGCTGCTGC	AGTCCAGCGG	240
CTACATGGGG	TTCAACAACG	AGCCGCGGGC	CGTCACGCGC	TCGTGTCTAG	GGGCGACACA	300
TCCCGAAGGC	CATTACGGCA	GGGACATGCT	GAGCAGCGCG	GTGGGGCACG	CCGCGTGTTA	360
CGTGGGGGCG	CAGAGCCCGT	TGCTACCCTG	GGGCGACGCG	ATTGCGCCGG	CGCTCCCACC	420
CAAGCCATCG	CATCGCTGCG	TCGCGGGGAA	CGCGCAGCTG	CGCGGGCCAG	TGCTGCCCAT	480
CGTGGGGCCC	GCGGCGTCCC	ACGCTACGAA	ACGAACAAGA	CATGCCTCGT	TTGTGGCAGA	540
CGATGTACCC	GTCCCAGCAC	GCTCAAGAAC	ACATGCTCAT	CCACACGGGC	GAAGTGGCTT	600
TCAGTGCAGT	TGGCCCGGGT	GCTCCAAGCG	GTTCAACGTC	AGGAGCAATA	TGAACCGACA	660
TGTGAACTCC	CACAAGCGCC	CGCTGATGAA	GGAAAGCAAG	AAGAAATCCA	GTTCTCCC	

1523RP

	GATCTTATCT	AAACCGCTCC	GCGATGATGC	TTTGGTAGCA	ACGGAAGCCC	GCATTTCAAA	60
	GTCAACATCA	GCGGAAGCTT	GGATAGATGA	GAATAATCACA	GGTGTACAT	GGCGCGAGAG	120
5	CTGAATTGGA	TTACCCGCTT	TGCTATCAGT	GGGTWAGAGG	CGTTCACCTG	GCTGTTCTGA	180
	ATTTGAACTT	CTGGAGCTAT	WCGAGGGGTT	ATGAGCAAGT	CCAAGTTCCC	GCGTGAAAAG	240
	CTGATCCTGG	TAATACTCGG	TGTAATCCAC	GCTTTTCTGC	CAGCAAAAAG	CTGGCGAGTT	300
	TGGAATCTTT	CCTTTATCGG	CGACGTCCGT	GCGTACATGG	CGTTCAATGG	TATTTGCTGA	360
	TGTAACCTGT	GGGAGAAGTC	GTAGGGAATG	TCTAGATAAG	GTTGACGCTG	AAAAGCTATT	420
	ACGTTGCAAT	AGCTGCGGTT	GAGAATGGTG	TACTTGGGCA	CAGCAACCTG	CTGCGCTGCA	480
10	TCTGGGTGAG	CTATTAAAAA	TCTCGGCCAC	CGAATAGAAG	AGCATCTTTG	GGTGAGCGCG	540
	ATTCAGTTCC	ATGAGATCAA	CAAAGGATAA	AATCCGGAGG	TTATCAAGGG	AGAATTTGTT	600
	ATCATACAAG	AGCCAATCAT	CACTGCAGTT	GGCTATATTT	GGATTATTGT	GATATTGCCT	660
	CACAGCAGTG	TTTATCCGGT	CTTTTTTCGA	GTCATATACC	ACAATGGATT	GT	

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1523UP

	GATCGACAGA	ATGAGCAGAG	CCATTCTGAG	AAAGCAAACA	CGGCCCATTG	CGGTTCTGGG	60
	ATCCCTGCCA	CAGAGCGAAA	TGGGCCCAGA	AGGTTTGTAC	TCGCCGATCA	AGGATCATCT	120
	GGCCTTAGCG	CCATGCGACG	TAGTAAAAGG	ATGGCATGGA	TGCTGGTCCG	AAATGCGGTG	180
20	CGACTGGCGC	AAGACATGGA	TTTTATCAAC	ACCAGCTCCA	AGATATTCTG	CGCAACACAC	240
	ACTTCGGAGA	CGAATTGCGC	AATGAACATG	GGTCAAGAACA	GTACATTATC	CCATTCTCTG	300
	ATGAACGCAA	ATATTATAGG	CTCAGAGTCA	AGCACGGCCA	TTAGCAATCC	ACCTATGCCA	360
	TCTGAAACTG	AGGAACGTTA	CAAAAGTGTT	TTACAGAGAC	TCGGTAAGCA	TGTCCCTCGG	420
	GGTAGAGGCC	TATCTCAGCT	TTATAATGAG	TTTTTGGAGG	ACGAGCGCAT	CCTCTACGGC	480
	TTAGGTGGTG	GAAGTGAATA	TGTTGAAGCA	TACTGCCGATA	GTTTGGATCA	AACAAAAAAC	540
25	AATGTGAGCA	TCGAGACTGC	GTATGAATCT	TCTTTGCTAG	AGCGCGGGGG	CCAGCAGGTT	600
	TTTCTGTCTT	TCGCCCAACG	CCCGAAGATA	GAGCTACTGA	GGATCATGT		

1524RP

30	GATCTTTTGA	AACAAGTGAA	TTTCTGGAAA	TCGAAGTGCG	GTGACTTGGA	CAAAATTAAG	60
	CAGGACTTAC	TGGCCAACAT	GGCGACGAAA	GAGACGGACT	TCAACAATCG	ATGCACCGAC	120
	TATGAACGTA	ATATAGTTGA	ACTTCAGCGT	CAACTATCAG	AAAAGTGCGA	CGCTACAAAC	180
	GAACGCTCTG	TCACTTCAAC	CTCTGCCGAT	GTACCTGGAG	AAACCAAAGA	ATATATTGAG	240
	TCTCTCAAGG	AAGTCAACCG	TAGACTGGAA	GAAGATATGT	TTGCTGTTTT	TGCGGGGAAC	300
	ATAGTGTTAC	TGGAGAACAT	CGGCCGTGCT	CTTTCTAGAG	GCCCTGACAA	CAAGTTACAG	360
35	ATTATACCGG	TTAAAGGTTT	AAGGAAAAAC	ATAGATGATA	GTATAATAAA	GGACAGCAGC	420
	CCTGTAATAA	ATTCACATAT	GGTGAAAGAG	ACAGTTTTC	AGGATGTGAA	GAACCTTATT	480
	GACGAGCTTC	AACTGAGCCA	AGGTGTTAAC	GACCAACTCC	ATTTTGTTAG	TGAGCTGGAA	540
	CGCTTTTATG	AAGAGGATCT	ATTTCCAAC	TCCGTGATCA	AGAGGTTTAC	CGATGTAGAG	600
	AACCTGGCTA	AGAGCTCAGA	AAGGAAAATA	AGGCTAAAAA	AAGCGTATTG	AAAGACACCA	660

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1524UP

45	GATCTATCGA	AAGTGTTGAAG	CTCCTAGACA	AGTTCGTCCA	TCCCAAAACC	GGGAGAACC	60
	CTTTGTGCTA	CCGTATCAAC	TACCAGTCCA	TGGACAGGAC	TGTTACCAAT	GCCGAGGTCA	120
	ATGTCCTTACA	AGAGCAGGTC	AGTCGGGAAC	TAGTCAGGCT	TTACAACGTT	CAATTGAGAT	180
	AGCCCAATCA	GGCCGAGACT	AATAAACTTG	TATATACAGC	TTTGCGGACA	TCGCACCCAT	240
	GTAACGTATA	GTATGATATC	TGCTTACTCA	TATCGCACCT	GAATGCTAGC	AGACTTCGAG	300
	AAATGCCTTA	ATACGCAGCA	TATCCGATAA	CTAGTGCCTA	AAGCCAAGTT	CTTGGATCTT	360
	CACAGCTAAC	CGTTTTTCTT	TGCTCCTGAT	GGCAGCTACA	AGAATAGCAA	TCCTTTATGG	420
50	ATCTGAAACC	GGTACTGCAC	AGGATTTTCG	TAATATACTG	TCCCACCAAC	TACGTCGTTT	480
	TCATTACAAG	CATACGGTGT	GCTCTATTGG	AGAATATAGT	GCCCAGAATA	TCCTCGCATG	540
	TCAGTACCTA	TTTGTCTATT	GCTCCACCAC	CGGGCAGGGT	GCGCTGCCGC	AAAATGCGCG	600
	GCAGTCTCCG	CAGGGCAAGG	TGGAAGGTAC	ACCATGGAGT	GTGCTCAAAA	GAAGCTCTCT	660
	CCCACCAACT	C					

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1525RP

	GATCTTCTCT	CGCTGGAAC	GGTGATGCGT	CCAAAATTTT	AACTTAACAA	TTTTTCACCT	60
	TGACCTCGCC	AAGCATCTAT	ATCACGTGAT	TCCATCTGAC	CAACCTCATC	CCAAATGCAG	120
5	GCCATTGGCT	GCTGCATTAA	CGGTCTCAGT	GCCCCGCTAG	AGAACTAGCG	TTACGCTTTG	180
	GGGTTTACTA	GCAAGTGGCC	GTGCCGTGGG	ATTGCGCAATG	TGGGCGCGCA	CCTTATCCAC	240
	GCGACACAGA	AGTGGGTATT	TTCCGCTTGT	TACATAGATG	TCCAAAAACA	GTACGCGCAA	300
	AGCACCAAGC	AAGCTTCAGC	AAGACTCAGG	GAGGTGTTAG	AGGCGATAAT	CCAACTCTGTG	360
	CTGAATGGAG	CAGGCGACGG	GACCAAAGTG	GATATTTGCA	GGCGAAAGTG	AGACGATGGC	420
10	AGCGCAAGAG	GGCAATGGAG	TAAACGGGGA	CCTGGACGGC	GGCATGCGAG	AGACGTTCAA	480
	CCCCGTCAAG	CCGCTGGACT	TCAACGTGAA	TTTGGCGGTT	TACCGGGGCA	AGGCGGGGCT	540
	CGGGGAGACC	CTGAAC TGCG	GCGCGGCGGG	GCAAAAAGCTC	AGGGTCGGAG	GAGGAGACAG	600
	ATAGCGAAGC	GAGCGGGAGC	TCCAGCCGGG	GGCGGGGGAG	TGCAGACACG	TCTAGTCTGG	660
	AGCCCCCGAA	GGTGGACCGG	TCGTTGACGC	CTTGGCGGCT	GAAGTCGTCG	CC	

1525UP

	GATCATCGCG	ATTTTCGGTG	GCGTTGATGA	GAAAGGCCCT	CAC TTATACA	TGCTTGAACC	60
	AAGTGGCGCT	TACTGGGGTT	ATAGAGGAGC	CGCTGCCGGA	AAGGGCAGAC	MAGCCGCTAA	120
	AGCGGAGCTG	GAGAAACTGA	TTGGGAACGA	TAAGTCAGAG	CTGTCAGCTA	GGGATGCAGT	180
20	GAAAGAAGCG	GCTCGGATCA	TCTACGTGGC	CCATGAGGAT	AATAAGGAGA	AAGAATTCCA	240
	AATFGAGCTG	AGCTGGTGCT	CCGTTCGGA	GACGGATGGC	TTGCACAAGG	AGGTACCAAA	300
	AGAGCTATTT	GATGCAGCGA	TTGAGTTTGC	GAAGAAGGAG	ACCGGTCAGG	AGAGTGATGA	360
	TGATTCGAAGC	GATGACAACG	CATCTGGAGG	TGAAGAGTCC	TCAACAAAGA	AGGATGCTGA	420
	CGGTGATGTC	CAGCTTTTCT	GATAACAGCC	CGGCATTATG	TGGAGGTTCA	TTTCATGACA	480
	ATTGACGGAT	GTTACTAAGT	GTATATTAAG	TTAATCCACC	TATATAAAATT	AATAACATGC	540
25	AAAGCAATTT	AGAATTTGTC	GGAAAGCAGG	TTAAAGCATG	TCTACTCTCC	TTAATCTTTC	600
	GCGAAGCTGT	ACATTTTCTT	CTCAAGTGAA	CGAATTCTAT	CCACCGGCTG	CGTCTGATTC	660
	TAATTTCTCTA	CGTTCGCGTT	CTGTGTACCA	TTTCCGCGTC	AGC		

1526RP

	GATCTGGCCG	CGACCTTGAG	AGGCGTCTGT	ACCTTCTTTC	AGCACAAC TA	TTGTGGGAGC	60
	TTGGTTTCCA	AAGTTCATCC	TGAGCTCGGT	GGTCTGTCAG	ATATGGTGGG	TGATGGCCTC	120
	GTCACGGTCT	GTCAGCTTCC	TGTACCGACG	ATGACGGCAG	TTTTTGCCAC	TAGGCCATTT	180
	TTTTTTTTCAG	CTCTAAGATG	GCAGACGGCA	AGGAGAATGC	TCCAGGACAC	CGGATAGAGC	240
35	TCCAATCTCA	GCAAAACATC	GCCTACTGGC	CCATTGCTGC	TGCTGCATAA	CAC TTCTATG	300
	GC TTAGTTTG	TGCACGTGGT	CGGCGCTTCA	CATTGTATCT	CGTGAATTGC	GTACCGGTAC	360
	TATATTACGG	TTGTGTGGCC	GAGCGGTCTA	AGGCGCCTGA	TTCAAGTGTA	TGCTTACAGC	420
	TGTTACAGGC	TGAACACTCA	GGTATCGTAA	GATGCAGGAG	TTCGAATCTC	CTCGCAACCA	480
	ATATTTTTCG	GGGCGTTTTC	GGGCGGCCAG	CGAAACTGAA	CCGCACACTA	TTTCGTGGTA	540
	CCGTTGGAGG	TAAACTGTTG	GAATCCGACA	GTGGGGTACC	GAAACCATCC	CAGCCTCTTA	600
40	TTACTAAGCT	GGATCGTGCA	CTGCAAGCGG	TGATATTGGA	ATCGTCCCCA	CGTATTATTA	660
	CTAAGCCGCC	ATCTTGCCGG	CCATGAGGAG	GGTACCGAAA	ACCAATCCCC	AATTTGCATT	720
	ACTAA						

1526UP

	GATCGTCAAC	AGGTCCCCGG	TC TTCCGGGAA	CGTCTTGCCA	TCGCCCTGGCG	ACAGTCTGTC	60
	GATCTTACAG	TTACCTTCGA	TTACCTCCGA	CATGCTCGTT	GCTGCTCCCG	TGGCTGCCCG	120
	AGAGTGATCA	AGTGC GTGT	ATTAAGGCC	CCAACGCCAC	CCGCC TGGCC	GGGTAAACAG	180
	TGCCCCGCGG	CTCGCGCGG	TGGGGCTGTG	CGGCCCGGCC	GCCCCATGCA	CCGGCAGCGG	240
	GGCCGGTGCA	CCGCGTGCGC	GCAC TTGCG	CCCGCCGCGG	CGCCCACTGC	CCGAAGCGGT	300
50	AAACTTAGTA	CGCAACCGCC	CAGCGCCCGT	CATAGCATA	GGACGCCAGA	CGGGGTAAGG	360
	CCGTAGCCCA	GTCCGGGAATG	CGGGCAGGAT	ACCTCTTTAG	GCAGGATACT	ATTTTAAGGC	420
	GTACAGGCGC	GCAGCCCATC	GTGCAGGCTG	CAGTAGCAAG	CTGAGACAGG	CTGGGCAAGT	480
	CTAGACCTGG	GACACAGCCC	GCAACCTAGA	GGCCGCGGTG	CGCCGAGGCG	GTCAGACATT	540
	TTCCGGTGCGA	GGGCGCGTGG	CAGCAGGACA	AAGAGCCGCG	AGAGAAGCAA	ATGCMCAACT	600
55	AAACGGGGAG	GAAGGGCAGC	GGATTTC TTT	TTGGGCTCTT	GTGCGAGGTG	GAAATTGTAT	660
	AAATAATGGG	AGCGGCGGCT	GGTCTTGCCG	GCTGAGACTG	T		

1527RP

	GATCTTGCTG	CTATCCAGAA	ATGGGAAGTT	CTTAGACAAC	GGGAATTAA	GCCCCTTTTC	60
	CAATATTTTG	AGCGTCGTGT	CATAGCTCGG	AAGACGCAGC	AGAAGCCCCC	CCAGTAGTGT	120
5	CTGTTTCATGT	TCGCTCATGA	AAGGTGTCTC	TATCAAATCT	AGCTCCATCA	TCGCAGAGTA	180
	GTTATTATCT	TTCTTCCAAG	ACAGACGCAC	ATGCCGCAAC	TTCGTCAGGA	TTACAGTAAA	240
	ATAATGGTAG	AACCGCGGAC	TCACAGAAGC	GACGACCGCT	CGAAATGAAG	TCGGCCCCGTA	300
	GAAGATCGTG	CGGCCCTGCT	TCTCTATCAC	AAGATGGAAC	TGCGAAAGTC	TGTTACACGGG	360
	GGACACCGTG	CCCATAACGT	GCTTCTGCAT	GAACAGCTGC	GGTACCATCT	CGCTCTTCAT	420
	CCGCGCGAGC	TCAGTCTCAA	GCTCGTCGAT	CCGTCGCAGC	AGCTCCACAT	TGGGCGTCGA	480
10	GCTGAACAGC	TCCCGTGAGT	TCACGTCGTG	CGTAAACTCA	GACAGGTACA	CACACTCGGG	540
	CAGGCCCTTC	CCAATACATG	TATAGCACTT	CGGCCGCGCC	TTGTTGCACT	TGACGCGCCG	600
	CTTGCGGCAG	AACACGCACG	ACTTGCTGAC	CTTCCGCCTG	GTTTTCACAA	TC TTGCCATC	660
	GGACTCTGCC	ATCCCGCCAG	CTTCAAGCAA	AATGATTAGG	CTATA		

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1527UP

	GATCGCGGAC	GTGGAGCACT	GGCCGGAGAT	GCGCGCGGCC	ATCCTGGTGG	TTTCTGCGGA	60
	CCGCAAGGAC	ACGCCATCGA	CGAGCGGTAT	GCAGCAGACG	GTGCACACGT	CGGACCTCTT	120
	CAAGGAGCGC	GTCGCGACGG	TGGTGCCGCG	GCGGTACGGA	AAGATGGCGG	CGGCGATCCG	180
20	CGCGCGCGAC	TTGCGGACGT	TTGCGCGCCT	GACGATGCAG	GACTCGAACT	CGTTTCACGC	240
	CACCTGCCTG	GACTCATTTT	CGCCGATCTT	CTACATGAAC	GACACTTCGC	GCCGGATTGT	300
	CAAGCTGTGT	CATCTGATCA	ACGAGTTCTA	CAACGAGACC	ATCGTGCGGT	ACACGTTTGA	360
	CGCGGGTCCG	AACGCGGTGC	TCTATTACTT	GGCGGAGAAC	GAGGCGCGGC	TCTGCGGCTT	420
	CCTCTCTGCC	GTCTTTGGCG	CCAACGACGG	CTGGGAGACC	ACGTTCTCGA	CGGAGCAGCG	480
	CGCCACCTTC	GCCGCGCAGT	TCGACGAGTG	CGTGCGCGGC	AAGCTTGCGA	CGGACCTGGA	540
25	CGACGAGTTG	CACAGAGGAG	TTGCCCGCCT	CATCTTCACG	AAAGGTCGGG	CCAAGGGCCC	600
	AGGACACTAA	ATCCTCGCTC	ATCGACCCCG	AGACGGGCCT	GCCCCGCTGAC	GCTATTCTCC	660
	TGCTATTTTC	TGCTCTGTAT	ACCCTGCCAG	AACGCGCTAT	ATATATAGAA	TATGCATT	

30

1528RP

	GATCACTGTA	TCGAATTTGA	CACCCAAGGA	AGCCAAAACA	TCGTGGGCGG	ATCCCGACAA	60
	TGTGGAACAT	ATGATATCGC	TTTCTGCAAG	GATGCGTGCC	TGAGCTTTCC	TCTTATTCAA	120
	TTCTCTATTT	CTATAATTCA	CCGCATTCCCT	TTCCCTCAGC	TCATCGCGCT	GCTTACCTAG	180
	CTCATTAAATC	TTCTTGCTCA	AGTCCCTCAA	CTTTAGCTGT	ATCTTAGATA	TCTCATCAGT	240
35	TGAGAGTTTA	CTAGTCGGCG	AACCATCCTC	TTTATTTCATC	ATATCCCTGA	GCTTTCTCCT	300
	CTCCGCTACG	GCGTCATGAA	AACCTCTGATC	TAAGTTTCGGA	TCGTGATTTA	TTTCGTACGA	360
	CTGATTCAA	GCTCGCTTGT	CAACCAGCTC	TTCCAACGTT	AGGTCTCTGA	TAGCAGCGTT	420
	AACCTGCATCT	GATTTACCAA	TCCGCACTAA	TTTTGGTTTG	AACAACCTGC	CGTCAGTATC	480
	GACCAAACCT	TCTCTCAGAC	GCAACACAAG	CTCGTCAACG	GCTGCATTAC	TGGGTGCACA	540
	TATCAGAACT	TTTTGTTTCT	GTAGTAACAT	CTCAGTAGAG	GTAGCGTTTC	ATTCTGTGGG	600
40	ATTTCTGATA	ACATTTGATG	GTAGTGCTTT	TGCGGTAGTT	AGGAAAAAGC	CGACGACACC	660
	AAGAATAGTC	TTAGTCTTAC	CAGTACCAGG	GGGTCCCTGG	A		

1528UP

45	GATCCAGCAT	TTGCGGGTAA	ATCGGCGTAT	TCCGCACGCG	AAGGTGGGAA	GCTTCAACGA	60
	GTTGATCTGC	ATGTGGCGGG	CGCAGATGGT	TCTTCCACTG	CTGCGAGACT	TTGATGCCTG	120
	CAAAGTATCA	GATGCTGTTA	TTCTGGCGAT	GTATGAGATA	CTGCTGAATC	CGCAGATGCT	180
	CCGGTGCTCG	CCGGAACCTA	AGTACTACTA	TGATCTAGCA	TTCAAGGGCA	TGTATGAGAC	240
	GGGACATAGG	CTTTTAGACC	ACACAAAAGA	ACAAGGTATC	AATCTGCTCG	TACCTGGAGT	300
	CGTATATTCA	CAGATGTACG	GCTGCCCTGA	ACAGAGTTCT	TGGGCAACAC	GTCTCTTCCG	360
50	GCACTTCTTC	GAGAACGAAT	ACTCAATCAC	AAATGAAAAC	GTGACAAACG	AACTGCTTGA	420
	CGAAATCACC	TATCATTTTA	TTTCAATTACA	GTTGAGCAGG	AGCAACAGCT	CGTATTTGAG	480
	CATGATTGGA	CTATTCTGGA	GCAAGATGTG	CCCGTTCTTT	GCGCTGATGC	ATGTTGATGT	540
	CTTAAAGGAG	TACTTTTATTG	AGCTCAAGAA	TATTAAGTCA	TTGCGGTCCA	CGACTAATGT	600
	TCATATTGAA	TCTGTTTTCA	AGGTATTTTA	TCACCATCTC	ATAATGCAGG	TAAGATCAAA	660
	ACCGTTGGAT	ATTCTGCTCC	GTATTTTGA	ATTATCCTGG	AAAACTAGG	G	

55

1529RP

	GATCAAAAAG	AAGGCGATTG	CTATGGCGAC	GGTGA CTGCT	GCTACCGCCG	TCTACGCTCT	60
	ATATCCTTCC	TCTCCGATGT	TGGTTGACAG	CTCCGCGTTG	ATCAAGCTAG	AAGGCACCAT	120
5	TTCTCTCAGT	AGCAAAGGTG	CTACTAATGA	TACTGATGTT	TTCATATTAC	CAGAAAAACA	180
	TTCTGCTGTT	CCGGGCTACA	ACACAATCAT	TCGTTTCCTC	GTACCCGCCA	TGAATGCCTT	240
	CAGGCTTTAT	GGCAGGCCGA	AAACACTATC	GGCGAGCAAG	GATGACACAA	ACTCACTCCT	300
	GTTTAGTCTA	CCAGCGCTTC	CACATGTGCA	CTACTTGCTG	GTCTAGGATT	TGCTTCCATT	360
	AGTGAATTCA	GCCTCTGGCT	CATGGACGAC	GCAGGAGTGG	CGGAGACAAA	TCAAGGCTCT	420
	ATTACAACGG	AGGGTAGCGG	CTGGCTATCA	GGGATGTGGT	TCAAGCTCCG	GTCTATCCGG	480
10	CGCTCTGTCC	TCCCCTGCTC	TGGGTCCATT	GAGTCCTACT	TCTTTGTTCAT	CGCCGCATTT	540
	TGCTCCGTCC	ATTGCGTTTT	CGCCTACTGA	GTCCAAC TAC	ACTTTTATGT	CAAGTCACTC	600
	AAGAATAACT	TCACTACATG	ATAATATCCA	GAGACCATAT	TGAATACCGT	GGCCAGCACA	660
	TCCGATAATA	CWCTGCACCC	AAACAATATG	CTATCTCCCG	CAGGTCTTGC	CCCTGATGCA	720
	TT						

15

1529UP

	GATCCCGCTC	AATGCCAAGT	AGAATGTTTT	TCGGGGGAGC	CCATACAGTA	CCGCCTCCTC	60
	CTCATCCCCG	CTCTCCTGCT	CCACGTCCTC	TCGTGCAACA	TCTAGCAGTT	TCCCGATAAC	120
20	ACTGGGGATG	GTCATGCTCA	CGGCTCCGGA	TATCAGGATC	AGCACCAAGG	CGCATACTAG	180
	AGACTTGAGC	TCAGGCCGCG	CCAATTGGAA	CAGTCTACGC	ACATCCTTGG	CACCTGATGC	240
	GTTGCCCGTC	GCCGTCGACA	GCTCGAGTCT	TTCTTGGTGG	GGTTTCTCTT	CCGTACTTGC	300
	CCGAGGGTTT	GCTGTTGAGT	TTAGCCTCGT	TTGAATTCTT	GTGATGCGC	TGAACGAAAA	360
	CCGGGTGCGT	TGATGTAGAT	GATTGAACGG	CGGCCATCGC	TGCATCCCAA	TAACAGGCCCT	420
	CGGCACCTGC	TTAACAGCTA	GCGATAGCCA	CATATATGTT	CTCCTCGAGG	TCATATPCCC	480
25	AGTTTTCTTC	TAACCTCACC	AGCCTTGTAG	GCCTCTCGAG	TTCGCTGTAA	GTGGTGAATT	540
	TGCCGATCGG	ACTCATTTTT	CATGGAGAAT	AAATAATTGT	ATTACAAAAT	AGAGATGCAT	600
	GCCGAGCTAG	TCGAGGCCAG	CTACTATACA	GCTCCTGGAG	CTTTGCAGTT	GTAGCGCACC	660
	GGTTTTCCGC	TCCATGTGAC	TACAACATTT	T			

1530RP

	GATCCCTCTG	CTACAAACAC	ATACCTAGAT	TTCTCATATT	TTATACTGAA	TACATATAAT	60
	ATATCATTTA	ACTGTCTTCA	TTCATGAGAC	GTCGTCTAAG	TTCTGTGCTG	CTCAACTTGT	120
	TTTCCCACTT	GTCAGCCTCT	TCGCCCCCCA	GTACGTTTAC	CACATGCACG	GCTAGCTTCC	180
35	TCATTCCTTT	GCTCTCACGC	GTATCGTTGA	TTGTCTGGGC	ACCGGCCACA	GTTTCCTCAC	240
	TCACTACCAG	GGCTTCGATA	CCAGGTTTCG	TACCCGTGGG	CCCGCACACG	TCATGTAACG	300
	CAAATATTTT	GATTTCCAGC	CCCGGTTTCA	GCCTGTGAAG	GAAGCTGCAC	ACGTTATCGC	360
	ATCGTTTCGT	GAAGGACTGA	AGCTGCTCCC	TGTATTTCTT	GTTCCGCAGC	AGTTCTTCAT	420
	CTGTAAATCCC	CACGATCAGC	CGGGACGCGC	TCACGAGCGC	GGCAACACTG	AGCAATATTT	480
	TATGTCCGTC	GTGTAAGTGG	TCGAAAGTGC	CTCCAGCGC	GCTAACAGCG	TACTTGTCTC	540
	TACCGCCACT	CTCGACCGGG	CCCGCAGCCG	CCATCGCCGG	ACTATCAAAC	AGCTCTATCT	600
40	GCCTGTGCGG	GAACGCATCC	TGCAGCAGGC	GATCGCTCAG	GAATACAACG	TCCCAC TTCA	660
	TTCCGGCTGTA	CGCTTCCATA	CTGACGTTGA	ACAAAACATT	TATCGGGGTC	GTGT	

1530UP

45	GATCCTGGGA	CGACATCGAC	ACCATTTCTA	TCGGTAACGA	ACTTGTGAAC	AACGGCCAGG	60
	CGACCGTGGA	CCAGATGGCT	GGTTACATGA	AAACTGGCCG	CAAGTGCCTC	GCTGAGGCCG	120
	GCTACAAGGG	CCCAGTTGTT	TCCGTGGACA	CTTTCATCGC	TGTAATCAAC	AACCCTGGTC	180
	TATGTGACCT	ATCAGACTAC	ATGGCTGTCA	ACGCCACCC	ATACTTCGAC	TTCCCACTT	240
	CTGCTGCTAT	GGCCGGCCCT	TGGGTTTTGC	ACCAGATCCA	GAGAGTCTGG	AGCGCCTGCA	300
	ACGGTAACAA	GAAAGTTGTC	ATCACCGAGA	CCGGCTGGCC	TACTCAGGGT	CAGACTTACG	360
50	GCAAGGCCAT	TCCATCCAAA	GCCAACCAGA	AGATGGCCTT	GGAATCTATC	AAGGCCACTT	420
	GTGGTGATAG	CGCTATCCTA	TTTACTGCTT	TCGACGACTA	CTGGAAGCCA	GATGGGCCCTT	480
	ACGGTGTCGA	GAAGTTCTGG	GGTATGCTAT	AAGTTGCCGT	GTGCTTCTTT	ATGACCTGTC	540
	TCTTTATTTT	GCTCGGAACC	CTTACATGCA	GATGGGGGGT	GGCGGTGCAT	GGGCCTGCAG	600
	CCTCCGGGCC	TGCAAGTTTC	TACATCGCCC	TACTTTAGCT	GCCACGGGAC	TTTTGAATTT	660
55	CTTTGGCAGC	TGGTACTGCT	GGCATCCTTC	TCATAGAACA	CAGTGTGCCC	ACAGGG	

1531RP

	GATCTGCATC	CTCGTGATGG	AAAATACGGC	CATGCAGCTA	ATTTTGGGAAT	GGTTTCTGCA	60
	TACCGTAAGA	GAGATGGCTC	CAAATCATAC	CCAGTTACTA	TCCTTGTGAC	TAACTTTTCA	120
5	AAGCCGACAC	CTACCAGACC	TGCTCTTCTG	AAGTTGGGAG	AACTCACAAC	GTCTTTTCAT	180
	GAGTTAGGCC	ACGGCATACA	CGATTTGGTG	GGTTCCAATG	ACTTGGAGTC	GCTCAACGGG	240
	CCTGGGTCGT	TCCCATGGGA	TTTCGTGCGAG	GCGCCCTCTC	AGATGCTGGA	ATACTGGACG	300
	GCACGGCGTG	ACGTTTAAAC	TATGTTATCC	AAGCACTACG	AGACAGGTGA	GAAAAATCCCG	360
	AAGTCGCTGC	TGGATGCCTG	GTTTAGTGT	GGCGGCCCTCA	ATTGAGGATT	GGCCAACTTG	420
	GGCCAACTGA	AACTTGGCTT	GTTCGACATG	TATGTGCACA	CCCGCGATTA	CAAAGGAGCG	480
10	GAGGTACGGA	AATTATGGAA	TGATCTCACC	AGAGAGATCG	GGCTCATGAA	CTTAAAAAAC	540
	TACACTAGCA	CCGGCTATGA	CTCCTTTTGA	CATATTATGG	CTGGATATGC	TGCTGGCTAC	600
	TATGGCTACC	TTTGGTCCCA	GGTTTTTGCT	GCAGATATGT	ACGACACAAA	GTTCAAGCCC	660
	AACCCATTCA	ATGCTACGGT	GGGTGTGGAA	TACAGGGACA	CTATTTTAGC	TACCGGTGGA	720
	CTT						

1531UP

	GATCCAATCC	TGGAGGCGGG	TTAAAGTGCT	CCTCAATGCA	GCGCAGCCGG	CACTGGAGTA	60
	TGGCACGGAA	ATCGCACTCT	GGAGGAGGCG	CGTGGTTGGG	AACTGGATCG	TCCACCTCGC	120
20	GCAGAAAGGC	CGTTTTCAAG	GCGCAGGCGA	GGACCGGAAT	GAGCAITTAAT	AAAGAGGTAA	180
	CGTGCAATGCT	GTGAAGAGTT	TCACTTTATG	CGTTGCATT	CTCCCCCCT	GAAGACGAAA	240
	ACACGGCGCA	CATGCGCTAT	ATATACCCTT	CGTGTCTACT	ATTGTGCGCT	GCCCCGCTCTC	300
	ATGTCAGTTT	TTACTTTTTTG	ACGCCGGGAA	CGCGACATCT	GCCACAACGC	ACCAACGCC	360
	AGTGACCAGC	TCTATGCCGC	TTGCTCTGCC	AATAACCAGC	CCCCTACTAG	CCGAGCATTT	420
	TGCCTTAGTC	CACCAGATAT	TCCATTGTTA	TCGTTGCTCG	CCAGCCTCGG	GCTGGGACAT	480
25	AAAGATCGGA	AGCTCCTGTG	CAAACCTGCA	CAGCGCGCCT	TCGAGAATAC	TCCGCAGGGA	540
	CCCCCCTCC	CATTAGTCCT	TGGCAGTTTT	TTGCTTTTGT	CCGCGATAAT	GTATCTAAAT	600
	ACAGAATATC	GATTACGGCG	AATAGGCAAG	TTTTGTGGTC	TGACATGCCG	AGTGTCAGTT	660
	CATGATTACA	TAATGTGTCT	TGCCATATCT	GT			

1532RP

	GATCTKTTGA	AAGAGTAACC	AGGATCAAGC	CTGCGGTATA	GCCAGCGAAA	TATGCATATG	60
	AAGTCTTTCT	GCGTGGGCTG	TTTCAATGAC	TTCAAGTGATA	TCGCATGCCC	AGTTTCTATG	120
	TCAAAATTGC	GCGACTGCAG	ATAATCAAAT	ATCTCCTGCT	GCAACACTGC	CTGGTAGTTT	180
35	TTGTACCGGA	GAGGTGCGCG	GTCGCGGGTA	CTCTGCAGCG	CACCGTAAGC	TGACGGAGCC	240
	CCGCCGGGAA	CAATCGAAGG	CCGCTGCGAA	GATCGCAGAC	TCCGCCGGAG	AGACTTTTCG	300
	ACCTCGGGCA	CAGGTCTTGA	AAGAGAGCTC	CGGCCGTTCC	GTGCCAGACT	CTTGTTTATC	360
	ATGTCCGTAA	GAGCAGCGTT	CGTGCCAGGT	ACGCCCTTCT	TGTTTCGTGTT	TCCACCAATT	420
	GATGGAATTT	GAGACGTGAA	CCTCTGCGGA	TTCAAGCTAT	TGAGCACACC	ATTGGCACCA	480
	CTTGAGCCCC	TTGCTCTGTC	CATCCCTAAT	CGTCCATATC	TACGGGCGGC	TAATAAGTTA	540
40	CTACCAGACT	CTGGCCCTCA	TCTGGGACTG	ATGTTATCGT	CTGCAGCCAG	ATCCTGTTTG	600
	TGACCCGATC	GAAATCATCG	AGTACGAATA	ACCACGTGAC	CATTATTAC	GTGATGAATT	660
	TGCGGTCCC	TGTTGCCGAC	TCTTACTCCA	GGTTAACCAT	GACTAGATGG	GCATACCTCA	720
	GA						

1532UP

	GATCATCTGA	ACGCTCATGA	ACAGTTGCGG	GAACATCGTG	TCCACGACTA	TGCACTGCTG	60
	GATGTCCCTC	TGGCCGAAGT	ACGCGCGGTC	CGGAGCAACA	ATGTTGACCA	GCTTAGCAAC	120
	GACCGTTCGCC	ACACCGCGGA	AGAAGCGTGG	ACGGGTGCGA	CCCTCCAGCA	TCTCGCTGAC	180
50	GCCAAGCACC	GACACAAACG	GCCCGCGCTG	CGCCTCGACC	TCCAGTGGGA	TGCCGCGCGG	240
	GTACATTTCC	GCGGGAGAGG	GAGCAAAGAG	CACGTCCACA	CCGGCCTCTT	CCAGCAACGC	300
	GCGATCCGCT	GCCAACGTCC	TGGGATAGCG	GTCAAGATCT	TCGTTGCGCG	CAAACCTGCGA	360
	AGGGTTTACG	AAGACTGAGA	CAACAGTAAA	GTCGTTTTC	GCGCACGATC	TCCGCACGAG	420
	CGTCATGTGT	CCCTCATGTA	GGCAGCCCAT	CGTTGGCACA	AACCCAAATCG	TCTGTGTCTT	480
	GCAATCTACC	GTCTGCTTGC	GCCATTGCGA	GACTTCCTGG	ACCTTATTTGA	GCACGTGCAT	540
	GAGGCGTATC	GCTTTGATGG	TTTACGCTTC	AAGTTTGTCT	GTGTGCATCT	CACAGATTAA	600
55	GGAAGCTTGC	GCACACTAT					

1533RP

	GATCACGAAC	TCCATCATT	CAAAGTCCAT	CGCGTCGATA	CGAAAACAAA	ATGCACAGCC	60
	GCTACCGACC	TTCCGAAACC	TCGAGAAGAT	CAACCAGCCG	CCAAAGAACG	CTGACCATGC	120
5	GTGGGAGTAC	ATAAAATCGT	GAATTATTGG	GGTTGTATGT	ACTATATACT	ATCGCTCTGC	180
	CGCCCAATGA	TGGTTACGCC	TCTTGCACAT	GCATTCTGGG	TGACGAGGTT	GTCTCCGTAC	240
	ACCTCTACTA	TTTCCAGGTT	GGGCGCACAT	TCGCTGATAT	GGGCGAGCAA	TTTGTCGTCA	300
	ACGCAGCGGA	CGAACCCTAC	ATTCAAGTTG	TGCAAGTTTG	GACAGGACAT	TAGCTGGAAC	360
	CCAGCTGCCG	TCAGGTTTCT	GGCTGAGTTC	AAGTTTAGCT	CTTTGAGGAA	TTTGGAACAT	420
	GGATTCAACC	ATATCTCCGC	AATTGATGCA	TCATCCAGCT	GATGGCAGCG	CCTCAAGTTG	480
10	AGGTAGTGAA	GTCGGGGAAG	CTGGACCGAA	GAGAAAAATG	TAATGAATCC	ATCGGACGTA	540
	ACCTGGTCCA	ATTCTCTAG	GGAT				

1533UP

15	GATCCGGAGA	CAGACGTGTA	TCTGAGTTCT	ACCGCTGGGC	GCTGAAACGC	ACGTCGTTAG	60
	CGCACATCCT	GTGTGCTTGC	ACCGGCCCAT	AGCAACCAAG	TATTCTTATA	TTCTGTAAAA	120
	CTGCGGTAAT	AACCATGTAG	AAGATTCCGC	GCCCGAATAC	CCGTTTTACC	CCAATATGTC	180
	CGTCATGTGA	GCTATTGGAT	CGAAGAGTTT	TTAATGACGT	ATCCCTTATC	ATAAAGCGGT	240
	GCTGGATTAT	TGGAGCATGC	ATCTGGTTCT	GCTCGGGCGT	GCCAAATATA	TGGTGCAAGA	300
	AGAACTATC	GTACCAACCC	CGTCTGTGTC	GACCTGTGTC	CTCTTAATCG	GCATGACTAA	360
20	TATGGGGTAT	CCTTAAAACC	TTTAAGATGT	TACCTCCGGT	CTCCAGGCGG	GTTGTCTAGT	420
	TTACAAGAGT	AAATACCACC	TTGCCCTCGG	GAGGGTTCTT	ACTTTACAGT	AGGAAAGAAT	480
	CGATACCACT	GGTGGGGGGA	TTTGGTATAT	TTTGAAAGAT	GGATGGAATG	GAGGGCTCCT	540
	TATTGACAGC	AAAGCCACTC	CGACAGAATA	CCCACACCTT	GGATTTGGAA	GCTGCGGATC	600
	GACAGAACAT	GGTTACGTAA	TCGAATTGTC	CTGTCGGGCC	GCCCTTCCGG	TTAATCAAGA	660
25	AGAACAACCG	CGGGGCACGC	AGGGAACAT	TGAATTTCAGT	GCTGCCAAGC	CTAATTTATG	720

1534RP

30	GATCCACATT	GGAATATGGG	TATGGGACTT	GATGGTTGAA	CGCTTCGCTT	CAACCACTGC	60
	AACATTGGCA	AACCGTTTGA	AGTGCTGGAT	GATTTTCTCC	TTCTGGATCG	CAGTCAAGAT	120
	GTGGCCGAAT	CGTTTTTCGT	TGTATAGGCC	TTGCTCATCC	TGTGCTTCAT	CCTCATCAGA	180
	CGCTAATGGA	ACGTCTGGCA	CAATCTCGAC	GCCATCGCAG	GATGCGATAC	TCAAGGTATT	240
	GAGCATGTTT	AAGGCATGTT	CCCTTGCTAC	TTTAAACCCT	GCATCAACTT	CCTCCTCGTT	300
	TTTCCATAGG	CGAGGGACAT	CGTTTTGATC	GTAACGAAAC	TTACTTTTCAA	AGCGTTCTCT	360
35	CAGTATAGAA	ACCACATTGT	CTTCTTCAA	ATACTGGTGG	ATAATATCAT	ACAGAATAGT	420
	CCATGCATTT	GACCGGATCT	TCAGGTATAA	AGCATAATTG	TCCTCCTCGA	TGAGGTCGAG	480
	CTGGAAGTCG	TAAGCGGTAC	TTTCATCGGT	GACATCCCCT	AAATTGGGTA	GTTTATACTT	540
	TAGAACTGAA	CGCGGGAATA	CATCATCAAA	GTGGTCCATA	ACAAGTTGCC	AGACGTTATC	600
	CTGTGGATGG	GAGAGTAAAGT	GGACAATATC	GTCTCTAGTA	TGTGTGAATT	GGTACTTTTT	660
40	CGCCCTCAAT	ATAATAGCTT	TCATCTCCTT	ACCACGCTCT	CTTTCCGCTA	GTTCACTATC	720
	TTCTCCA						

1534UP

45	GATCAGCGTG	GACTTGATCA	TGGTGTGTCT	CGTGCGGCCG	TGTGGTAGGC	GGGGGACGCT	60
	GCTGCTGTCC	TTTGTGCGGC	CCGCGGCGGC	GGCGATCAAA	GATCGCGCAC	CACGGTCGCC	120
	GCCGGGGGGG	CTCCAAGACA	CACGCGCACA	GCAGCGCGCG	CGTGCCGGGC	AATGCAGCGC	180
	GCACAGCTAT	CCTCGCGCCT	CGTACCGGTG	GCTGCCTTCG	GGCGGATTGC	GCTCGTCAGC	240
	GGTCACGTGA	CCCGAGATAT	GTTGCAAACC	AAGCCATCGA	TCGGCATAGG	AACGCATTAC	300
	CAGCCGATTG	GAAAACCCCT	ACAACCCGCC	ATCTGCTGGT	ACGACCACCG	CAAGTCGCTG	360
	GCATCGGTTG	CACAGTGGTA	AGGTCTTCGT	TCAAAATTAC	TCTGCCAGGG	CCGCTCTCAA	420
50	AACCTGTCAA	GTGCAGACGC	ACTGACAGTC	CGTCAAGATG	CGACATTACA	ATGCTCTGGA	480
	AGCTCTCCAG	TAGGTTCTCG	CGCGCGTGCT	AGACAGTCAG	GGGCAGGCTT	CATCGACAAA	540
	GACGCGCAAG	GATGTCGCAA	TTCTGTTGCA	CAGTCCACTC	TAGGGTCGGA	CGGGAAAAAC	600
	AGCGTACTC	TGCGTTGACT	GGGGCGAGAC	TGGTAGCCGG	CTGCGTGGCC	TCAATGAGGA	660
	CAGACCAAGG	TGATCATGAT	AC				

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1535RP

5 GATCTTGCTG CTATCCAGAA ATGGGAAGTT CTTAGACAAC GGGGAATTAA GCCCCTTTTC 60
 CAATATTTTG AGCGTCGTTT CATAGCTCGG AAGACGCAGC AGAAGCCCCC CCAGTAGTGT 120
 CTGTTTCATGT TCGCTCATGA AAGGTGTCTC TATCAAATCT AGCTCCATCA TCGCAGAGTA 180
 GTTATTATCT TTCTTCCAAG ACAGACGCAC ATGCCGCAAC TTCGTCAGGA TTACAGTAAA 240
 ATAATGGTAG AACCGCGGAC TCACAGAAGC GACGACCGCT CGAAATGAAG TCGGCCCGTA 300
 GAAGATCGTG CGGCCCTGCT TCTCTATCAC AAGATGGAAC TCGGAAAGTC TGTTCACGGG 360
 GGACACCGTG CCCATAACGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT 420
 CCGCGCGAGC TCAGTCTCAA GCTCGTCGAT CCGTCGCAGC AGCTCCACAT TGGGCGTCGA 480
 10 GCTGAACAGC TCCCGTGAGT TCACGTCGTG CGTAAACTCA GACAGGTACA CACACTCGGG 540
 CAGGCCCTTC CCAATACATG TAGAGCACTT CGGCCGCGCC TTGTTGCACT TGACGCGCCG 600
 CTTGCGGCAG AACACGCACG ACTTGCTGAC CTTCCGCCTG GTTTTCACAA TCTTGCCATC 660
 GGA

1535UP

GATCGCGGAC GTGGAGCACT GGCCGGAGAT GCGCGCGGCC ATCCTGGTGG TTTCTGCGGA 60
 CCGCAAGGAC ACGCCATCGA CGAGCGGTAT GCAGCAGACG GTGCACACGT CGGACCTCTT 120
 CAAGGAGCGC GTCGCGACGG TGGTGCCGCG GCGGTACGGA GAGATGGCGG CGGCGATCCG 180
 20 CCGCGCGGAC TTCGCGACGT TTGCGCGCCT GACGATGCAG GACTCGAACT CGTTTCACGC 240
 CACCTGCCCTG GACTCAATTC CGCCGATCTT CTACATGAAC GACACTTCGC GCCGGATTGT 300
 CAAGCTGTGT CATCTGATCA ACGAGTTCTA CAACGAGACC ATCGTGGCGT ACACGTTTGA 360
 CGCGGGTCCG AACGCGGTGC TCTATTACTT GCGCGGAGAAC GAAGCGCGGC TCTGCGGCTT 420
 CCTCTCTGCC GTCTTTGGCG CCAACGACGG CTGGGAGACC ACGTTCTCGA CGGAGCAGCG 480
 CGCCACCTTC GCCGCGCAGT TCGACGAGTG CGTGCGCGGC AAGCTTGCGA CGGACTGGAC 540
 25 GACGAGTTGC ACAGAGGAGT TGCCCGCCTC ATCTTTCACGA AGGTGCGGGC AGGGCCCAAG 600
 ACACTAAATC CTCGCTCATC GACCCGAGAC GGGCCTTGCC CCGCCTGAC

1536RP

30 GATCATTTGT CTTGCGAGCA CAAACATCCA CAGCTGTGCG ATTTGCAGTT GCAATCCGGA 60
 GCAGCAGCTC CTTGCGAGCA TTTGCAAACG CCAGGCTCTC CCACCTCTTT CGCATGTTCT 120
 TCTGACATTT TTGTTTGTTT TAAATCGTGA TTTTGAGTCG ATGGTTCCGA GACCGCCGCA 180
 GCTGACTATA GGGGGGACCA AGACCCTTTA TATATTTTCG CAACCAGATA CATTAATGCG 240
 ACGCCAAAAC ACTATCAAAA ATAAGGTATA GCCTCATTTT TATTGTGACC CATGGGACAT 300
 GCTGTAATCG GATTATTCTA ACTAAGCTAG TATTATGTG GTATCCTTTT ATTAATTACA 360
 35 ATCACTGCTG AGTTCGGTA TCGTGCAGT GCACACGCAG CTCATCAGTG GTTTCGTTCC 420
 CGCGCAGATC ACGTGCCTGC GACATGGCGA CTTTCATCCAC TGGCGCCCAG CTACGTGGTA 480
 TATGACATTA TGGCCGAGAG GTTAAGGCGT GAGACTCGAA CTAAATTGAG GGATCTCTTG 540
 GGCTCTGCCC GCGCAGGTTT GAATCCTGCT GATGTCGTTA TTTTGTGCTT GCGCGGCCTA 600
 CGGGGGGCTG TATTTGCTTG TTGCTATTTA GATAAACGAG ATACTAAACT ATGGGTAGAA 660
 CTCGCGGTAC TTCCCGTAGT AGTAGGCTGT GCCGAAACCG CCGAGGGCGG TGAGCAC

1536UP

45 GATCAGCTCG GTACTGGAGA AACAAAGCTA CTGTCCCTTG CCTTGACGAA GTTACGCGAA 60
 ATCGAAAGCA GCAGCAACAA GCAACATAGC AAGACCCTA AATACATTCT CAAGTCATTG 120
 GAATAAGCTC TAAAACTACC GATACGTATA TTTACTGCGT TAACGTTTAT ATACATATAT 180
 CTAGGCGTGC GTATGGGTGT TGTACGTGTA CATCTAACCA AATAACTCCA CTATAGCTGT 240
 AGTACATGGC ATTCCCTTGT AAGCAACTTC AGGTCTGGA CTACCCAATT GCTGTCCCGC 300
 ATCCAGCCT TGGGGTCGTG GCCCTGTGTT GACCTCAATT TAGCGAAGAC CGACTTGTAG 360
 TCGCTCTCAT ACTGCTTGAA TTCGCGAATG ACGCGGTTAG AGTCGAACTC AACATACACG 420
 CGCGTATCGA CTATCTGAA GAGGACATCG TCCACACGCA GGAAGAAACG ACTCAAAATC 480
 50 AGCATACACT GTTTCATCAC TCTCACCTTA ACATTAGAA TGCTAATGCC ATTGTCCGCT 540
 AGTTCGTCTT CAAATAAAAT CATGTCGTCG TAGAAAAGAA TGGGGTCCGG GCTCGAAAAG 600
 CTTGCGCAGA GGCAGCTCCA CGCTGTCGTC TCTGACCATC GCCCTGCCAT CTATGGTGCC 660
 CTGGTAGAGC GTCGTGTACG TCCAGTCGTA CTGGTGGGAT ATGTTTAGGG

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1537RP

	GATCTCCGTA	CTTTAGGATG	GCTTTATAGA	GGGCACGAAT	TTCCCTTTTCG	CCTATAGAGT	60
	TCAGGTTGTT	GGATTTTCGCA	CGTTTTTTTGG	AGCGTGAATC	CTCTTTGTGCG	CTTAAGCTCT	120
5	GAGCTCCATC	TCCATTGACG	CTATTTTTTA	TCTTATTTCAG	AGCAACATTTC	CTACGATTCA	180
	TCATTTGCAG	TTGTTCCCTGG	ACATACTCTT	CATCCTTCCG	CTTCTGTTCT	TCGTCTTTGA	240
	GTTTGCCTAG	CTCGTCTTCC	GGAATGATAT	CATCCCATTTC	CACGTCAGCT	TTATAATCGG	300
	TGACTTCAAA	CTGTTTTAGG	AATTCCCTCAC	CTCCGAGATG	AGACTCTCCC	AAATCTGGTG	360
	TGGTGACGTG	ATCTTCCGCA	TGATTCAAGA	CATCATCCAA	GTTCAAATCT	TCAAGCTTCT	420
	TTTGATTATC	ATGCGCTTTG	AACATATTGC	CTGCACCAA	CTTGAGAATC	TCAGACAGCT	480
10	CTCCTGCACT	AGGTTCGGCT	TTGCTCTTGC	TCGTATATTT	ATTCCCCTCT	GTAACACCTA	540
	ACGAGATGAT	AGCATACTCC	AAGATCATCT	TTTTGCGTGC	TCTTTCTAAG	ACTTCTTCTT	600
	CAACGGTATT	CTTAGACACA	AAACGGTAAA	CCATAACATG	ATTCTTTTGA	CCAATTCTAT	660
	GCGCGCGAGC	CATTGCTTGG	AGATCGGCCT	GTGGATTCCA	GTCGGAATCA	AATATGATCA	720
	CAGTGCTGTC	CGTCATC					

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1537UP

	GATCTAGACC	ACCCGGGCTC	GTTACCCGGA	TACGAAGTAA	AAGCAGTCGG	GAGCGGTCTT	60
	CTGGCAACGA	CGTTTTCTTC	TACACACCTC	CTCGCACAGG	ATCCAGCATC	CTGCCGCATA	120
20	ACGTCAACGC	CGGCGTTGTG	ATGGTTCCCA	GGTGCCACTG	GCGCCAAGCG	CTGCGTGAGA	180
	AACAGCAGCG	CTGCACCTCG	CTGCTTCCGG	GAGGCTCCTG	GGAGTGGTCC	GGGGGTTTGT	240
	CCACCGCTCA	ACCTAGCGGG	GCGTCGCTGT	GCCGGGCTCT	CCATGCAACT	GGGGCGCTCC	300
	CATGATGGCG	GGGGCCTTAC	CAGGGTGGTG	TTTGGGCTGC	CTGGCTGTGC	GTGGCCACAC	360
	GATGGCCTGC	TGGAGGAGCT	GAACCTGCTT	CCGTGGTGCA	AAGGTGTGTG	CGACAGCGCA	420
	CCTGCGTGCA	AGCTGTGCCT	GCGGGGGCGT	GTCGATTGCT	GCGTCCGCGG	GTGCAACTGT	480
25	GGTGACAGCG	CTTTGCAGGC	ACGTGATGGT	TGGTGCGGGG	CCCAGACGTG	CTCGGTGTGT	540
	CTCAGACAGC	TTTTCCGCGG	GCTGCGGGCT	CGCCGTTGCC	GCCATATGAT	TGATTCCGTC	600
	TCGATTAGTG	CATGGTGGTC	AGCTTCCAGA	TGGCCAGGCT	GTACTTGTGC	TTGCCCCGGG	660
	CCGGCAGGCT	CTTTGGCTGT	GCCGGTGGGT	CTTGCTTGTC	GGGCTGGCGC	CGTTCT	

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1538RP

	GATCCCTCTG	CTACAAACAC	ATACCTAGAT	TTCTCATATT	TTTACTGAA	TACATATAAT	60
	ATATCATTTA	ACTGTCTTCA	TTCATGAGAC	GTCGTCTAAG	TTCTGTGCTG	CTCAACTTGT	120
	TTTTCCACTT	GTCAGCCTCT	TCGCCCCCA	GTACGTTTAC	CACATGCACG	GCTAGCTTCC	180
35	TCATTCCCTT	GCTCTCACGC	GTATCGTTGA	TTGTCTGGGC	ACCGGCCACA	GTTTCCCTCAC	240
	TCACTACCAG	GGCTTCGATA	CCAGGTTCCG	TACCCGTGGG	CCCGCACACG	TCATGTAACG	300
	CAAATATTTT	GATTTCCAGC	CCCGGTTTCA	GCCTGTGAAG	GAAGCTGCAC	ACGTTATCGC	360
	ATCGTTTCGTC	GAAGGACTGA	AGCTGCTCCC	TGTATTTCTT	TTTCCGCAGC	AGTTCTTCAT	420
	CTGTAATCCC	CACGATCAGC	CGGGACGCAG	TCACGAGCGC	GGCAACACTG	AGCAATATTT	480
	TATGTCCGTC	GTGTAAGTGG	TCGAAAGTGC	CTCCCAGCGC	GCTAACAGCG	TACTTGTCTC	540
	TACCGCCACT	CTCGACCGGC	CCCGCAGCCG	CCATCGCCGG	ACTATCAAAC	AGCTCTATCT	600
40	GCCTGTGCGG	GAACGCATCC	TGCAGCAGGC	GATCGCTCAG	GAATACAACG	TCCCACCTCA	660
	TTGCGCTGTA	CGCTTCCATA	CTGACGTTGA	ACAAAACATT	TATCGGGGTC	GTGTACAGCT	720
	TCTGCTTCAG	AAG					

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1538UP

	GATCCTTGGG	ACGACATCGA	CACCATTCTT	ATCGGTAACG	AACTTGTGAA	CAACGGCCAG	60
	GCGACCGTGG	ACCAGATGGC	TGGTTACATG	AAAACCTGGC	GCAAGTGCCCT	CGCTGAGGCC	120
	GGCTACAAGG	GCCCAGTTGT	TTCCGTGGAC	ACTTTTCATCG	CTGTAATCAA	CAACCCCTGGT	180
	CTATGCTGAC	TATCAGACTA	CATGGCTGTC	AACGCCCAACC	CATACTTCGA	CTTCCACACT	240
50	TCTGCTGCTA	TGGCCGGCCC	TTGGGTTTTG	CACCAGATCC	AGAGAGTCTG	GAGCGCCTGC	300
	AACGGTAACA	AGAAAGTTGT	CATCACCGAG	ACCGGCTGGC	CTACTCAGGG	TCAGACTTAC	360
	GGCAAGGCCA	TTCCATCCAA	AGCCAACCAG	AAGATGGCCT	TGGAATCTAT	CAAGGCCACT	420
	TGTGGTGATA	GCGCTATCCT	ATTACTGCT	TTTCGACGAT	ACTGGAAGCC	AGATGGGCCT	480
	TACGGTGTCC	AGAAGTTCTG	GGGTATGCTA	TAAGTTGCCG	TGTGCTTCTT	TATGACCTGT	540
	CTCTTTATTT	TGCTCGGAAC	CCTTACATGC	AGATGGGGGG	TGGCGGTGCA	TGGGCCTGCA	600
55	GCCTCCGGGC	CTGCAAGTTT	CTACATCGCC	CTACTTTAGC	TGCCACGGGA	CTTTTGAATT	660

TCTTTGGCAC GTGGTACTGC TGGCATCCTT CTCATAGAGC ACAGTGTGCC ACAGGGTATC
ACTGG

720

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1540RP

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GATCTTTTCT	TTGTCAAAGT	TCAACACCTG	TAAGCCGCCT	CTAGATACCG	CTCTAGAAAG	60
GGCCACATAC	GCTTGGCCCT	TTTCAAAAAC	ACGTCTGAGA	TCCACTTTCA	CTTTGTTTAG	120
TGTTTGGCCT	TGAGATTTAT	GAATGGACAA	GGCCCATGCA	AGCATGAGTG	GCAATTGAAC	180
TCTCGTACT	AGAGGCTTCT	CATTTTCGTC	CTCGATAGCC	CATGCCTCTT	CTCGAACTAA	240
AACTGTTCTG	GTGGTATTGT	CGGGCTGGAA	GAATTGCACT	AATGGCAACT	TCTTACCCCT	300
TGAGCTCATG	TGAACTTCCT	GTAAGAGCTG	CTTCTTCCGT	TCTAGATTGG	CCTTCACTTC	360
AGGATCTGTG	ACTTCTCGAT	CATCCTTTAA	GAAATCGAAT	ATCGTGTCCG	CCAAGTGGTC	420
TACAGTGTCA	TCTGTGTCTA	TCGTCCCTAAA	CTTCTCTCGC	AGAGCTTTCT	TGACCATGCT	480
TGTGCGGGTC	TCCTTCTTGG	GCTCCTCATC	CTCATCAAGC	TCGGGGGCGT	TCCAGTCGTT	540
TTTCGCTAAT	GCATCCCAGT	ATTTCTCCCA	TTCTGCAACG	TCAAGATCAT	CATCGCGAAC	600
ACTTTGATAG	AACATAAATG	TTGCCTCATC	GATGAAGTCA	ATGACCTTCC	CCAGTGATCC	660
GTTTACGAGT	GTATCATCGA	AGTTCTTAAT	GTTCATAACC	TGTGCGCCGA	CTTTAA	

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1540UP

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GATCTCCTGC	GCGAAGAGCA	CGCCCTGCGC	CCATCCGGCA	TAGGGGCCCC	ACTTTTGTAT	60
GAACATTTCC	CGCACAAAGT	CCAGCTCCAT	GTTTCAGTTT	TTGCGCACAC	TGGGAAGGTC	120
CTTGATTCGC	GCTTTCAGCG	CAGCGATCTT	CGCTGCCGAT	GCATTGAACT	TGTAGTCTCT	180
TTGTGCGATC	CTGTTGATGT	GCACGTCTAC	AGGCACATGG	TCGTCCATCT	GCATGCCCCAT	240
GAGGCAGACG	CAATCTGCGA	CCTTCGGACC	CACCCCGGGA	ACCTCCATAA	ACCGCTGACG	300
GATCTCCTCC	CGCGATATCA	TGTCTAGCCA	GGATTCCAGG	TGTTTCAGTAT	CGCTCATGTG	360
TGCCGGTTTA	CTTGAATCCA	TCCATTCTGC	CGCAGCCATG	ATATACTTGG	CGCGATACCC	420
AAACCCCAAA	TCCCGCAGTG	CGTCTCTGCT	AGCGCCTTCC	ATCAGCTGCT	TGCTGGTGGG	480
GAATGAGTAG	TATGGAGTAC	CGTCGAGCTC	GCCGAGGAAG	CTCCCGTACT	GCGAACACAG	540
TGCATGGCAC	ATCTTCGTGA	TGCGCCCGAT	ATTGTTGTTG	CTAGAGCAAA	TAAACGAGCA	600
CAGTGTCTCC	CAGGGTTCTT	GTCGCAGTAT	TCGCACGCCA	CGA		

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1541RP

	GATCGAACAA	CCATACTTTA	GGCCACACG	ACCGTTCCCC	TCGGGGATAT	CCTGCCGCCC	60
	CTCTACAAGA	TTGGATTCAA	TCATCACCCC	ACAAATGGCA	TTCTCACCTT	TACTCAGCTG	120
5	CTCATAGATA	TCTTGGGCGA	CTTTCGGCTG	GTTGCGGTAA	TCCTTGTTGG	AATTTCCATG	180
	CGAGCAGTCA	ATCATAATCC	TCCGCTGGAC	CCCAGCGCTG	TCAACTAGCT	TCGCATTGAC	240
	CAAGTCCTGC	TTAGCCTGTT	GTACACTGGC	AGCGTCATAG	TTTGTGCCAT	CTTTACCACC	300
	GCGTAGAATG	ATGAAGGTGT	CCTCGTTACC	TTCAGTCCCA	ACAATCGCAG	TCACTCCAGG	360
	CTTGGTAACC	GAAAGAAAGT	AATGAGAGTG	AGCAGCGGCA	CGCATAGCGT	CAATAGCAAC	420
	CTGTAAGCAG	CCATCTGTCC	CGTTCTTGAA	TCCGATCGGG	AACGATAGTC	CAGAAGCCAG	480
10	CTCACGGTGC	AGCTGCGATT	CTGTCTGTCG	GGCGCCAATG	GCGCCCAAGG	AGAAGCAGTC	540
	GCTTAAGAAC	TGCGGCGATA	TGGTGTCTAG	CATTTCGCCC	GCAATTGGAA	TGTGCTCCAC	600
	CAGCTGCGTG	TACATCTCCC	GCGAGATACG	CAATCCCTTG	TTTATTTGGA	ACGAATTATC	660
	GATGTCCGGG	TCGTTGATGA	GCCCCTTCCA	CCCCACCGTG	GTCCGCGGTT	TTCCAGATAC	720

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1541UP

	GATCAGCTGA	TGAAGATTGT	ACGTCATCAC	TGCTATTTAA	CACAAACATA	ACATAATTCA	60
	TCCGCGATAG	TTTAATGGTT	AGAATTCGCG	CTTGTGCGCG	GCGGGATCGG	GGTTCAATTC	120
20	CCCGTCGCGG	AGCTTTTTGT	GACATTTATT	GAAACGGTTG	TCGTTATAAC	CGTTCCGATG	180
	GAATGTGGCA	GGACCCTGTA	ACGGCGACGT	ATCCTGCAAC	TTCGACGTGT	TGTCGCGTCT	240
	ACGCCAGGGC	TTGGGCTTCC	AGAAATTGGC	TTTCCCGGAG	CCCGAGTTTT	TGTGACCCAA	300
	TATTTGAGCT	GCTGATCATC	AAGCTCTAGT	CGCACACAGG	GGGCCCCGAGT	ATCCATTGAC	360
	AAAGGTGCGC	GCAACATCCG	ATCGCCGGGT	CCCTTTATAT	ATAAATATAC	ACTAATGACA	420
	CATGCGAATA	CCCCACTGCC	GTGGATAGGG	GACGTTTGAG	GCCTCATACC	CCTCAATACA	480
25	GATAACAAAA	TTGGAATATA	GGAGAAGAAA	TGTTTCGAGAG	GCTAAAACTT	AGGTTCCGGC	540
	GATGCAGAAG	ACTCAGAGCC	AACCGTTTAG	CAGACGTTCC	ATACCCGAAT	CCCACGTTGA	600
	ATTCCGCAAT	CATTTCCAGA	ATCGACACAA	TCACGGTGTC	AATCTCGGGT	CGCTATCGTC	660
	CTTGAGAAGT	GGATATCGAG	TCGATGTTCC	AATGTGGCGG	CGAGACCGAG	CATGCGGGGA	720
	TCAGGAAGAT	GA					

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1542RP

	GATCATGTGG	AGGAACTCGG	GCAGCGTCTC	GGAGCCGGCG	TAGTGGGCTA	CTGTGGCGGC	60
	GCGGGCAGCC	GACTGCTCGG	GGTATTCGGG	CGCCGGCGCA	GCGGCGTGTG	AGCCGATGCT	120
35	GCTTCCGGGG	TGGCGGGCGG	CGAAGGCGTC	TGCGCGGGCG	CGACGGGCGC	AGGGCGAGCC	180
	CCCGTCGGAG	AGCGCGAGCA	CAAGGCAGTC	GAGGGCGAGG	AGCATGAGGG	TGGTGGCGAT	240
	GGTGGGGGCG	TTGAGGCCGT	CCTGGACGAC	GCGCTCGCGC	AGGTGGGGGG	GCTGGAAGAC	300
	GGTGATCAGC	TGATGCGCGC	GGCGGGCCAG	CGTCCAGGCG	GGATCGCCCG	TGACGGCGAT	360
	GAGCGGGCTG	GCGGGTGCGA	AGCGCGCGCT	GCGCAGGTAG	GCGGCGAAGT	GCAAGAGCTC	420
	GTCAGTCTCG	CCGGAGTGGG	AGCAGAGCAG	CAGGGCGTGC	CCGTGCGCGA	CGATGCCGAT	480
40	GTCGCCGTGC	ATGGCCTCCG	TGGGGTGGAA	GACGGCGGCG	GGGATGCCGA	ACGAGTGGCA	540
	GGTGGCGACA	GTCTTGCGGA	TGATGCCGAA	GGACTTGCCG	CAGGCGACGA	ACACGAGCTT	600
	GCGGCGGTCC	GCGA					

1542UP

	GATCACTTTAC	CTACGCATCG	GCCTGCCGCG	CATTGCCGCA	GACGGATCGC	TGCGAGACGG	60
	CTACCTGGAA	CACTACTACG	AGAACGCGTA	CGCCGCGGCC	CTTCTGGACG	GCTGCCGTGT	120
	GCAGCGCCTG	ATAGGACTCC	ACGCGCTGCC	GCTGTAGCGA	GTCATGCCGC	TGTGCCGGAC	180
	CCGAGCGGTT	TGCCGTCTCG	GGAGCCTCCG	GGTTTCGCACC	GCTGGAAAAA	GGAGGGCCAC	240
50	GCTGGTATAT	AAACGGCACA	CGAGCCATCC	GGCGTCAGGA	ATAGCGTGAG	TCGACAAGAT	300
	GGGTGCGGAA	CACGGTCCTA	AGGACCTTCA	GAAGAAGCCT	GTGAGCTTTT	CCAACATTGC	360
	CCTGGGAGCG	GCGTTGAATA	TGTGCGAGGT	CACGACGCTT	GGGCAACCGC	TTGAGGTCAC	420
	CAAAACGACC	ATGGCCGCAA	ACCGGCAGTT	CGGCTTTTTCG	CAAGCGGTGC	GGCACGTGTG	480
	GTCCCGTGGG	GGCGTGTTCG	GCTTTTACCA	GGGGCTGATT	CCGTGGGCTT	GGATTGAGGC	540
	GTCCACCAAG	GGCGCGGTGC	TGCTGTTTGT	TTCTGCCGAA	GCCGAGTACC	AGTTTTCGGCG	600
55	GCTTGGTCTC	AGCAACTTCG	GTGCAGGCAT	CCTGGGCGGG	TGTCTGGCGG	CGTA	

1544RP

	GATCTCAACA	AGATCAATAG	GCATATCCTG	CCGGCTAGGG	ACACCACTGA	ATTTTATGAC	60
	GAGAAGGCCG	AAGAGTTCGA	CCGCAGTGTG	AGAATGGAAG	AAATGGCCAT	TCGGATGGGC	120
5	AAACGGCGCA	AGTGGCTGAT	GAAGCACTGC	GAGGGCGATG	TGCTAGAAGT	TGCATCTGGT	180
	ACTGGTAGGA	ATATAGATTA	CCTAGACTTG	AGCAAAATCG	ACACAATCAC	CTTTCTGGAT	240
	GCGTCTAAGA	ATATGATGAA	GATCGCCAAT	AAGAAGTTCA	GAGAAAAATA	CCCACACTTC	300
	AAACAAGCTG	CATTTCGTAGT	TGGAAAAGCA	GAAGATTTAG	TGGACCTGGC	GACTGGGCAT	360
	TGCGCTCAGC	AACAGAATCT	GGAATTGGTC	AACTCTCCTG	AGCAGGTGAT	CCCGGAGTCC	420
	AAGCCCAAGG	TTAAATACGA	TACCATCATC	GAAGCCTTCG	GTCTGTGCTC	TCACCATGAT	480
10	CCTGTACGGG	CATTGAAAAA	CTTTGCGAAA	TTGCTAAAGC	CTGGCGGAAG	AATAGTTCTG	540
	CTTGAGCATG	GCAGAGGGAC	CTATGACGTT	GTGAACAAGA	TTCTAGACAA	GAGAGCCGAG	600
	CACCGTCTCG	AGACCTGGGG	CTGCAGATGG	AACTTGATA	TTGGCGAAAT	TCTAGATGAC	660
	TCTGATCTAG	AATCGTCACC	GAAAAA				

1544UP

	GATCAAATTC	CAATCTCCGT	CAGCGTCAGG	CAGCCGCGTT	ATGTGTTGAA	CTCTTCGCTG	60
	CTTCTCTTCT	CTTCGCTGAA	CCCAGCAAGAA	AATTCCACCT	CACGCCGAAC	CAGAGGCCGAA	120
	AAACTGAAAA	TGAAATAAGG	CGCCGGCTTC	CGAGGACGTT	GCGGGCTCGT	GCAGCTCTAC	180
20	TTGCAATACC	CGCAATAGGA	CTACCAGACC	TTATTAGACA	CTGTAATATG	TGGGCAGCAG	240
	TAGGTGCAGT	CTACAAACTT	TTATAGCGCA	GCCGGGCGTA	TTACTCTTTT	CTGCTCCCGC	300
	GTCCGCGATA	AGTTGTGACT	CACAGTCCCG	CGGACGGAAC	GTGCGACCGA	GTGCGGCGAA	360
	TAATGAGTAA	TGTTCTATGT	ASTGGTTGCT	AGGGGGCTGA	AGGCTATGCT	CTGGGGTAGC	420
	TGGAATGTCA	CGCAGAACAT	GGGCTTCGTA	GGTGCCACTT	TGCGCACGAG	GTGGAACGAC	480
	AGCGCAGTCA	TGGGCAGGAT	GTCTGCGCTG	GTGTGCATTA	TCTCGAGCAC	ACGGCGGTGT	540
25	ATGCGGGCGT	GCAGGTCTGC	TGGCGCGGGC	TCGGGGCTCGT	CGGGGGCTGTA	TTTCTCGAAA	600
	CAGTGACAGT	GGATGTAGGG	CAGCACCAAW	TGCTGGGTCG	GCAGCGGCGT	CCTCCGAGAT	660
	CCGTGGCGCG	AGTACAGCCC	GGC				

1545RP

	GATCATTAAT	CAGCCATCGC	ATACCCGGGC	AAGATGACCA	TTAGCTCCTG	CTTTCGACAG	60
	AAACAACGGA	CTATGGGTAT	AGAACTTGAT	GATAGAAGGT	TGAGGCATTT	AAAAAAGTGG	120
5	CTAGACCGGG	CTTTAGATCC	GCCTACGACA	GACGAGAGCG	TCACAGCCCT	TGTGAAGGAC	180
	TATGTACTAC	AGGTACTACT	AGAGTGCAC	ATCGCAGCTG	TGAAGGGCCG	AAAGAACGAG	240
	TTCTGCGAGC	AGATGAGCCA	GTACCTGGCA	GGTATGGTGA	AGGACCACAG	CTGTCTAGAT	300
	GGGTTGTTTT	ATCAGCTAGT	GGACTTAGGC	GAGCCTCCCG	CGGGGAATAG	TTGCGGGCGA	360
	CAGCTGCGTG	TCCTGAAAAT	CCCAGCGGAC	CGGCTTCGCT	GGGAAACCTT	GCGTGCGGAG	420
	TTTGCGCCTT	TTGGAGCGGT	CACCAGGGCG	AGGATTGATT	ACGTGCATCG	TGAGGCATTC	480
10	TTGGAGTATG	CGGATGCGGC	CAGCGTCGTC	CGATGTTGTT	CGGTCCGGAA	GGCTTTCTTG	540
	GGGAACCGGT	TCGTTGAGGT	GCAGCCCTGC	TCCGCGAGCG	TGGGAATCAC	TAAGCGGTGT	600
	CGACGTCTGG	CCGCCGGATC	ACGAAACAAC	TGTGCCCGAG	CATGGATCAT	CTGGGGTGCC	660
	TCCGCGAACT	GGTGTGTCT	TGGATCGTGG	ACGTGCGCCT	CCGCCTGTCA	TCTT	

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1545UP

	GATCATCTTG	CAGGGACCGC	WCCACGTGGC	GTAGAAGTCC	ACGACCACGA	GCTTGTCCGA	60
	GGCCACGGCG	GACTCAAATT	CAGAAAGGGA	CTTGATTTTC	GACACCATTG	CGTTCTGTGT	120
	GGCTGACTGT	ACCTTGTGTA	TACGCAGTAC	CCAGGAAGCC	GGGCGGAGCC	CCGCCTTTTA	180
20	TACCCGGCCG	CCTGCGGTCA	CGTGTCACCA	CGTGCGGGGT	CTCCCCCTTA	TTTCCGCTCA	240
	GGAGATAAGG	ATGACAAACG	CGTCTCCGCG	CGGTCCGCAT	TGACGTCTTC	GACAGCAATG	300
	GAACCTCTGC	TATAAGCGGT	GTCTGCGCGC	CGAGCCTTCT	CAATCGTCCG	TCTCTCTGTT	360
	CGCTTTGTGT	ACGCCAGGCG	CGGGTTTGT	TACGTTTCGG	ACGGGGTTGG	ATCTCCAACG	420
	CACGGTCGAA	TAACGAACAT	GAAAGCCAGT	TGTACAGTAG	CTACACCCCA	GCAGACGAAG	480
	CATCAGCAGG	CAGTTGAGAG	CGCGTACGAG	AAGTTCCGTT	ATAGAGCACA	CTCGAGACCA	540
25	TAGAGGTCAT	CCGCTAGGCG	GTACTTCAGG	TCAGGC			

1546RP

	GATCTTGCTG	CTATCCAGAA	ATGGGAAGTT	CTTAGACAAC	GGGGAATTAA	GCCCCTTTTTC	60
30	CAATATTTTG	AGCGTCGTTT	CATAGCTCGG	AAGACGCAGC	AGAAGCCCCC	CCAGTAGTGT	120
	CTGTTCAATG	TCGCTCATGA	AAGGTGTCTC	TATCAAATCT	AGCTCCATCA	TCGCAGAGTA	180
	GTTATTATCT	TTCTTCCAAG	ACAGACGCAC	ATGCCGCAAC	TTCTGTCAGGA	TTACAGTAAA	240
	ATAATGGTAG	AACCGCGGAC	TCACAGAAGC	GACGACCGCT	CGAAATGAAG	TCGGCCCGTA	300
	AAAGATCGTG	CGGCCCTGCT	TCTCTATCAC	AAGATGGAAC	TGCGAAAGTC	TGTTTACGGG	360
	GGACACCGTG	CCCATAACTG	GCTTCTGCTG	GAACAGCTGC	GGTACCATCT	CGCTCTTCAT	420
35	CCGCGCGAGC	TCAGTCTCAA	GCTCGTCTG	CCGTCGCAGC	AGCTCCACAT	TGGGCGTCGA	480
	GCTGAACAGC	TCCCGTGAGT	TCACGTCGAT	CGTAAACTCA	GACAGGTACA	CACACTCGGG	540
	CAGGCCCTTC	CCAATACATG	TAGAGCACTT	CGGCCGCGCC	TTGTTGCACT	TGACGCGCCG	600
	CTTGCGGCAG	AACACGCACG	ACTTGCTGAC	CTTCCGCCTG	GTTTTCACAA	TCTTGCCATC	660
	GGACTCTGCC	ATCCCGCCAG	CTTCAAGCAA	AATGAGTAGG	TCATATTATT	TACCTGCTGG	720
40	TAATCTTGAA	TAATGCTCAC	T				

1546UP

	GATCGCGGAC	TGGAACACTG	GCCGGAGATG	CGCGCGGCCA	TCCTGGTGGT	TTCTGCGGAC	60
45	CGCAAGGACA	CGCCATCGAC	GAGCGGTATG	CAGCAGACGG	TGCACACGTC	GGACCTCTTC	120
	AAGGAGCGCG	TCGCGACGGT	GGTGCCGCGG	CGGTACGGAG	AGATGGCGGC	GGCGATCCGC	180
	GCGCGGACT	TCGCGACGTT	TGCGCGCCTG	ACGATGCAGG	ACTCGAACTC	GTTTCACGCC	240
	ACCTGCCTGG	ACTCAATTTCC	GCCGATCTTC	TACATGAACG	ACACTTCGCG	CCGGATTGTC	300
	AAGCTGTGTC	ATCTGATCAA	CGAGTTCTAC	AACGAGACCA	TCGTGGCGTA	CACGTTTGAC	360
	GCGGGTCCGA	ACGCGGTGCT	CTATTACTTG	GCGGAGAACG	AGGCGCGGCT	CTGCGGCTTC	420
50	CTCTCTGCCG	TCTTTGGCGC	CAACGACGGC	TGGGAGACCA	CGTTCTCGAC	GGAGCAGCGC	480
	GCCACCTTCG	CCGCGCAGTT	CGACGAGTGC	GTGCGCGGCA	AGCTTGCGAC	GGACCTGGAC	540
	GACGAGTTGC	ACAGAAGAGT	TGCCCGCCTC	ATCTTCACGA	AGGTGCGGCG	AGGGCCCCAA	600
	GACACTAAAT	CCTCGCTCAT	CGACCCGAGA	CGGGCCTGCC	CGCTGACGCT	ATTCTCCTGC	660
	TATTTTCTGC	TCTGTATACC	CTGCCAGACC	GCGCTATATA	TATAGAA		

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1547RP

	GATCCTCCGC	CTACACCAGA	ATATTTCTGG	CCAATTAGTT	GTTCAACATC	GCCCCGAACG	60
	TTGGTGAAGC	CACGGCCATA	CGCTGCCATG	CCGAGTGCAA	TTTTTCITGG	GCTGACCTTA	120
5	AATTGTTCCG	TCATCATGAG	TATCGCATCA	TGTGCATTCA	ACTCATCAAA	GTTGTCAATA	180
	CCCATATCTT	CATACCGACG	CTTATCTAGG	TGCGATTTGT	ACGGCGAATT	CGTAGCATTG	240
	TACAAGTTGC	TATGGTAGCC	TGTTGCTCT	GACCATGCAC	CGTGGTAGTC	GTATGTCTATC	300
	ATATTCCACA	TGCTGAGATA	CTTGTTTCATC	TCCTCAACCG	GGAAAATGCC	AAGTGTCTGA	360
	GGAAAGGCCG	GTGCTGCCAT	GCTTAAAGTGG	AAGCGCGGTT	CTGTAGTCCC	GCCGGGGCCC	420
10	CAGATATTGT	CTTCCAATTC	GTCCATCTTG	TGTCGCAAGC	GGCTACACAT	TTCTAGATAC	480
	ATCTGGGGTT	CGTAGCCATC	ATCCTTAGGG	AACTCCAGT	CAAGATCTAT	CCCATCGAAG	540
	CCGTACTCAA	ACATTGCGTC	GATCGCCGAG	TCGATGAAGT	TGTTAAACTT	CTCCTCGTCA	600
	CGCACAATTT	TATGGAACGG	CTCCCGATTG	GAACAGCCGC	CAACGGGCAT	CATGAGCTTG	660
	AAATCGGTCC	CTGGCCGCGT	CTTGAGGTAA	TTAAGCTTCG	CCTATTGCC		

1547UP

	GATCTCTGAG	GGTTCCAAGG	CAAGCCCGCC	GGAGCTTGCC	CAAATTGTGT	CACCCGCTCT	60
	CGAGTAGATG	GTGGCCTTGT	CGACCTTCCC	GGTTGCTAAC	AAGTTGTCAG	TGTAGGCTAA	120
	AGCTCTAGTT	AGTACCCACG	AACGGGCCAC	GAGCAGAACA	CGTAAAAACA	CATACCTTGC	180
20	CAAGACATGA	TGCGTTCGCG	ATGAAATCTG	AGTTAGTGCT	AACACTCGCA	GATGCTCTGG	240
	TGAGTGGAAT	CTACGTATCA	ATAGTATTGA	TTTGTCAATA	AATATACCTT	GGCTTTTTGT	300
	AATCTTTTTA	TATAAGGGGT	TCCGATCTGC	TGACATCATA	GCACACGAAT	TAAGTATCCG	360
	GGTAACGAAC	TGCCCCGGTA	ATGCGGGGCA	CAGGGCAAGT	GCCGGGTAAC	GGCATCCACA	420
	TACCGCAGAG	ATGCACTGGC	GGCTACATAC	TGTACACAGG	CTCGCAGCTA	CTCGTCTGCT	480
	GAGTCGAGAA	CAGCCACCTT	GCGACGCTTG	AGAGCGACCT	CTTCATCTGC	GCGCGGGGCC	540
25	GGCGGGGCAG	CAGCGTACTT	GGCTGCGCCC	TCGCGTTTCA	GCTGCTGCAG	ACGCGCGGCG	600
	TTTAGGTC						

1548RP

	GATCATCATT	GCTCGGTTAG	CGATTGCCGG	CAATTTTACA	GCTGGTTCAT	CGCTAGGCGG	60
	TAAGGCGACC	GCGGGTAGTT	TCCTGTCCTA	CGGGTCCGTG	GTGTTTGGTT	TTGCATCGGG	120
	ATGGACAACA	TATGCTGCAG	ACTACACTGT	CTACATGCC	AAAAATTCTA	ACAAATACCG	180
	CATCTTTTTT	TTCATGATTG	CGGGTCTTGC	GACCCCGTTG	CTGTTACGCT	TGATTCTTGG	240
	AGCTGCTGCC	GGCGCTGTG	TGCACACAAA	TCCTACGTGG	GGCGAATATT	ACAAAAACA	300
	TTCCGTGGGA	GGTCTGTGCT	TTGCTATACT	GGCTGAAAAC	GCTCTGGGCG	GGTTTGGGCA	360
35	GTTCTGCTGC	GTGTACTGG	CCATGTCCAC	AGTTGCAAAC	AATATTCCAA	ACATGTATT	420
	CATCGCTCTC	AGCACCCAGG	CGCTGTGGAG	TCGTTTCGCG	CGTGTGCCAC	GAGTGTCTG	480
	GACCTGGGTC	GGCAACGCAT	GCAGCTTGGT	CATTGCAATC	GTTGCGTACT	ACAAGTTTGA	540
	GACCTTCATG	ACCAGCTTTA	TGGATTCAAT	TGGCTACTAC	CTCTCCATAT	ACATCGTAAT	600
	ATGTGTCACT	GAGCACTTCG	TCTTCCGCAA	GGGCTTCCGT	GGTTACACGT	CAGCCACTGG	660
40	GAACGTCCCG	ATCTTCTCTC	AGCTGGTTAC	GCTGGCTGCG	CTGCGC		

1548UP

	GATCGACAGA	TTACAGTTAC	AAGCGAGAGT	TCGGCCTATT	TAAGGAACAG	AACCTATACC	60
45	ACATTTGAAG	CTCGAGTTTT	GGCACGCCAA	GACCGATTTG	CGGATTAAGT	ATCTTGAAGT	120
	TTGCACTCAG	ACTCAAGAAC	TACTATTACG	ATACTATAAC	AAAGACGATG	ACTAGCACAG	180
	CCGACCACAA	GCAGCCCAT	TCGTTGAAGG	TTAACGGGGC	TCTATTTCGAC	GTCGACGGGA	240
	CCATCATCAT	CTCGCAGCCC	GCGTAGCCGG	CCTTCTGGAG	GGAGTTTGGC	AAGGACAAGC	300
	CGTACTTCGA	TGCGGAGCAT	GTCATCAGTG	CCACCCACGG	CTGGAGAACC	TACGACGCCA	360
	TCGCTACCTT	CGCGCCAGAC	TATCTGAGTG	AGGAGTACGT	GACGAGACTG	GAGGGCGAAA	420
50	TCCAGACAA	GTACGGCAAG	TTCTCCGTGG	AGGTTCCCGG	CGCTGTTACG	CTCTGCAATT	480
	GCCTTGAACR	AACTTCCGAA	GGAAAATTGG	GCCGTTGGTA	CTTCCGGCCC	CTTCCAGATG	540
	GCACCAAGTG	GTTTCGATGTC	CTCGGCATCA	AGCGTCCTAG	CACCTTCATT		

1549RP

	GATCTGCTTG	GTCTGACCAC	CGAAACCGA	CTGCTTACGG	TCATATCTTC	TCTTACCCTG	60
	AGCAAACAAG	GAAGCCTTAC	CGGCCTTGTA	CTGGGTCACC	TTGTGCTGGG	TGTGCTTGCG	120
5	GCAGGCCTTG	CCCTTGCAGT	AAGTCTTTCT	GGTCTTTTGA	ACGTTAACTG	CACACGTTAG	180
	TATACGTCCT	CTTGGCGAGT	CCCTTTTCGA	TCTGCAGCCG	CGCCGTCAGA	AGGCCCTGCT	240
	GTAGCGAGCC	GTGGCCCCCT	GGCGGCGCTC	CGCGCTTCCC	CTCCGTCATA	TTGAACATAC	300
	CCATTGCGAG	AAGTAGCTTC	TGTGATGCTC	TGTGCTTACT	ATCAAGCAGG	ATGACACCCG	360
	GCCTTGAATC	CTGAAATTTA	CCATGTTTTT	CGCTTCGCGA	GGTCCGGCCC	CGGGCCGGCC	420
	GGCTGCCCGC	CCGGAAGGTC	CAGTGCTGCC	CGGCCTGCGT	CGCCCCAGTT	CACCCGGGCC	480
10	ACCACGCAAG	GTGGTGATGC	ACGCATGTGC	AGTATGTGTG	GGTGTGTAAT	AAATAGATGT	540
	ATGGGTGTAG	TCACATGTTT	GTCACAGGCA	CTCCTCCGCG	GCTAACGCCT	CGAGATTGGC	600
	CAATGCGTGT	GGCGGCATAG	GCGATGGCAG	CCATGCCTTG	AGCTCTGCGC	GGGGTTAGAG	660
	CCCAAGTCAT	TAGACTGCGG	CACTGCAAGC	GTCTGACCGG	CAGGTTTTAA	GCTGGTGTGT	720
	GGCCCTGCGC	TACGTT					

1549UP

	GATCCATGTA	TAATCACCCC	ACAGCACCTT	TTGCAGGTTT	TCGCGCTTGG	CCCCAGCTT	60
	CTGCTCGTAG	AACCTTCGAA	ACAGACTGAC	GTTGAACCCC	CACCCATCTG	CAGCAGAGGC	120
20	AAAAATCACA	TTGTTCCGGG	ACGGGTCGAA	GTATATGTCC	GCATCATCCC	GCTCCACATA	180
	CTCGGCCTGG	GCGTCTTGCT	CCAGTTTCTC	TCTCCACGAG	AGGTCATCCA	GCAGCCGCTC	240
	CCCGGCAAG	AAGGACCCCA	GTACAGAGTT	GACCTGTTCA	ATCGTCTTCG	ATAGATGCAC	300
	GTAGGCCTCC	TGTGGCGTCA	GCTGGAGCTC	CGTGATCAGC	CGATCGATCT	TGTTTCAGCAC	360
	CAGGATTGGT	CTCAGCTTCT	CCGTCCAGCA	CTGCCGCGAG	ACCGTAATCG	TCTGCGAACA	420
	CACACCCTCG	ACCACGTCCA	CCAGCACGAT	CGCGCCATCA	CATAGCCGCG	ACGCCGCGCT	480
25	AACCTCGCTG	GAGAAGTCTA	TGTGGCCCCG	AGAGTCGATC	AGGTTGATTA	AATGTTTCGTT	540
	GACCAGCGGC	TCGCTGCTCC	CCTCCTGTTT	GTGAAGCACT	CCGAAGTTAC	AGAGAAATCG	600
	CACTGGACTC	CATCGTGATG	CCTCGCAGCT	GCTCATCTGG	CCGCGAGTCT	AGGAATCGCA	660
	CTTTCCCCGC	TAACCGCTGT	GAGATAATAC	CGTTGGATGC	GAGGAGG		

1550RP

	GATCGAGTAC	ACAAAGTACA	TGGATGCTGC	CAATAACTAT	AGTCTGAAAT	CAATGCGTTT	60
	CTTAGCGAAT	GCAGATGAGT	TGGCGCAGCT	GGCATCATTT	AACTCCATCA	GCCATTATTT	120
	ATTGGCTGAA	TGCCCATCTG	TCCAGACACT	ACAATTTTTA	TAAAGCTCAT	CTAAATTGTA	180
35	CCCAAAATTA	ACGAAGGAGA	ATCAAGAATC	TGCAATTATC	GAAACACTGC	TGTCTCTCAG	240
	TGAATTTACG	TTGCTGCACG	ACTTCTCTCT	CCAGGCAGGT	TTCCAGGTTC	AAAAATCGGT	300
	CATTTTGAAG	TACTTTTGGC	GCTTTTTTCA	CAGCGCACCA	AATGGGTCCA	GGGGACCGGC	360
	CAGAAATGAC	AAAGGCGAGG	AACAATCTTC	GCTTACTGCC	CAAAAAGGAC	TATTATTATC	420
	TTGAGACTCT	TCTTGATGTC	GCAGACGCCT	TGGCAAAGTA	TTGCTAAGC	TACTCACGTG	480
	GACAACCCCT	CAGACCATCG	CATATATTGG	ATCTCAAAGA	TGATCCATTG	AGAATCATAA	540
	GCAAACTGCT	AGAAACGAAT	CCCAGTCTGT	ACCGTGACGT	TGAAACGACT	TTCGAAATCC	600
40	TCAAGCAATT	ATATGAAGGA	TTGCAACTGC	AGCCTCATGA	TCCAAAGTAC	ACAAGTGAAT	660
	ATACCCGTTT	GCTAGTCTGT	CACATTGATT	GTGCATTGGC	AAATAT		

1550UP

	GATCTCCTCC	CGCGATATCA	TGTCTAGCCA	GGATTCCAGG	TGTTTCAGTAT	CGCTCATGTG	60
	TGCCGGTTTTA	CTTGAATCCA	TCCATTCTGC	CGCAGCCATG	ATATACTTGG	CGCGATACCC	120
	AAACCCCAAA	TCCCGCAGTG	CGTCTCTGCT	AGCGCCTTCC	ATCAGCTGCT	TGCTGGTGGG	180
	GAATGAGTAG	TATGGAGTAC	CGTCGAGCTC	GCCGAGGAAG	CTCCCGTACT	GCGAACACAG	240
	TGCATGGCAC	ATCTTCGTGA	TGCGCCCGAT	ATTGTTGTTG	CTAGAGCAAA	TAAACGAGCA	300
50	CAGTGTCTCC	CAGGGTTCCT	GTGCGAGTAT	TGCGACGCCA	CGATGTGTTT	TCCCGATGAA	360
	ACGTGTGTCT	GCTTCTTGCC	ATTCTGTCTA	CAAAGCCTCT	AGGTTACCTT	CCATCCGTAG	420
	GTAGCGCATC	AGCCATTGTC	GTGCGGCCCC	GCTGCAGTCG	TCATCTTTAT	TCCCGCTAC	480
	GCTGAATTCA	ATACTGCACT	GATCGGGCTG	CTTCAATACA	ATAATACGAT	AGCCCGAGTT	540
	GTCATTTAGT	AGCATGCTCG	CGGAATAGTA	CCTTTTCTCA	TGATTCCAGA	TCCACCTGAA	600
	CGCTTGACCA	CATTGCAATA	CATGGTCCAG	GACTATTTCT	CCCTTTGGGA	ATATCAATCT	660
55	GTTAAACTTC	ATAACTGTGC	ATACAGCACT	GACCTCGCTC	TAATAATCAG	CGTCACGGCG	720

CTGGCTCGAG CATGTT

1551RP

	GATCTCACGT	GAATCGGATA	TCTGCTCAAC	GGCCAATTCT	CGTATATTCT	GACGAGATCT	60
	TGGCGTCAAT	TACGTGCACT	TTGGCCGAAG	CCTTCGCACG	AGCTTCTACG	ATACAGAATG	120
5	CTGCCAGGTG	CATCTTAAAA	AGCGGGTTTA	CAGTGAGCCC	TCCGTCCTTC	AGGGCACCAG	180
	CCCCTAACTG	TACATAGTTT	CTGTATAGTA	GTTTGCCTTT	CCTCGCGATG	CCTGCCTCTT	240
	GTGGAACAAA	AACAGGCGGT	AGAAGGAAAT	TCCCGTGCGT	CATCGGTATC	GGACGGCGTC	300
	TGCCTGGATC	TGCGGAGTAG	CTTTATGAGC	CATTAGTGAG	GAACGCCAGT	TTCGACGACA	360
	GATTTAGTCT	TTTCTGTGTT	CCTGCAAAACA	GGCTTGGAAT	GTATCAGCGC	GCTGGCGCAG	420
	CGACAGGCGA	CACCGCTTCA	CATAGGGAGA	GGCCACCCAC	TGAACACGCG	GTGCACTGTC	480
10	AGGGGGCGCA	GCGTACTGCC	TACAATGGTA	TCGTCCGCAA	ACGGCAGGCC	AACCGGCAGA	540
	GCGGGCATT	AGATCTAAAT	TTATCAGCCC	ATGGACGGAT	GGATTTACGG	CAGCGTGTCT	600
	CCGCAGCAGC	GGGCACGCCA	GACTGCGAGG	TGGCAAATAA	TTACATAGC	AACCTGCATT	660
	ATAAACATCC	CAAGTCATTA	AACCTACTAA	ATATTGTTGC	GT		

1551UP

	GATCCCGGTG	AAGCTGCGCA	ACTGACCGGT	GCGCTACGAG	GACCCGGGCG	GCGCAGTGGA	60
	GCTGGCGCAC	TACGACTACT	CGAGCGAGCT	GGACGCGTAT	CTGAAGGATA	TCGAGGTGGA	120
	GTACGAGGTG	CTGGCGTACA	ACTGGCCGAC	GTTTCTGGCG	TACGTGCAAG	AGCTGGAGGA	180
20	GGGGGAGTTC	CGCGAGTTCT	TCGTGCGAGCT	CTGCGCTAC	GCCGCGGAGA	ACGAGGTGTA	240
	CGGCGCGAAG	CTGTGGGCGG	GGCTCGTGAA	GGAGCGCTCG	ATGCAGGAGC	TGATCAGCGC	300
	CAGAAAGCGC	TCGTCACTCA	CGCCTGTGTC	CGCGCGAGGA	GGAGACGCAG	CGACGGCAGG	360
	TGGAGGACGA	CTGGCACAGC	AAGCTCGACG	AGCGCGACCG	CTTCTGCGG	CTGCGGAGCA	420
	AGCTCGTGCG	CAAGCGTGCC	AAGAAGACCA	AGGACGCGCT	GTGGACGGTG	CTGTGGGAGC	480
	GCTTCCAGAG	CGACGCTAAG	ATCGAGAAGA	TGCGGCGCCG	CAACGAGGCC	GCCACGGCCG	540
	AGGCGGGCGG	CGACGAGCTC	CTGACGCCGG	CGGAGCGCTA	CGCGCTGGAG	CAGGGGCAGG	600
25	GCTTCTTGG	CGCCTGTGCT	CCCTGTGCGG	GAGCCGGCGC	CGGCCCTGGC	CGTGCCCTGC	660
	AACGAGCTTC	CCGATGAATA	CTGCATCACC	AAGACTGACT	TCGACCGGCT	CGCTAGCCAC	720
	GGCATCCCGG	TCGAG					

1552RP

	GATCGTCGGC	TCATGCCACC	ACAACCTCCA	CGTCCACTGC	ATCTACCAGT	GGCTCAACAC	60
	CTCCACGTCC	AAGGGCCTCT	GTCCGATGTG	CAGGCAAGCG	TTTTCACTCC	GGGAGGGCAT	120
	CCGCATTAAC	GAGCCCCACC	GCGACAAGTT	CGAGAAGGTG	TTGATGAAGG	CGCGCCAGCA	180
	GAGCGTGGTG	AGCGTCGCGG	GCGCCAACCC	GGTCGGGCGG	GACCAGGACG	ACGTCAATCAT	240
35	CKACCAGGAG	TTTCATCCGCT	GACACTAACT	AGCCTGTGTA	CCCATGTAAA	AATAATGCTT	300
	CCAACCAGAT	TCGAACGTAT	GATCTCCACA	TTACTAGTGT	GGCGCCTTAC	CAACTTGGCC	360
	ATAGAAGCAA	TACGAGCGTC	TAGCGGACTG	CGCCGGGCTA	TATGCGCCGG	GCGTGACCGC	420
	GACGAAACGC	TGGCGCCCAA	ATACCTGATC	CCAGGTTTCC	AACGCTGGTC	ACGCAACTTC	480
	TGCCACGTGC	ACTGCACACC	ACGCCAGCAC	TATATAGCCC	CGCACCCGCC	AGGCGTTCTT	540
	GCCAGGTAC	CGCGTCCAGC	TGTGCTGCA	GCATTCCACC	TGAaaaagTT	TCACCAGCAG	600
40	AAAGACTTTT	CCACTTCTCA	ATAGCACTTC	TATCCCCTAT	TTCTCTAGCA	GTTTTGCAAT	660
	GAGCTACaCT	ACCAGACAGA	TTGGAGCTAA	GAACACCTTG	GACTACCGGG	TGTTTCATCGA	720
	GAAGGCGGCA	AGGTCGTCTC	GCCGTTCAC	GACATCCCAT	TGTaCGCGGA	nGAGaAACC	780
	aATCTTChAC	aTGGTGGTGG	AnAT				

1552UP

	GATCTTGCAG	ACACGCCTGC	GCCCGTAGTC	CGTGCAGAGTG	CAGACTGCGT	CGCCGAATAA	60
	ATAGCTTTGT	GCCAGGCGGT	CGCCGAGGCG	TTGCGGGACT	CACCGCATAA	AAGAAACACG	120
	CTGCGGCCGC	GCGGCCGCAA	AGCAGCCAGG	CGCAACGGGC	GCGCCGCAAA	AGCAACCGTG	180
50	ACACACGATA	TGGCAGATT	ACRTACATAT	TATACATAGC	CGGCCGCGGC	ACGCGGCTCA	240
	GCCGCCGAAG	CCGTACAAATG	TGCGGCCCTG	GCGCTTGAGC	CGGTACACGA	CGTCGAGCGA	300
	GGTGACGGTC	TTGCGCTTGG	CGTGCTCGGT	GTAAGTGACG	GCGTCGCGGA	TGACGGACTC	360
	CAGGAACGAC	TTGAGCACCG	CGCGCACGTC	CTCGTAGATG	AGGCCGGAGA	TGCGCTTGAC	420
	GCCGCCACGG	CGGGCCAGGC	GCGCGATGGC	GGGCTTGGTG	ATGCCCTGGA	TGTTGTTCGG	480
55	GAGGATCTTG						

1554RP

	GATCAAACTA	GGAATTTTGT	ATAATACTGA	AGAAGGTCCC	ATATTCAAGT	CTCTATCCAG	60
	CGATGATGAG	GAAGTGGGTG	AGATTGTGCT	GCACGACCTG	ATGAACAATC	TCGATTTTCAT	120
5	AACTATGGAT	CATCCTGACA	GATCGAGAAA	CCAAACTCAT	CAAGATAGAC	CGATGATGAT	180
	CAAGAAGTAG	TTTGAGATCC	CTCTGCTACA	AACACATACC	TAGATTTCTC	ATATTTTATA	240
	CTGAATACAT	ATAATATATC	ATTTAACTGT	CTTCATTCAT	GAGACGTCGT	CTAAGTTCTG	300
	TGCTGCTCAA	CTTGTTTTTC	CACTTGTCAG	CCTCTTCGCC	CCCCAGTACG	TTCACCACAT	360
	GCACGGCTAG	CTTCCTCATT	CCTTTGCTCT	CACGCGTATC	GTGATTGTC	TGGGCACCGG	420
	CCACAGTTTC	CTCACTCACT	ACCAGGGCTT	CGATACCAGG	TTCGCTACCC	GTGGGCCCCG	480
10	ACACGTCTTG	TAACGCAAAT	ATTTTGATTT	CCAGCCCCGG	TPTCAGCCTG	TGAAGGAAGC	540
	TGCACACGTT	ATCGCATCGT	TCGTCTGAAG	ACTGAAGCTG	CTCCCTGTAT	TTCTTGTTCC	600
	GCAGCAGTTC	TTCATCTGTA	ATCCCCACGA	TCAGCCGGGA	AGCAGTCACG	AGCGCGGCAA	660
	CACTGAGCAA	TATTTTATGT	CCGTCTGTGA	AGTGGTCGAA	AGTGC		

1554UP

	GATCACTGAG	GAAATCAAAA	CCTTGAGCAG	CTTCCCTGTG	TTGCGGTGTG	ACGGTGTGGA	60
	CTGTGCCCAA	GTGAGACTG	TCCTCCAGGC	CAAGGCTCCA	GGCCAAAAGC	TCTTCCTAGG	120
	TATCTTCTTC	GTCGACCAAA	TTGAGGCCGG	CGTGAAGGCC	ATCAAGGAGG	CTGTTTCAGAA	180
20	GCATGGATCC	TGGGACGACA	TCGACACCAT	TTCTATCGGT	AACGAACTTG	TGAACAACGG	240
	CCAGGCGACC	GTGGACCAGA	TGGCTGGTTA	CATGAAAAC	GGCCGCAAGT	GCCTCGCTGA	300
	GGCCGGCTAC	AAGGGCCCAG	TTGTTTCCGT	GGACACTTTC	ATCGCTGTAA	TCAACAACCC	360
	TGGTCTATGT	GACCTATCAG	ACTACATGGC	TGTCAACGCC	CACCCATACT	TCGACTTCCA	420
	CACTTCTGCT	GCTATGGCCG	GCCCTTGGGT	TTTGCACCAG	ATCCAGAGAG	TCTGGAGCGC	480
	CTGCAACGGT	AACAAGAAAG	TTGTCAATC	CGAGACCGGC	TGGCCTACTC	AGGGTCAGAC	540
25	TTACGGCAAG	GCCATTCAT	CCAAAGCCAA	CCAGAAGATG	GCCTTGGAAT	CTATCAGGGC	600
	CACTTGTTGGT	GATAGCGCTA	TCCTATTTAC	TGCTTTTCGAC	GACTIONTGA	AGCCAGATGG	660
	GCCCTACGGT	GTCGAGAAGT	TCTGGGGTAT	GCTATAAGTT	GCCGTGTGCT	TCTTTATGAC	720
	CTGTCTC						

5

GATCATACAC	GCATTGCAGG	TATACATTAT	AGTGCTCATA	ATTATCGGAT	TGCAAATAGA	60
ATGGGGCCCT	TACCGTAGTA	CTGTCTTGGT	AATGCAGCGA	CGCTCAGGCT	TAAGAAGCTT	120
TTTGTTCCTC	GTGTATTACT	AACAAAATAA	TTTCTCTCGAG	CACAGGGAGT	AGAGATGAAT	180
TACATAATCC	ATATGGACAC	CTCGTCACTT	TCCAGCGACA	TTAACATTTC	CTTATGAATG	240
CCCAATAATG	GTGCCTTAAAT	GATGTGCTTG	GTGTAATGCG	CATTATAAAA	TGTATGTGGA	300
TTATATATTG	TTTGTAGCAT	CTAGTAAAAAC	CATGGTAGCG	AGGTCTTTGG	CCATACCCCT	360
CTGAAGAGAG	ACATAGCAAC	AGTGTCTTTGT	GCAGACAGTC	TGCCGTCGAA	TGTTGCCTTG	420
AAGTAACCAT	GAGTACCAAG	ACTCTCCCTTA	ATGAAGCCAG	AGCGTCCAGA	TTTCGTGAAT	480
AGTGGGATCG	ACTTGAACCA	CTCGACATCT	TCTGGCCTAA	AGAACATATA	GCGCACTGTG	540
ACGACGCGCT	TGTGGAACTT	GAATGGATGG	GCAGTTAATA	TGATPTCTGT	GGCCAATATC	600
CGTGTGTGGT	CTGCGTTTCAG	GAACGTGCCG	TGGCCACAGA	ACGTCAGGCC	CTTTGGATCA	660
GAAGGGTTTT	CTTTGAAGTA	GACTGGCCGT	GACTGGGTCA	GGTCCAAGGG	AA	

75

GATCTGGGAA	ACAAGCATTC	CAACCTAGTT	GGAATGGCTG	GCAATTAGCA	GCTGCGGCAA	60
GGCAGATAAA	GCTAACTGTG	GCATAGTPTC	CGTGAGTTTT	GATTCGGTTT	CTCAAGCAGG	120
AATACTTTGC	TGGCCGCCAC	GGNCGCCGTT	TTTATACTGT	CAGGCCAGCC	CGCGCCCTGC	180
CGGGTAATGC	CTGGCAGACC	CGCTCTAGGG	CACGCCGAAT	CGCCCCGTAC	AACGCCTGCC	240
CGCGCAAGAT	GAGCACCTAA	AGGGCCGGCA	GCCTCCGCTA	GACAACTGA	TGGTAACGTC	300
GTATTGTAAT	ACTTAACTTA	TACAGGGTPT	ATTGATTATA	TTACTCAGAA	ACTGCCGTGA	360
GACCCACAGC	CCGCCCGCCG	AATTGTGTAC	AGTAGGCGGC	AGCGGGCCGC	CCGCCGCTCT	420
TAAACGTTACT	TGTGGAAACC	AATGTCGTTG	GCCTTCTCTC	TGAAGCACTG	ACGGCAGATG	480
TTCAAGCCGT	ACTTTCCTGAT	CAAACCAGAG	TGCGAAGCGC	ACACGCGGCA	CTGGCGGGAG	540
CCCTTACCCT	AGTTCCTTGG	GTGGGAGAAC	CAAACGTTTT	CGTGAGCCAT	CTTGTCTGCA	600
ATGCGTTAGT	ACTCTGTCTG	ACCGCTTGA	AACGCTCCGG	CCCTCGTTGA	GCTGCCCA	660
CGCTCGGCT	CTGCGGCGTC	CTCATTGCC				

3

GATCAACCAG	TCGGCCGAGT	CCTATACGAC	CGGCATCACC	CTGGTGTTCG	AACTTCTCGG	60
TGACCCCTCCG	ACGTACTCTGC	CTAAGGATAG	TTTGCCCGCCA	GAACACCCCT	ATGAGGGCTT	120
CACGAGTGCT	TCTGCGTCCG	AGCTGCGACG	CCGCTTTGCA	TTCAAGTGTC	AAAATCCACG	180
AGTCACCCCT	GTAATAGACT	TCACGGTAGA	CGTATACCCG	GCCTCAACCT	TCCAGTGTCT	240
CAATGATAAT	ATCTGCTTGT	GTTTTGATAT	TCTGAGAAGG	CAGAAGTGGT	GGCACACCGT	300
CTTATATCCT	ATTTCCTCAAC	TTTGCTGCA	TCAAGGCCAG	GATTCCTGCG	TAGGAGACGC	360
CCCAGCACCC	GCAGCCCCAAC	CCCCCTTCCA	CCGCCGCCGA	TCAAGCAACA	AGGGCTGTCT	420
CCGAGCAAGT	CGCGCCGAGT	CACGCCAGCT	AGGGGACGAA	AATATGCACC	AACTTACCTT	480
AACGGAAATT	ATGAACAAGT	CTGTGATTCC	CGAAGATGAC	CGATGATGGA	TGACCGCATT	540
GAGCTCTATG	TTAACGAGAA	CTACGTCTAT	CTGGGGACCA	GGAGGGTTGC	AGCTTCTATA	600
ACGATCCGAT	TGAGAGGTGG	GAGGCGTTTG	TAGAGTCACT	AAGACAGATG	CTTACGTAGG	660
TATATAATTCT	TCATCTCACG	CCTGGTATGT	ATGCGCTTGT			

4

GATCCGAATA	ACGTCCACAT	AAGGGAGAGA	CTAGAGGCTT	TGACTGCCCA	GCTAGCCAAC	60
CCAGGGGGCCC	AGCAGCCTCA	GCAGCAGCCT	CAACAGCAAC	AGATGCAACA	GCCTAGAGGG	120
CCAGCACCCCA	TTATGTTGCA	GCCAAACATT	CAGCAGCAAG	ACCAAAACAA	TCCGTTGAAT	180
AACAAACCTG	CGTCTTACCG	GCTCTCTCCC	CACGGAGTTG	CGGTTGCCGG	AACAGAGTCC	240
GCAGGCCACA	CACCAATGTC	AGGACGGCCT	CAGCCGTTGC	AGCAGTTGAA	CAATAACGGA	300
AGTATCCTGG	AACCGTCATT	GTTGCCGCAA	AAGAGGCCTA	TGGAGGGTGG	AATGGATACA	360
TTGGTAAATG	CCATTTCGCA	CAGGAGTTG	CAGCAACATC	AGAAGAAACA	TATGCTTCT	420
CAGAACCATC	CTAGTTTGGC	CGTGGCTACA	GGACAGCCGC	AGCAGTTACC	ACCCGATGCC	480
GCTCCCATAA	TACCGCCCGA	AAAGAAAGGT	GCGCCTCTCC	CCCAGTTTCA	GAAAAC TGAA	540
CCAGAGCATG	CGGCAAAAAG	ACTGAAGCAC	GAGCAGAATA	ACGTTTAAAG	GCAACCGGTC	600
CGGTCTCGAA	TATACCTTCG	ATTACGCACC	CAGCTTCCAT	GGAAACATTCT	GGTCCGGGGAG	660
ATCAGAAATCA	CATTCTATCT	GGGCCCTCAG	TCCACGCAAC	CCACGTTTAA	CTCCGGGTA	

EP 0 866 129 A2

1557RP

	GATCAGGCGA	GACATTGCGT	AGAAATATCA	ATTGGTTCCA	GAGGAGATCT	GTCTCCTGGT	60
	CATTGTAGAG	AAGCGGCCAG	ATATAATTGT	CCAAAGTGAA	CTCGTCTTTT	TGAGAAAACA	120
5	CGCTTTCATA	CACAGCGTCC	GACTTTTGGG	CTAGACCATA	AGCAAGGTCT	ATAACTTCCG	180
	TGGCAGTATA	ATTCCAGACC	GGCGGTGGTT	GCGGCGGGAC	AAGGGACTCC	CAGTACCCAA	240
	GTAAATCCTT	CGTCATTGAG	CTTTTTTAAC	ACAGAGCCAA	CTAAGATCGA	CATGGTAAAC	300
	GACGCGATTA	MTTTTGTACC	ATTTTATAG	GAGACCAGAT	ACATTTACAG	AAGCACCAAC	360
	CGCAATCGTT	TTAATCGGTG	CAATCAGTGC	CATTCTTGCA	GCTGGGTCCA	AACTCTAGAT	420
	TTACAAACCC	CGCACGAATT	AGCTAGTGT	GAACCAAGCA	ACATGTAAGG	AGTTTCATTT	480
10	CCCCACACTA	TTGAAAACCTA	CTGCGGTGAA	CGCAGGTGGG	GCCGCATTAA	CGCCATATAA	540
	CTGTGCGGTT	TGATAACAAT	TATCTCATAT	TGTCTTTTTT	ACGCACAAAT	ACATCCACTC	600
	ATAGAGAGCA	TTACGCCAAT	GCAGTCAAAT	ATAACGGAGA	ATTTGCATAT	CAGTACGTGG	660
	AATCGCAGCA	GTTGCTGTGA	TTTTACTATT	GATAACGGGC	GCAGCATAAG	GGCTGTGTTT	720

1557UP

	GATCCGCGGA	TTTGGGCACC	ACAGGGTAGT	GTGGCCGCAT	CAAATGATGG	CACACACGCG	60
	ACGTGCGTAC	TCAGCCCCCT	TATTTGATTT	GAAGAACAGA	TTGATTAGGT	CTGATCCTAT	120
20	AGCTCTGGGC	AAAGCGGGGC	GCCTTGGCGC	CTGTGTGGCC	GCGAAGTATC	GCTTAGGAAA	180
	ATGCTGGTGA	ATGTATATTA	TACGCTGACG	GGAGCATTCG	AGTCAGGTGT	CATGTATGGA	240
	CTTGCCTGCG	ATTAACATATC	GCAGCAGCCA	TCTGATGCTT	ATGCACATCA	ACTAGCACAG	300
	CAGCCATATG	ATGCTTATTC	ATACCGGCGG	CCTATCGCCA	TCTTCTTCAT	ATAAAGGCAG	360
	TGTGTACAG	ATAGGTGCAT	TGTCCTCTGA	ATTCCAAAAG	CTCATCGCGA	GTGCAGATGA	420
	AAGATCTCGC	TTCTTTGGTC	CCGCCGCAGG	CGGCACCATC	GTGGAATTTT	AGTGCACAAG	480
	ATGTTATTAG	TCTTAGCCAT	CAATTGATCA	ACCAAACCGA	GGCGGTTTAC	CACAACGTGT	540
25	TACAAGAAAA	GCCACCAACA	ATTGACAATT	ATATCATGCC	TCTAATATAC	CATGAGGAGG	600
	AAACAGACCT	GCTATGGAAC	CAGTTGGTGT	TTCTCCGCAA	TGTTTCGCCC	GATCCGGAGA	660
	TTCTGTGAAGC	GTCGAAGAAC	GCAACATCCA	TGCTGGACGA	CTGGATTATT	GGCCTTACGT	720
	CAAAGT						

1559RP

	GATCCAGAAT	CCAAGTTGCG	TGTTTCGTAGC	AACCGCCGCC	TGCGCAGGTT	ACGAAGCAGG	60
	CTAAGGAAAA	GGGGCCTGGA	TGCCGAGCAC	ATCTCAGAAG	TAGTACAACG	CATAAAGGAG	120
5	AAAAGCAAGC	CAAGCGCTGA	AAACAAGACC	GTGCGTGAGC	GGACTCCCTC	ATCCGCTGCG	180
	GTTGCTGATC	CTAAGAAGCG	GGTAGTTCGAT	GTCCCAAACA	ACCCGCCAAA	CAAAGTATTG	240
	CTCGTACAGG	ACCTGCCAAC	AGACATTACC	GAGCAAGAGC	TGGTGGATAT	ATTTGCAAAC	300
	GATAAGTTGC	TCCAGGTAAG	ACTAGTCCAA	GTCCGGCAAC	TGGCGTTTGT	AGACTACGCC	360
	GATGTACAGA	GCGCTACGGC	GGTCAAGAAC	AAACTGGGTA	CAAATTATGT	GATCAAAAAT	420
	CAAACAACCA	TCATAGGGTA	TGCGAAGTAC	ATAGGGCCGT	GGGGATATGG	GTTCTTACCA	480
10	GTGGGTGGGA	ACCCGACAGA	TCATTTAGGT	AAC TACATAA	TGATAGTATT	TACMAGACTC	540
	CTTAAGTCGC	ACGTGCCCTCG	ATGTCATTTT	CCAAAGAGGA	CTGTTCTCAT	AGCTGTGAGC	600
	AACGACTCTT	TGCTGCGTCC	TT				

1559UP

	GATCCGATGA	CCGTCATGTT	CTTCTACAAG	AACAAGCACA	TGCGATGCGA	CTTCGGCWC	60
	GGGGAACAAC	AACAAGATGA	ACTTCGTCGT	TGACAACAAG	CAGGAGATGA	TAGACATCAT	120
	AGAGACGGTC	TTCCGCGGCG	CCAGGAGAAA	CAAGGGGCTG	GTGGTGTGCG	CGTATGACTA	180
	CAACTACAAG	CGGATACAAT	AGAACATTTT	TTGCAGCTAG	TGTTGTCCCA	CGATAGAAAG	240
	TTTATACGCA	ACCCGGCACA	GGCGCCGGGT	TGCTTGGCTC	CACAGCTGGC	GATGGAGCCT	300
20	TGGGTAGGGC	CCTGCTGGCC	ATTATTCCCT	TGACTCGACC	TTACGCCTAT	AGATGGTGTG	360
	TGGGCTGTTT	TGGCGGTGAT	AGTGAAAATT	TTTTGGCTTT	ACGCTCCACC	GGGTTTCAGG	420
	CTAGGCAGCA	GGATAAGTAC	WTAGGTCTTT	CTGCTTCAGG	CATTATATAA	CCTCAAGCGA	480
	GCTTTTCAGA	CCTTTTAGGC	CAATATATCT	CCAAAGTGTG	GGCATCTGGA	CTATTAAGCA	540
	GGAGGTTCTA	TTCCAGCGTC	ATCAAGAAAT	CTGTCAGAAT	AAGAACCATG	GCCTCAGAGG	600
25	ATGTGCAACT	GGCCAGGAAG	GCTGTTGAGT	TTAACAGGGA	GAA		

1560RP

	GATCGCGCGG	AGGTTCTGTA	AAAACCTTCC	ATGCACAAAC	CCCACACCAT	GCTCCCGCTC	60
30	GTCTCTTTCA	AAC TCTTCG	CACTAATGGT	GCCGTGCTCC	ACGACTTTAT	CATTCCCGTC	120
	AAACACTAAG	TCAGGGATC					

1560UP

	GATCCCTGAC	TTAGTGTTTG	ACGGGAATGA	TAAAGTCGTG	GACGACGGCA	CCATTAGTGC	60
	GAAGGAGTTT	GAAGAGGACG	AGCGGGAGCA	TGGTGTGGGG	TTTGTGCATG	GAAGGTTTTT	120
	ACAGAACCTC	CGCGCGATC					

1561RP

	GATCCAAATA	AGCGTGCGGT	CCATACAAAT	GAACGGTTGA	GTGAAGCTAC	TTCGCTCGGT	60
	CGCGTATGAT	TACTCGCACC	AGGCTCTGGA	TGACGCCGGG	GGAGATGGCG	CTGCTGCTAC	120
5	GGCAGCCAAT	ATATACATCT	TCTATAGGTC	TAATTCATGT	CCGCTTTTTA	AAAAATGGCT	180
	TGCGTCAATT	TGTATGTAGT	AGGCTATGTA	ACGGCTCAGT	CGGTGGACTC	GGCGAAGCGT	240
	TCCTGGATGG	AAGCAAAGAG	CTTTTCGAAC	TCTGCGTGGA	CCTCGCGCTC	GCCGCGGCTG	300
	GGCTCGAAGA	ACTTGGAGGA	CGAAACGGCG	TGTTTCACGT	CGCCGGTTGC	CTCCGACAGC	360
	ACGGCCCACT	TGGCGCCGTT	GGACACGCTC	TTTTGTGCCT	CGTCGAAGTA	GGACACAAAC	420
	GCTTTTCATCA	TATCGTAGGT	CTTCCAGATG	GGGCAGAATG	CGTCGTAGGT	CGAGTAACCG	480
10	TTCTGCTGCA	AGAAGTCTTC	TTTGATTAGC	GTGCGGACAT	CCAGTACGAT	CTTGTCTTTG	540
	TCAGAGAGCG	CGGACTTACC	GACCAGCTGA	ACAACTTGCT	CCAATTCTCT	GGCGTTGGAG	600
	AGGATCTCCT	TGATACGGTC	TCTCAGGACT	GGGAACCGGG	GTAATTGCTA	TCATAGTATT	660
	TGTTTAGGAC	GTTGGTGTTT	CTTCGAGT				

1561UP

	GATCGCAGTC	TGTAGTTGCT	GGTACTGGAG	TCTTGACTGC	TCTATGCCTC	TTGCTTGTGC	60
	TAAAAGCGAA	GGAGACTCGG	TTACTTGTAT	GTTTTGCTGA	CCTTCTGGTG	GCAAAAGGGG	120
	TGGGGCGCGG	GGTCGGACAC	TATTTTGGAG	CGGAATCAGC	CTGAGTGTTT	TTTTTGTGTT	180
20	CACCAAGGGC	GGTAAACCTG	GCGCCAGCCG	CTGGCCGGCG	AGGTGATGGG	CCATGAGCAC	240
	AGCAGGTATC	GCGGGAATAT	GGAGTGTCCG	GGGGCGCGCT	TATGTAGACC	CAGCACGGTC	300
	CCCAGCCATC	GCGCGGAATT	GCGGCTTTTG	TAGAGTCCCG	CTAGGCGCGC	TGCCGCGGGC	360
	GTCAGCGCCT	GTGACACAGA	CAAATAAAAT	TGGGCAAGCG	CGAGACACAA	GTCCCAACAG	420
	CCGCCACTGC	ACGAAGCTAT	GCACGCATTC	AAGGAAGACT	TACCCCATAC	CGTGGGTTT	480
	GCCCTCGACA	ATGAGGAGAT	CACATTCCCC	AACTACGTGC	CCACGCATGT	GCAATCGTTG	540
	CCCCACACGT	CCAACGGGAT	CCGACAGCTA	GTCATAGATA	AGCAGAACCA	GCGCGTCCTC	600
25	CCCACATATA	ACCGCCTACT	CGACCGCATG	GAGGACGCGC	TCGTGCGCTG	GCGGCCGCCC	660
	GCCAGCTCCC	ACGTCGGCTC	CTCGCTAGCA	ATCCACGGCA	CGCACCCGTA	C	

1562RP

	GATCATTTGA	GTGCAAAGGG	AGAAGTAGCG	CTTTTGACAG	TACGTGCGGT	GTGTGGACAT	60
	CCTAGGTACT	GTTGACATTC	ATGTGGGTCA	GTCAGATTAC	AAGTACACAA	AGTCGATATG	120
	ACAAGCCACG	TGACCATATA	TCCAAGACGC	CCCCCAGCGC	ACGCCCTGCTC	TGTGCATAGG	180
	ACTGGCTACC	TACCAGTTAC	AATGGGGTTT	GCAACTTAAC	TGCTCTAATC	CTCACACGCG	240
	GAGTTATATA	TGTGCTATAG	GGCATGCTCC	CGGGGCGCAA	TTCAGGGCCA	ACGGCCTGCC	300
35	ACCATGCCAG	AGCAGCCATA	CCAAGCGCTG	CAACAGGATG	CGATATCTCG	TTCTATATAT	360
	ATACAGATAT	ATATATATAC	TGTAACAAAA	TCCCTAGCGA	TCTCGCTGTG	AAAGGCCGGT	420
	ACTTAAATCA	TATCGTCGTC	TTCTTCAGCC	CCGATCGACA	AAGCCCGCCC	ATCGTTCCGG	480
	AAGCTTGGA	GCTCGGGCGC	AGAAGAGCTC	AACTCGAGTG	CCGCGCATAT	AAAGCCGGTC	540
	ATGAAGAGCA	TTGTAAATGC	GCAAACCTTG	AAAAAGCCTG	CTGGCAAAAG	CATCACTGCC	600
	AGGAGGAGTT	GTAGGAGGGC	GCGACCCATG	TAACTATAGT	AGAAGGACGC	GTATTGTTGA	660
40	AGCAATGGTA	CTGGTCGGAA	TTGAGGTAT	ACCAGCAGGA	CGGAGAGTGG	AAGGCCGAAA	720

1562UP

	GATCTGGCGT	GCATATATAA	CGTATCTGCG	CTCACGCGAC	CTGGTGCGGA	CTTCTTTAGC	60
	CGGCTACTAA	CTCTGTAGCT	GTGGGGGCTG	CCTGCGGGCG	CGCCGGGCGA	GCTTGGCAGA	120
	ATCCGCCGTT	GCGTCACGGC	CAGTGCCAGC	CGAACAGGAC	GCCCTTTTCT	AGCAGCAGCG	180
	CTTCCGCAGC	GGTTTCTTTT	TTTTCCCAGC	TAAGGTCGTG	TATTTTCTCG	CAGAGGGTTA	240
	GAAAAGTACA	CTTTACATCT	GAACACACCA	CAAAGTCGTT	CTGATTGGAG	AGGCACGAAA	300
	CCAAACAATT	GAAAGGTATG	TTGAGTGCTA	AGCAGACGGT	ACACTGAGCT	GGCCGTCTTT	360
50	TAGCAGCTGG	CGGCCACCCG	CACTTTCTCT	TTTTCCGCTC	TGTTGCTTCT	TGCGCGCCCC	420
	CTTGGCCTGG	ATCTCGAGAG	CCGCGGAGCT	ACCGCCCGTC	CCGCGCCAGC	CTGGGCTTCC	480
	CAGGCGGCCA	GTGGTCAGAG	CCGGTCGCCC	ACGGCAGCCG	GCTTCATGGG	CGGCTGGCGG	540
	CTCTGTTTAC	AGGGATCGGT	CACGTGCCGT	GTGAGGCTAA	GCCGGTGGCG	AG	

1563RP

	GATCCTCGCT	ACTTTGACAA	CATCAGGAAG	GCGCTTGCTG	CAGGCTTTTT	CATGCAGGTA	60
	GCGAAGAAAC	GCTCGGGAGG	GAAAGGCTAC	ATTACTATCA	AAGACAACCA	AGACGTGCTC	120
5	ATCCACCCTA	GCACGGTCAT	TGGCCACGAT	GCAGAGTGGG	TAATCTACAA	TGAATTCGTG	180
	CTGACTACTC	AAAACFACAT	ACGGACGATC	ACCTCCGTCC	GTCCTGAGTG	GTTGATTGAA	240
	CTCGCACCTG	CGTACTATGA	CCTTGATAAC	TTTCAAAAAG	GTGATATCAA	GCTCAGTCTG	300
	GAACGGATTA	AACAAAAGAT	GGATCGCATC	GAAGAGCTAA	GTAAAGAGCA	ATCCAAGAAG	360
	CATAGACAGA	GCCGCGCGTA	NTTCGTGAGC	TTGTTGTAGC	TAAATATCTC	TCTGATATAG	420
	CATGTACACA	ATAATAGGAC	TTTGTAGCTG	TCCTTCGTTA	CTTCGGATTA	GCAAATTATC	480
10	GCAGAAAGTTA	GCAGGCACCG	CCGCCCTTGT	TGGTGCCTT	GCACGAAAGC	AGCTGGTGAT	540
	GTTCCGGCGTC	GCTAAAAACC	CTCATTTGTG	CCTATCATAT	GCCCAGCGCT	ACAGAGTCTT	600
	CGCATCATCA	TGTTTGAGAA	GGACGAGATA	CTCCCACTTG	ATGAGGCCAG	GTCCCAAAAG	660
	ATAAAGGAGT	TCCTGAGCCT	CTCCCTCGGG	CTGATCACCG	AATCCATCGA	AAAGAAAGAA	720
	TATGACTCCA	TA					

1563UP

	GATCGGTTGT	CTTCCGACGC	TGGTACAGGG	CTGCGATGCG	CGTCTGCGGC	TGGCGGTGCA	60
	TATCGGAGAT	ATGGCGCCGT	GCCCGTACGG	CAAAGAATCA	GCAAGACACT	AGCGTCTGGC	120
20	ATTCTTTTTT	AATGCATTAT	TTAGCTTTTT	TTTTTTTTTT	TTTTTTAGTA	TAGACACAAT	180
	ATAAAGTAGA	GTTCGTCATC	AGTAGCGCTC	GTAAGGTTAG	GGGCCGGCTT	CACGCCATAG	240
	TAGCATCTCC	GTCAGACTCC	TGGATTGGCG	CTTGCTCTAT	GCCGGCGGAT	TCCGCAACTG	300
	CGTAGGGTCT	TTCTGTTAGCG	GACTGCTTCC	CACCGGCGGC	ATGGGCAGGC	CACGAGGGAG	360
	CTCCGGTAGC	AGCCTGTGAC	TTGTCTGGCA	GCGAGCGGCC	TGGTGGGTGC	TGGAAGAAGC	420
	AGTGGGCGTT	GCGACATTCC	GCGCCGAATT	TGCAGGGCTC	GTTGATGGGG	TGGCCGAAAA	480
	AGCAATCTAT	GCGCGTGAC	GCAGCGCCCT	CGCGGCACAT	AATGTGTGAA	CGCGCATGGC	540
25	GGTACTTTACA	CCGTTTGTTT	GTGCACTTGA	CGCCGAACTT	ACACTGCTCG	AGCGAACGCT	600
	CCGCTGGTGC	AAACGCACCG	GCTTGGGAAG	ACGTGGCGCA	GCAGCAATAG	GCTGAACATC	660
	TCGTATCTTG	GACAAGGAAG	ATGCGCCTTG	TCGCAGTCCT	CTTGTCACAG	GTTAGGT	

1565RP

	GATCACATGT	TTTCCCCAGA	GAGGGACCTG	GCGTTGAGAG	AGCGATGGGC	CGTTATACCA	60
	CTGAGCCCTA	TTAGTTGCTG	GATTTGTGTT	TCCAGCAGCT	GCGCATGGGG	CCGGATTCCG	120
	TCAAGTGTA	TCCGCAGAT	GTTGGTTTTG	GCTCGATAAG	TGCATAAGGA	AGCTGCTCTG	180
	TTAGTACATG	TCACATAGGA	GGCTTCCGCA	TTGGCGCATG	GCATCCAGTG	GCGGGCTTGT	240
35	GGCGCGACGG	GTATTCCAGT	AGCCGTCCTG	GAACCGTATT	CAATCATCTT	TGGCCCAGCG	300
	GTATATAAAG	CGGCTGATGA	GCCTGGATGC	AATGGGGTGT	AGCTGCGGAG	ACTGCACCGA	360
	AGATGTCTAG	CAAAGTTTCA	TTCTATTGTA	ATTGGCAGCC	TGCGCCATAC	CACATTGCGA	420
	TTTTTCTAGC	CCAGTCCAAG	GGCTACTTTT	AGCAGGAGGG	TGTGGACATT	GCGCTGCTCG	480
	AGCCACGAA	CCCGTCCGAC	GTGACGGAGT	TGATCGGTGC	GGGCAAGGTT	GACATGGGCC	540
	TAAAGGCGAT	GATCCATACG	CTGGCCGCTA	AGGCACGTGG	TTTCCCGGTC	ACTTCTGTTG	600
40	CATCGCTGCT	GGATGAGCCG	TTCAACGGGG	TTCTGTACCT	GCGTGGCAAC	GGAGTCACAG	660
	ATACTTTTACG	CTCTCTTCAG	GGGAAGCG				

1565UP

45	GATCCCTTTC	ATACAGGTCA	ATATTTTATG	CAGAGACAGG	GGCTGGACGT	TGTAAAGGTC	60
	TTTCATCCAG	ATATGCTAAG	AGGCGAAATT	TCATGCACGA	GTATGATCAC	AAAAAATGAC	120
	ACAGCCAAAC	AAATTGCCAT	TATTTTATGA	GGATCTACAG	TGATACAGGA	TTGGATTATC	180
	GATGTTCTAT	CCACCCCTAT	TCCATTCAAT	CTCGCTCCTA	CCCCCTATCA	GCCCCGTCAGT	240
	GGAGCTGCAA	AGTGCCGAGG	GAACGTCTC	ACGCACACTG	GCGTCTACGA	TCAAATTTAAA	300
50	AAAGCATTTA	AGGATATTTA	TGCTGTTTTT	AAGCCGCTAA	AAGACACACA	TCCGGATTAT	360
	GAGGTGATAG	TTACTGGTCT	TTCTTTAAGT	GGCGGCTATG	CTCACTTTAT	GGGTATTGAA	420
	TTGCAACTTC	TGGGCTACAA	GCCTCATGTT	TGCGCCTTTG	GATCATTGCG	TATAGGCMAT	480
	AAGGACTTTA	ACGATTGGGT	GGATGATATA	TTTCCGTCGG	AAGACGTTTC	GAGAAGAATC	540
	CCAAATAATG	AGATGCCC					

1566RP

	GATCGCGAAA	CACAACGCGC	GCGGCGCGGT	AGCGCCGCGG	GCGCTGCTGC	AGGACGTGCG	60
	CGACGCGCTC	GCGGCGCACT	ACGGGGTAGG	AGTACATCAA	CCGGTACGTG	GAGGACGAGT	120
5	GGGTGTTCAA	CAACGCGGGC	GGCGCTATGG	GGCAGATGCT	GATTCTGCAC	GCGTCTGTGA	180
	GCGAGTACCT	GATTCTGTTC	GGCACGGCCG	TGGGCACGGA	GGGCCACACG	GGCGTGCACT	240
	TTGCGGATGA	CTACTTCACG	ATCCTGCACG	GGGAGCAGAG	CGCGGCACTG	CCACACGCGC	300
	TGGAGCCGGA	GGTGTACACG	CCGGGTATGA	CGCATCACCT	GCGCATGGGC	CACGCGAAGC	360
	AGTACGCGAT	GCCGTGCGGC	TCTTTTGCGC	TGGAGCTGGC	ACAGGGGTGG	ATCCCGTGCA	420
	TGCTGCCGTT	CGGTTTTCTG	GACACGTTCA	ACAGCACACT	CGACGTGTAC	ACTCTGGCGC	480
10	GCACCGTGCA	GCTGACAGCG	CGCGACATGT	TCAAGAACTT	GGTGACAAT	TTCAAGTTTT	540
	AGCCTAGATA	CATAACCACC	ACCAATGTCT	GCGCAGGCCT	CGCCCGCGAC	AGAGCTGCCA	600
	GAACCCGACG	CTCGGGCAGG	TGTACGCCAC	GCTGACGCGC	CACTC		

1566UP

15	GATCCTCAAG	TCTACGAACG	CCTCGAAGGT	GTTTACGACG	GCCGTTTTGG	CTGATGTCAT	60
	CACAGCTGAG	GCTAAGGGTG	ATTTTGACGC	GAAGTCTGCT	GTCCCAGGTC	ACGTGCAACA	120
	GGGCGGCCTA	CCATCGCCAA	TCGACAGAAC	CAGAGGAACT	CGTCTCGCGG	TCCGTGCGAT	180
	CGGCTTCATC	GAGGCTAAGC	AGGACGTCAT	TCGCGAAGCC	AGGGGAAAAT	GAGGAGGCCT	240
	TTGACTGCGC	CGACAAGGCC	GTCTCTCACA	CCGCCGCCGT	CCTCGGCATC	ACCGGCTCCC	300
20	AACTGAAGTT	CACCTCCATC	AGGCAACTCT	ACGACCTGGA	AACAGAGTTC	TCCAAGCGTA	360
	TGCCAAAGGT	TATCCACTGG	GAGCCTACCC	GCGCGATTGC	GGACCATTTA	GAAGGCCGCA	420
	AGAGGGTAAC	AGTTTAGTGT	CTCTGTTTCG	CCCGCTGCCC	CACTATATGT	ACCACTAGAT	480
	ACCACGATTA	TGGATAAACT	TAACATGGCA	GAGTACACTC	TCATCCACCT	GCCATGTATA	540
	TAATGTGATT	TTACTGACGA	AAACTGTTTT	AAACGCCGTT	GCAGGGTCCG	TCGCAGCTCG	600
25	TATAAATATC	TTGACGCCAC	CTCGATCTCC	ATTGGTGAGG	AAGTACCCGT	CGAGATACAA	660
	TAGTGCCAGC	TTGCTAAGGG	GTAAGCTGAC	CACTCTACAC	A		

1568RP

	GATCACGAAA	CGGTCGCTAT	TAGGTTCCCA	TGCAAAGCGC	ATGCAGCGGT	CCTTAATCTC	60
	CACCTTCTCA	AATGGAAACT	CTCTGGCAGT	CAAAGAGCAA	ATCTCCATGT	TGGTGAAGAT	120
5	GGTCTTCCTA	GACTTCGTGT	GACGGTCCAC	CTGTACACAG	AGGAACTCTG	CCTGGTTCTG	180
	CCAATGGAAG	GAGACATCAG	TAACCTGCAC	CAAGTTGATG	GTACGCAGAA	CACGGCGGTT	240
	CGGTAGCTCA	ATCAGGACAG	CTTTACACGA	CTGGTTGTTC	GACTCTGGAG	TCCAGTATAC	300
	CATGACAGTA	GATGGTGGGT	CGTTGGGTCT	GTTTGACGCC	AACCTGATGC	CCTTAGGAGC	360
	AAAGGAGAAG	TCCTGAACAT	CCTCGATCTT	CATCACCTTA	CCGCCCAACA	GCTGGAAGTT	420
	CTTCTCGGTC	TCGTACACAG	CAATTGCGCC	AGGGCCAAGA	CGAGCGCAGA	ACTTGTCGTC	480
10	AAAGGACCAC	TTGACCATAG	GCCATTGCAG	CTGCTGCTGA	GGCGGCAGCG	CAAAGGTCTT	540
	CACGCAGACA	CCTGTTGCCA	CATCCCATAT	ACATAGCTGG	TGGCCCCGCG	ACTCGGGCCC	600
	GAATGGACAA	GCCTCGTTAG	GTTTCATCCGA	GACTTCTAGA	GGTTCGACG	AAAAGGTAAC	660
	CAGGTACTTC	TCGGTCGAGG	ACATGGAGAT	CGCCTT			

1568UP

	GATCATCTAC	GTGGCCCATG	AGGATAATAA	GGAGAAAGAA	TTCGAAATTG	AGCTGAGCTG	60
	GTGCTCCGCT	TCGGAGACGG	ATGGCTTGCA	GAAGGGAGGT	ACCAAAAGAG	CTATTTGATG	120
	CAGCGATTGA	GTTTGCGAAG	AAGGAGACCG	GTCAGGAGAG	TGATGATGAT	TCAAGCGATG	180
	ACAACGCATC	TGGAGGTGAA	GAGTCCTCAA	CAAAGAAGGA	TGCTGACGGT	GATGTCCAGC	240
20	TTTCATGATA	ACAGCCCGGC	ATTATGTGGA	GGTTCATTTT	ATGACAATTG	ACGGATGTTA	300
	CTAAGTGTAT	ATTAAGTTAA	TCCACCTATA	TAAATTAAATA	ACATGCAAAG	CAATTTAGAA	360
	TTTGTGCGAA	AGCAGGTTAA	AGCATGTCTA	CTCTCCTTAA	TCCTTCGCGA	AGCTGTACAT	420
	TTTCTTCTTC	AAGTGAACGA	ATTCTATCCA	CGGCTGCGTC	TGATTC TAAT	TTCTTACGTT	480
	CGCGTTCTGT	GTACCATTTC	CGCGTCAGCT	CTTCTATCAT	TAATTTTGAA	TGCTGATCAA	540
	ATGATATCTGA	TTCATCCGAG	CCCTGCGACA	CCTGGGATAG	ACGTTTGATT	CTTCTGTCTT	600
25	TTTCCTTTAA	CAGCAGCTTT	ACATGTTTCT	CCACTATTGA	TGATGTGGCA	TTTGTGGGATG	660
	AACATATAAA	TAGAATCCCA	TTTCAGCTGG	TTTCTTC			

1569RP

	GATCCGATAT	ACGCTGAGTG	CTATATTACA	AACCATCAAT	TTGATGTTAT	CTTGGACGTA	60
	TTGTTGGTTA	ACCAGACGAA	AGAACTTTTG	AAAACTTGC	ATGCGCAGTT	TGCAACCCTG	120
	GGCGACCTGA	AGATTATATG	CAACCCTCCA	AGCACCAATC	TAGTTCTCTA	TGGTTTCCAC	180
	AGATTTAGCG	TTACAGTGAA	GGTTTCAAGT	GCCGATACTG	GTATAATCTT	TGGGAATATA	240
	GTTTATGACG	GTGGACACGG	CGAAGATGCA	CGCTATGTGA	TCCTTAAATGA	TGTCCATGTT	300
	GCTACAATGG	ACTACATTAA	GCCTGCAGTT	TGTGATGAAG	CTTCTTTCCG	CAAGATGTGG	360
35	AATGCATTTG	AATGGGAGAA	CAAAATGGTT	GTCAAATCTA	AGCTACCGAC	TCTGCATGAC	420
	TACTTGAATA	AGCTGATTGA	GGTCACCCAT	ATGAATGTCC	TGACTCCTGA	AGAATCATTT	480
	GCCGACCCCG	AATGTCGTTT	CTTAAGCTGC	AACCTTACT	CGAAGTCCAC	CTTCGGCGAG	540
	GATGCTCTGG	CTAATTTGTG	TATCGAGAGA	GACCCTACTA	GTGGTTCCAT	CATCGGAGAA	600
	GTTTCGCATCC	CTTCGAAGAC	GCAGGGCCTT	GCTTTGACCC	ACGGAGACAG	TATTGCGCMC	660
	ATGGAAAGGT	CC					

1569UP

	GATCTGCAAT	GCTCTTCAAC	AATTTGCTGC	AAGCTATTCT	CCTGATGACC	TTGCCATCTT	60
	GAGTGAGCTT	TTTGATTCCA	ACAGCAAATC	TGAATAGGCC	TCTATCTCCT	TTAAAAGCAG	120
45	CGTCGTGCAT	GGGGCTTTGG	GTTTACATTG	GAAAAAGCCC	CAAAGAACAA	GGTAATGCAT	180
	GCCAAAAGTA	GCCCTTAATC	CACTTCACAT	TTAGATATTG	TTACGCAGTG	TATCTATACA	240
	AAAAATAACG	ACAAATAATA	TCTTTTAGAG	CTGGTTCTTT	AGACTAAAAT	AGGGCTCGGT	300
	ATGCAATACC	TCAGATGCTA	TCTTGATATC	CGTGTGGATA	TCCTCGATTA	AAGCCTCTTT	360
	CGTGGTGTAG	TTTAATTCCG	GCCGGATGTA	GCCAAGGAAG	CTGAACCTAA	TTTTGGCGCC	420
	ATAGAAGTCT	TCTTCAAAGT	CGTTTAAAT	GTGCAACTCA	ACCGTCTTCT	TACTGTTGTT	480
50	ATAGAACGGG	TTCCATCCTA	CCGATAACAC	GATTGGAAAG	ACTCCACGCT	CTGTTTCCGA	540
	CAGCTTGGAG	CCAAAGTTGT	ATATGACCTC	GCTCCCATCA	TTTCTGTGAT	GGGACCTGCG	600
	CTTCTTGGTC	CATATTAGCC	TTAACC GGCG	CCAGCCAAA	TATACTCCTG	TGGCCATTTT	660
	GTTAACTTCC	CTAGGCAATT	GTTCTATTGG	GAACATT			

1570RP

	GATCCACAAC	ACACACAGCT	TGCGGACTCT	TMTTCTCAAA	GACAGTTCAC	CAGTCCAACA	60
	CTTGCAAAAC	CATCTGCTAA	CGTTTCAACG	ATTGCGCAGC	AGCAAACCCA	GCCAACCGCT	120
5	CTCTCTCAAT	CTCATCCTCA	GCAACAACAA	GGTTCACAAG	CTCAGCAGCA	GCTACTTCAA	180
	CAACAACAAG	GTTTACAAGC	TCAGCAGCAG	CTACTTCAAC	AACAACAACA	GCAACCACCA	240
	CCACCACCAC	CACAACCACA	GCAACAAACA	CAACAACCAC	AACAACCACA	ACAGCAGCAG	300
	CAGCCCCAAC	CTCAACCGCA	ACTACAACAA	CAACAACAGC	TTGGTTTACA	GCCTCATCAG	360
	CCACAACCTGG	CGCAGGCGCA	GGCGCAACAA	CCACAACCGC	AGCAGCAGAC	GCAGCAGCAG	420
	ACGCAGCAGC	AGCAGCAGCA	GCAGCAGCAG	CAGCAGCAGC	AGCAGACACA	GCAGCAGACA	480
10	CAACACCAAC	CACAACCACA	ATTGAAACCA	CAATCACAGC	AACCACAACC	GGTTCCACAG	540
	CAAGTCCAGT	CTCAACAACC	ACAGCAAGTC	CAGTCTCAAC	AACAACCACA	GCCTCAGCAA	600
	CTTTCAACAG	CTGCCCAACA	ACAATCGCAA	CAACAACAGC	AGCAGCAGCA	GCAGTCTCAG	660
	CAGCAGAAGC	TTGCGCAAGT	GCAGCTGC				

1570UP

	GATCTTCGGG	CCCCGGGGGC	CGCTGGGCTA	CGTGCTGACG	CTGTATGCGA	ACGCGCAGTT	60
	CTTCACAACC	ATGATCGTGA	ACTCGCACCT	GGCGACGCCG	CTGTTGGACT	ACACCATTGC	120
	GTCGCTGATG	GGTATCCATA	TTGAGTACAA	GCGCCATAAC	CCTGAATTGG	TGGAGCCGGA	180
	GGCGTTCAGC	GCATACGATG	TGCTGACGGT	GCTGCGCCTG	GTCATGAGCG	TTGCCGTGAT	240
20	GGTGGTTCTG	GTGACCATCC	CGATTCTGGG	ACCTGTTCTA	CTGATGTTTG	TGATGAATGT	300
	AAAGTTTTC	TACGACTTCT	ACGAGCGGTT	CTTAATTCTA	CGGGGACTAA	ACCAGGTGCA	360
	GCGCCGTGAC	GTGTTCTACC	AGCATATCTT	ACAGTTTGCA	TACTTCGGGG	GGTCGTACAC	420
	GGTTTAAAT	TTGCTGCCTC	TATTCTCAGT	CTGGGGCTTT	GTGTGCTATC	CGTTGGCAAT	480
	CAAAATGTGG	GCGACTTCCA	ACATCATCCA	CTTTACAGCG	GAAGAAGTGG	AGTCCATCAC	540
	TGAATGAAAT	CATTCAATTA	ACATGTCCAT	CTATACATAA	AGATAGATAT	AGCCAGATC	600
25	AATACCCTGC	CCATTAGTAA	AGTACCATGC	TGTCGACACA	GCCGAATCCC	GCGCAACACC	660
	GCCCTCGTTG	GACGAAGGCA	ACTTGGAACG	CAGCAGCCAT	CCCAGCGTAG	TCGT	

1571RP

30	CGCAGGCCGT	AGGCAACACC	GTTGGATATC	TGCACCTGGC	AAAGGTCCTG	ACCCGGCAGC	60
	AGAAGCTCGC	GCGAACCGGT	AGTCCACGCA	TACAAGTCGC	CGCGGCGGTC	GATTGCCAAG	120
	TTGCAACCCCT	CCTCTGCCAG	CGCCACATCC	CGCAGCCGCT	CGCCCTCAAA	CCCCGGCACC	180
	CGCAACGGGA	ACCGCGTGGA	GCCAGCGTCC	TCGCCCAGCC	GCGCGCCCCA	GTAGTAGAGC	240
	CCGGGCTCTC	CTGGCTGCGG	CGCCGTCAAC	GGGATCTCGG	GGATCCCGCG	CAGCTCCTTC	300
	TTGCGCTTGA	TCTCCTTCAG	CCGCTCAAGC	GTGTTGTCTG	CCACCCGCGG	GTCGCGCGCT	360
35	AGAATCCAGC	CCTTGATCTG	CGGCCATTGA	AGATACACCG	TGCCTGCTAC	TCCGATCCCG	420
	ACGACCACCG	CCAGGCCCTG	GAACACCGCC	ATCAGCTTCT	GCATCTTCTC	CACCTTGCTC	480
	GCATACTCCT	GCTCCAGTTG	GCGCGGCGAT	TTGTCACTCC	ACTGGTAGTC	CAGCTTGCTG	540
	CGCTTGCCCT	TGTATGTGCC	ATGGTTTCAG	TGCTCTTGCC	ATCATCTCGG	GCTCATCAAA	600
	ACGCTGCCCC	TTGCGCAACG	CCCTTGCTTC	CATAGCGAGC	GCCTCGCCAC	TCGCAGCC	

1571UP

	GATCACGTGA	TGGGATGAAA	ACTCTGACAA	ATGCACCGGG	AATATATAAG	GCATGGAGCT	60
	GCGGACTCGG	CCAGACAGTG	CGAGCAGCGA	AACAACAACA	TCATCCAAAA	TGGCCAGAAG	120
45	ACCAGCTAGA	TGCTACCGTT	ACCAGAAGAA	CAAGCCTTAC	CCAAAGTCTA	GGTACAACAG	180
	AGCTGTGCCA	GACTCCAAGA	TCAGAATCTA	CGACTTGGGT	AAGAAGAAGG	CCACCGTTGA	240
	TGAGTTCCCT	CTATGTGTGC	ACCTAGTGTC	CAACGAGTTG	GAGCAGTTGT	CCTCCGAGGC	300
	TTTGGAAGCC	GCCCCGTATCT	GTGCCAACAA	GTACATCACC	AAGATGACCG	GTAGAGACTC	360
	GTTCCACTTG	AGAGTCAGAG	TGCACCCATT	CCACGTCTTG	AGAATCAACA	AGATGTTGTC	420
	GTGTGCAGGT	GCAGACAGAG	TGCAGCAGGG	TATGAGAGGT	GCCTGGGGTA	AGCCTCACGG	480
50	TTTGGCTGCC	CGTGTGCACA	TCGGCCAGAT	CATCTTCTCC	GTCAGAACCA	AGGACAACAA	540
	CAAGGACATC	GTTGTTGAGG	CTTTGAGAAG	ACCAGATACA	AGTTCCAGG	TCAGCAGAAG	600
	ATCATCATGT	CCAAGAAGTG	GGGTTTCACC	AACTTGGAAC	GTGCCGAGTA	CGTCAGA	

1572RP

	GATCTATTAT	TAGAGGTAAT	ACATTTAAAC	TATTATCTAA	ATTCTTCTTC	TTCTTATTTA	60
	TTCTTAACTT	TATCTTATTA	GGTAAATTAG	GTGAATGTCA	TGTTGAAGTA	CCATTTATTT	120
5	TAATAGGTCA	AAATTGTACA	TTTATTTATT	TTGCTTATTT	CTTAATCTTA	GTACCTATTA	180
	TTTCTATAAT	TGAAAAATAT	TTATTTTATT	TACTAAATAA	AAAATAATAA	TTAAATAAAT	240
	AATAATAATA	TTCATTAAAT	ACTTTAATAT	TAATATTTAT	ATATTATACT	TCTTTATCAT	300
	TTAGGAGGGT	ACCTCATATT	GCTGACTAAC	AATAGGGGGG	TGAACCCCTAC	GCACCTAAAT	360
	GATAAGAGTT	TATCATTTAA	TTATATACTA	TATATTATAA	GTAAATTATC	AAACCATATA	420
	TAAGGTATAT	ATATTTAAGAA	AGTTTGACTG	AGTGGTTTAA	AGTGTAAATAT	TTGAGCTATT	480
10	ATAAATCTTT	ATGATTTTCCT	AGGTTTGAAT	CCTATAACTT	TCGTATTAAA	TAATTATTTA	540
	AAATAATTAA	AAATAGTTAA	TAATAATGAG	AACATGATGT	TGGTTCAGAT	TAAGCGCTAA	600
	CTAAGGGACA	TTACACATGC	CAATC				

1572UP

	GATCCGTGTA	TTTTTTATTT	ACATTATTTA	ATTAAAAATA	ATGATTTAAA	TAAATATTTT	60
	TTATAAAAAA	TAATTAGTGC	ATTGTTACAT	GTTCAATTAA	GAATGATTAT	TATCAAAACC	120
	ATCAACTAAT	TGTTATATAT	TTATTAAATA	TTAATTTTCRC	TTAATTAAAG	ATTAGGAACT	180
	TTATCTATTA	GTCTGGGCTG	TTTCCCTTTT	GATTATTAAAC	CTTATCGCTA	ATAATCTGAA	240
	ATATTTAATT	TTAGATTAAAT	AATATATTCCT	GAGATTTTAA	ATTTTAAATA	AAATAAATAA	300
20	TTATTCCCTA	AATAATATTA	ATAACTATAC	CATATATATC	TAATATTTAA	ATAATCATAC	360
	TAACATATGT	TTCTGTAGAAA	ACCAGCTATT	TGCAAAATCAG	ATTTTGACTTT	CTCTACTTAC	420
	CATTATTCAT	CAGATAATAT	TGCTACATTA	ACCTGTTCAA	TCGTTTTTTAT	ATTTTATTAT	480
	ATTTTAAATA	TAATAAATAT	ATATTTTAAAT	CATTTGATAA	TAGTAAGATC	ATCTGCTTTC	540
	GGGTAAATTA	ATATTAACTA	AATTTAATTT	ATTTTAAATTA	ATTTTAAACAT	TGTTAAATAT	600
25	TTATATTATT	TTTAATATCA	TTTTTTATTT	TAATATTATG	CTAATATTAA	TTACTTGCTG	660
	ACCCATTATA	CAAAAGG					

1573RP

	GATCCGTATG	GAAATTATTT	TTTTATTTGA	ATTATCTTTC	TCCAGAACAT	CCAAGAAGAG	60
	TGTCAGAGTG	GTGGGCAGAT	ATGGCTTAAA	CTCTCCTTCC	AAAGATTTAG	AAATAGATTC	120
	GATAACAGAA	ATGATTGTAA	TTTGAGTTT	AATAAATGGG	AAGAACTCTT	TAATGACTTC	180
	AAATATTTTCG	TCAACATATG	GCCTGATATG	TTGCTTCACA	ATTGATACCA	TAACACCTAA	240
	TTGTTGAAAA	TAAAACTCAA	GTATTGATGG	AGGACAGCTA	CGCATCACAT	TAATCATTTCC	300
	TGGAATAATT	TGCTTTAGGA	AGGAGACGCA	GCGGAGTCCC	AATGTTTGGG	AGATGTGCTAT	360
	CACTGCCTGT	ATGACAGCAG	TGTGATGAGA	AGATAAAGAA	GGATCCTTCA	AAATTTTCAT	420
35	TAGAGTATTG	ATCACGACGG	TTGGATAATA	TTCTTCATTG	GAGGGTGACA	TACCTTGCAT	480
	TAACAAAGCA	ACATCTATGG	ATGGGGCATT	TTGTTTCGACG	GATATAGGCG	TGCTGGATGT	540
	TCTTTCAACT	TCTCTATGTT	TATAAGGGTC	CAGAGCTCCC	AGAATCCCTA	TTAGTCTAAC	600
	TGTTTCCCTC	CTTATGCTTT	GGG				

1573UP

	GATCSGATAG	GACAGCGAGT	ACGACGGCCC	CTGTGCCGCT	GCCAGCGCCT	CGTTGCCAAT	60
	GTAAAAGTCG	AGGTCTCTCCG	TCCCGCGCTT	CCCAGCCAGG	TTGTTTCGACA	TCAAAGAAGA	120
	TGACGTAAAG	CCCGTGAACG	ACGTCGCCGA	CGTCGTGTTG	CCAAAGAATG	CAGACCCGCC	180
	AGCGCCCAT	CCGCTCCCGC	TCTGGCCCAT	ACCGCTCATA	CTGCTACTCT	TGGCCGCTCT	240
45	GGAAGGCTGC	GCAGTCGCAA	TTGCCGTTGG	GAACACCCAT	GAGGGCGAGT	CGTTACCTGC	300
	AAATCCCAAT	TTGGTCAATC	CTGTACCATT	GTCCATGACA	ACAGCAGGAT	TATTGAGGTA	360
	TGACATGCTG	TATTCTCTGGT	CTCAAATGCT	TCTGGTAGAC	TTGTGTGAGC	CTTTGGCTTC	420
	GGATGGCTTG	TCACTTACTG	GCTTAAGAGT	GCTGGCAGTG	GAAAAGGGGT	CTAATGCGCC	480
	TTTCGTTTTA	GCAGTCAACC	ATCACCAACC	ACGGTACACC	TGACGAAAGG	CAACGCCGTG	540
50	GCTTGTGAAG	CCAGGAGAGC	CCTCGTAGGT	ATTCCGCGGA	GCCAATTGGT	GGCCCTCTGC	600
	GTTCCTCGAG	CGCTCTGCT	CCATCTGCCC	TCTTGACTCG	TTTATGAACC	TTGAAACACG	660
	GCATATAGCG	ACACGGACTT	TCTGCAGGTC	TGTAGAGTAG	CCCACATCCG	GCGAA	

1574RP

	GATCCCGAAG	CTGGTCTGTT	TCGAATTCGG	GATATTTT	GGAAGTACGT	TTGTTCCAAC	60
	GACGTTGCTT	CCATGCATCT	TGCGGGGTTG	TTGACGCAAC	ATTTTCAGTC	TCACATTCCC	120
5	TGAACAGCTT	TGCTATCTAC	TAGGAGTTAC	TGAAGCTTTT	AATGTCTGTT	AATAAATCTT	180
	TTGAGTTAGA	TAATTCGCTG	CGCTACAGTC	TCCATGGGTT	TCATTGGCC	AACCCATCTG	240
	TAACCTCTAAT	TGAAAGGGAG	AAGATCCTAT	ACAGGAAATT	AACAAAGGAG	TCTGTGGCAC	300
	TAGTTTCGGG	TGGGGGGTGC	GGACATGAGC	CTGCGCACAG	CGGTATGTT	GGGGAGGGCA	360
	TGTTAACC GC	GGCTGTCCGA	GGAGACATTT	TTGCGTCCGC	GTCGACGGCT	CAGATTTTGA	420
	CTGCAATAAG	GATTGCTACA	AAGCAAGCAG	CTGGAGCATT	GCTGATCGTG	AAGAACTATA	480
10	CTGGCGACGT	TCTTCACTTT	GGCCTGGCAA	CTGAGCGTGC	TCGGTCTATG	GGCATTGATT	540
	GCCGCGTGGT	TATTGTTGGT	GATGACGTAC	TGTTGGTCTT	ACCAAGGGTG	CAGGAATTGG	600
	AC						

1574UP

	GATCAAAAGC	GTGAAGCTGG	AGCGTAATGA	GGAGCAGCCA	GTTGTTTCGA	TGGACTGGGA	60
	CCAGCTGTAC	GACGTGTCTT	CGAACATAAT	GGAAGAATTT	ACAAAGGAAA	TGGACGAAAT	120
	AGTGGCAGAG	CTCAACCAGT	CGTTCAAGGT	ATGTAGCACG	ATGAACACGC	AGGGCGGGCG	180
	GGTTACTAAC	GCGATGGGTG	CAGAAGCAAT	TGCTTTGGCA	GGAGGCGGGC	TTTACCGTCG	240
	ACTCGCACAG	AGGCGCCACC	CGGTTCCGGC	CTGCGGAAAG	CTGGATGAAG	AGCAAAGAGA	300
20	CGCACCTGGA	ACAGAAGCGG	CGGGAGCTCA	ATGCATCCGG	GCGCATCATC	AAGAGCACGC	360
	TCGAAAATTT	GACGCAGGGA	TAGTCCCGGC	CGGCATCCGT	CATGCAATGC	CTTGCTCAAC	420
	ATTACATGGA	TGGGTATTTT	TGCCTATGTA	CAAACATAAT	TTACGCGAAT	TTAGCTTTCT	480
	TCCAAGGCCT	GTCCTCGGTG	TCTGCGCCAT	CGGCGGCTTC	AGTTTCACTC	TCCGAGACAC	540
	CGGCGTCTGA	GTCAAACTCC	TCCGCGACGT	CATCGTCTTC	CGACTCCGCC	TGGAAATCCT	600
	CGTCCACAGA	CTCATCGTCC	TCTGCAGCAG	AACCATGTTA	ACGTCTCAT	CTCGCTGTCA	660
25	GAACCAAGGG	CTGTTTGTAG	GCGCTGCTGA	ATCTCTTTCT	CTTCGTTTTT	GACGCGGACG	720
	TT						

1575RP

	GATCCAGTAA	ACTTCAGCTC	ATCGTGAGCA	ACCGACGTCA	CCCCACCACG	CGCAGGCGAT	60
	ACTCCGGTGG	AAATCACCTG	AGTATATGCA	GTACTCTTCG	AACCATCGTG	AGCAACCGAC	120
	TCCACCTCAC	CACGCGCAGG	TGAAAGTCCG	GTGGATATCA	CCTGAGTACG	TGCAGGCGAA	180
	CTGCCGTGCG	AAATCACATC	ACTATCAGCA	GGTGAAGTCT	CAGTGGAAAT	CGCCTGAGTA	240
	CGTGCAGTAG	GCTTCGACTC	ATTGTGGGCG	ACCGATGTCA	CCTCACCCCG	CGCAGGCGAA	300
	CTGCCGTGCTG	AAATCGCATC	ACCACGCGCA	GGCGAGACTC	CAGTGGAAAT	CACCTGAGTA	360
35	CGTGCAGGCG	AACTGCCTGC	GGAAATCGCA	TCACCACGCG	CAGGCGAGAC	TCCGGTGGAT	420
	ATCAGCTGAG	TGCGTGCAGT	AGGCCTCGAC	TCATTGTGGG	CGACCGATGT	CACCTCACCC	480
	CGCGCAGGCG	AGCTTCCAGT	GGAAATCACA	TCACCACGCG	CAGGCGAACT	GCCTGTGGAA	540
	ATCACCTGAG	TACTTGCAGT	AGGCCACGAC	CCANCGTGGG	CAACTGACT		

1575UP

	GATCAAATAT	CAACTAAGGC	ACTAGTTTTT	GGTGTAGCTG	CTCAAGCATC	ACCGGATGCT	60
	CAGAAGCGTG	TAATTAACCT	ACAATCTCGG	ACTTCACCAC	CCAAATCTGA	AACACATTCTG	120
	CATATACGGC	ACAACGCTTC	TAGCGTGTAT	CAGTCGGAAA	CAACAKATAA	TATAACTAAA	180
45	GATACCGGGA	TGTTTTCTGC	AGTGAAGTCA	GGCTTTCCCC	ATATACAACA	GAAAACCATA	240
	TCAGCAGGCT	CTGAACCTGA	TGACACTGAC	TTTCAGAGAA	CACAACTAC	CAGCACAGGC	300
	CCACTTCCAA	CTTCAAGCGA	ATATGACTCT	GCCCCGTGTA	CAGTTCATGG	AGGACTTGAT	360
	ATTTCTCCAA	GACCACCTTC	CTCTAGCTCC	ACAGATTTTC	ACGAGTATCC	AACTGGTACA	420
	ATAACAGAGT	CACACAGACG	GCCTTATAAC	GTTAGCCAAC	TTCCCAGAAA	TAATGGGAAC	480
	TCAGCTGCCA	CTCGTGTGAT	TAAGAGAAAC	AGTTCTGTTC	TCAGCTCGCC	TGGAAGCGTG	540
50	ACCACCACCC	CAATGGTTAA	TCRAGCTACA	GTACTCAGCG	CCTCGCCGGG	AGCGGTTAAA	600
	TTAACCGAGA	AACAGCATAG	TCCGGCATCA	TCTTCAGATA	TTTCCACAGC	CAATAAAACA	660
	CATTGGAATT	CTATTGATCT	AAAC				

1576RP

	GATCTTGTG	AGAACA	ACATCGCG	AATTGCAG	CCCCCGGT	CCATACCG	60
	TTTCTTGT	GCATTTCG	CATAGCTGA	CCGTCTTAC	GGACCTTTG	ATTCCACAG	120
5	TTGGCCTGG	TGTAGCCC	CAAACCA	GGATACCTT	CCGTCGAC	AAGATTGAC	180
	AATGATATC	AAATGGCC	CGGCAA	GTTGGAGAT	GGCGTGTAG	AACGCACTT	240
	TTCTACACCA	TCCAGCATC	CCTTTCGC	TAAATGAA	CCAGTAGGT	TATCAAGAG	300
	TTCCACGCTT	GAACGGAG	TGAATCTGT	TATCGCAGC	TTTTTGCTT	GAACGATCC	360
	TTCTTTCCA	TCTAATGG	TCCACTCAT	TGGAAGA	GAAGTCCTG	TTCTGTATG	420
	TAGTAGCAG	CGTGACCT	CAAACATTG	CAAAGCTAG	ATGCCTAG	GGTACCATG	480
10	GTTCCCCGC	GACCAGGCG	TAACAAGAA	GCCCAATGT	AAGATGCCG	TGGGGATGA	540
	GATCCCATG	ATGGGATCA	CCAATATCT	CATACCTCT	CGTTCGGTC	TACTAATAT	600
	TTGAAAGCT	GTCGTAGCT	TTCGTCTAG	AGGATGAG	CGGTAAAT	ATGCTTCCT	660
	CTAGTTCTAT	AAGCACGG	TCTTTGCA	TGGTGAAG	TCGTCTAAC	GTCATCATG	720
	ATCTGCCGAA	AA					

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1576UP

	GATCAGGCCG	GACGGGTACT	TGCAGGAAG	CCTCACGAAA	CCCAAGGGGG	GCGAGGAGGG	60
	CTTCTCGACG	TTTTTCAACG	AGACGGGCTC	GGGCAAGTTC	GTGCCGCGCG	CGGTGTACGT	120
20	GGACTTGGAG	CCGAACGTGA	TCGACGAGGT	GCGCACGGGC	GCGTACCGCG	AGTTGTTCCA	180
	CCCGGAGCAG	TTGATCAGCG	GAAAGGAGGA	CGCGCGGAAC	AACATACGCG	GTGGGCACTA	240
	CACGGTGGGG	CGCGAGCTCT	TGGACGATAT	CCTAGACCGC	ATCCGCAAGA	TCTCGGACCA	300
	GTGCGACGGG	CTCCAGGGCT	TCCTCTTCAC	GCACTCGCTT	GGCGGTGGTA	CGGGCTCCGG	360
	CTTGGGGTTCG	TCGCTTTTGG	AGCAGCTTTC	TATCGACTAC	GGCAAGAAAT	CGAAATTGGA	420
	GTTTGCCGTG	TATCCCGCGC	CACAGGTGTC	CACCTCGGTC	GTGGAGCCAT	ACAACACCGT	480
25	GTTGACCACC	CACACCACAT	TGGAGCATGC	CGACTGTACG	TTCATGGTCG	ACAACGAGGC	540
	CATCTACGAG	ATGTGCAAGA	AGAACTTGGA	CATCTCGAGA	CCTAGCTTTG	CGAACTTGAA	600
	CAACTTGATC	GCCCAGGTCG	TCTCCTCGGT	GACCGCGTCA	TTGCGTTTCG	ACGGCTCCTT	660
	GAACGTGGAC	TTGAACGAGT	CCAGACCAAC	TTGGTGCCAT	ATCCAAGAAT	CCACTTCCCA	720
	TTGG						

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1577RP

	GATCCGTTTA	GAGAAAAACG	GTAGCCCGGT	GAAATACGCA	TTTGAGTGCG	CAGAGCGGCG	60
	CGAGCCGTCC	GAAAGGTAGA	TTTTGTCCAG	TGGGAAGTTG	ACTCGTTTGC	TTATTTTCGAC	120
	AATCGACGTC	TTCAAGTCCC	CGTCTTCCAA	CGGGGTGAGC	TTGTTGAATA	AAGCTGTAAA	180
35	AACCTGGCTGA	AGAGCAGTCA	GCACCAGATA	GAAAGAACAG	ATCAGGATAG	AGACGTAGCT	240
	GACGAAGCCA	GTCGAGAACT	TTTCAATTAC	CTTCAACAGC	GCATAGGCTG	CAGGAGTGGT	300
	AATCATGGAG	GAGATCATAA	ACACTTTTTC	CTGGTCCGTT	AGCCATAGCT	TGACCGTGGA	360
	CTTGTTGAAC	CGTCAATTTT	CCTCGAGCAT	AAAGTTGTAG	TAAATAGCTC	CAAACAACCC	420
	CTGCCACCAG	TTCAGCTGTA	GGTAGACGAT	CAAAAAGTAC	AGCGACTGCG	AGATGGTCTGA	480
	TACTGGCACC	AGCATGGCGG	GCATGCGCTG	ACCTACCGCC	ACTCCTAGGT	TCCACATCCG	540
40	TGGCAGCCAG	TCGTACTTAA	TCATTACCAG	ATTTAGTCCC	AGGAACACCA	GATCTCTAAC	600
	CATACGGTAG	CGTTACTTGG	CCCCTCGTGA	CGCCTGCGTC	TTTTCATTTG	TTTCTTTATC	660
	AATAACGCCC	TCCAGTTCGC	TGGGTA				

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1577UP

	GATCTTCGAC	ACTATGTAGG	CCGCGTAGAT	GAGCAACATT	ACCACGCAGT	CCAGGACGGA	60
	CACAGCGTTC	ATCAGGCATA	CGTAGCCGAT	AATGCAGACG	GCCAGCATCG	CAAACAGTAG	120
	GTCCACGATG	ATCGAATGGC	GCTCCGCCGC	GCTAAGATTT	ACCCACGCAG	ACCTCATCAC	180
	CATAAATATC	GCGCCCTGTA	CCACACAGAT	GATAACGCCG	CAGGCGCCCA	GCACCTCACC	240
	CACAGACAAG	CGGGCGGCAT	TGTTGGCCGC	GTTCACGAC	ATCAGACTGG	AGAACAAGTC	300
50	GGGCGACGAA	TTGCACCATG	CCAGTAGGAT	GGCTGCCAGA	ATGCCCTTGT	GCGGCCGGTT	360
	CCGTTGGCTC	GTCGAAGGTC	CCACTATGGG	ACATAAATAA	TCAGAAGCGG	AAACGCCCCAG	420
	CAACACAAAA	CACACGCTCA	GATGTAGAAC	CGTCAGCACC	ACGAACCCAG	GGATAGCTTG	480
	TTCGTCTCGT	ATAGATACAC	TGGATGTGTG	ATCCGTGCCC	ATGTACTTGG	TGCATGGTCC	540
	ATCCTTGCAC	TCTGCCTTTC	CAGGTACTTG	GTAATAGTAG	TGGTAGCCAC	CGCAACACTG	600
	GTCAAAAAGC	ACACCTRAAA	CCTCAATATG	TAAGGCGTGC	GAATGGTAGA	TGCGTTATTT	660

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AAAATGCAGT GCTTGAGATG AACAGATAGA CTGGTGCCC

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1578RP

	GATCATCCTG	CTGCGAGTTG	AAGTCATCTT	GCGATTCTTT	CATGCATAGG	AGTTGGTTAG	60
5	CACCAAACAT	AGGATTTCATT	CTCAAGTCCA	CCTGCGTTAA	CCGTTCTGTC	CTATACCTTA	120
	AGTAGTCGAT	GAACGTCTTT	GTAGAGTGAG	CCAGGTTATT	AAAATTAAAC	CTGTGGGAAC	180
	TATCCCAGTC	TAGTCGGATG	AGATTATCGG	TAATCTTATT	CACGACACCC	CAGTCCTCGT	240
	TCGATAGACG	CTGGCTACCC	GCAGCCTCAT	TCCGCAACTC	CTTATCGATA	TCTATTCCAA	300
	GGATCTCGTC	CAGGAGAATG	CTACCATTTT	TATCGTTTCG	AATGAACCTG	CCTCTACATC	360
	GAGCAAAGCA	TAGGTGTTTT	ATGTGGATAT	CCGCTAGATC	GAACCCAGAC	TCATCGCCGA	420
10	CTTTCTCTGT	ATCTAGCCCA	AAACCATGCA	TTAGCAGCTT	CAAGACAATC	GCCACAAGCT	480
	GCGATTGTTT	CCATGTCCTG	CAAGGAAGCT	TTACGACATA	TGGGATTTCG	TCATCGCGGC	540
	CATGTTCAAA	GTTTTGCAGC	ATTAGCACGC	AGCTAGTGGA	TGGGGTGAAC	ACGATCCTAG	600
	TAAGGACCGC	GACGAACCTA	ACCTTCTGTG	CTACAATATC	ATCACTGGAG	AAAAACCTCA	660
	GAAGTTCCGC	GG					

1578UP

	GATCTTTTTT	TGGTCTTTTT	CCTTTAAACA	GAATAATAAT	TGAACAGGTA	CCGTATTATC	60
	GCCGCATGCT	AAGTGCACCT	TTGACCGAGA	CACTTTAGTG	ATATTTATTT	TGGTAGTGTC	120
20	CTCGTATACG	TGGGCCACGA	CTTTCTTGCC	ATTAATCTCG	TCCTTGCGGA	AGCCGTCCTG	180
	GTAGCATCCT	AACGCACCTA	TTAATGCCAA	TGATCGCGGG	TTGATCGCCT	CACGCCCATC	240
	CGAAACAACA	CAGACACATA	TCCGTTTCCA	GGCATCGGGG	CCCCAAATAT	CAGAACGCTT	300
	CCGTCGAGTG	AAATATTTTT	TGTTGTCCAT	GACGCCTTTT	AATGTCCGTG	CCAATAATAT	360
	GTCTGTTTTG	TTGTACATCG	TTATCACGAT	CATGATTTCT	GTCTTACGCG	GTACAGCGTA	420
	TTTTAATTGT	CTCACGGTAA	AGTTCCTTTAG	CTGAAACTCA	GCTGGCTCAC	AGGTGACAGC	480
	CTGATATCGC	ATGAATTTGT	ATTCGTTTCG	GAAGTAATCT	TCTCTCATGC	CACGTGCGTA	540
25	CTGCGACACT	AGCTGTTTAC	TGACTGGACA	ATCAAAGATA	AAGTTTCTCT	GATATAGCTT	600
	GAACCTTTCG	AATACAATGC	GATTTTTTAG	CTGTTTCGAC	TGCGGTAAAC	CACTCAGAAG	660
	CCGTTCTGAG	CTGAGATCGC	TGCAGTCGCC	AGAACCTTCG	GAACCGGAGT	ATGCCGATTA	720
	GGCGCTACGC	GAGAGAT					

1579RP

	GATCGAAATA	CCACTGATCG	ACCGCGGTGC	CTCGCTTTGC	AGCTGCTCCG	AGAGCCGCTC	60
	TCCGAGATAC	CGCGCAGAGC	ATGCCTTTTC	CAACACCATC	TTCTCGTACC	GTTCGGGAAG	120
35	TGACCCTACT	ATACTTATGA	TAATGACCTT	CTTGCTCTTC	AGAGTGCCCT	CTGTTTCCTT	180
	CTTCAGGTAA	AGGTGCGATT	CTCGGCCAGG	CTCGTAGTAG	CCACGGACCG	CAGACGCAAT	240
	CCGCGTCGTC	CACGGCATGG	GATGGAAGTA	CTCCACCGBA	GAGTGGCCCG	GCAGAAGCAG	300
	CGAGTTGTTT	ACGCCGACCA	CGTACTCCGA	CTGGTGCTCC	AGCGGACACA	CCTCGAGCGG	360
	ATACTCCTTC	AGCGGCAACT	GGCAGTTCTG	TGACCCGGTG	TTCCGCAACG	TCAGCTCGCC	420
	CTCGACCAGC	CCCCAGACCC	CCGCCATGTC	TCCCATGTCC	GGCAGGTACT	CCGTGTGCCA	480
	GCACCAGGAG	TCATTTCCCC	GCGCTACCGC	CTGCAGCGCC	TCCTGCTCCA	GCGTATGCAG	540
40	CTGCTTCGCA	GTCAGCTGAT	GGTACTCCGT	GCTCTGGTCG	ATCAGCAGCC	CGTCTCGGG	600
	GGTCTGCCAG	AACGGCATCC	ATCCACCAC	GCTTTGTAGA	AACGAGGTCT	TGGGGCGCCT	660
	GCA						

1579UP

	GATCGCACGG	ACCGCGAGAC	GAGTTCCTCT	GGTTCGTGTC	ATTGGCGATG	GTAGGCCGCC	60
	CTGTTGCACG	TGACCTGGGG	ACAGCAGACT	TCGCGTCAAA	ATCACCTTA	GCCTCAGCTG	120
	TGATGACATC	AGCCAAAACG	GCCGTCCGTA	AACACCTTCC	GAGGCGTTTC	TMGACTTGAG	180
	GATCAGTTTA	CCGTGCTTAC	CCTTCCCGTG	CGCCTTTTCG	AAGGACTCGC	GGAGCGTCTC	240
50	AATATCTTGT	GAGAGCTGTT	CCAGCGAGAT	ACCTCTTTCT	GGAACGTAGG	AAACCTGTGC	300
	GCCCCACGCC	AAGGCAGCAT	GCGTTGCCAG	ATAGCCTGAG	TTACCACCTT	GGACATCGAC	360
	GACAAAGACC	CGCGCTCTTG	TGGAGGCTGC	CGACTGCTTC	ACAACATCAC	AGTACTCCAT	420
	TAGGGCATTCT	AGAGCTGTGT	CTGAACCGAG	CGAATACTCA	CTGCCCCGGA	CGTTATTTCGA	480
	AAGTGTGCT	GGAATGAGTA	CCATTGGTAT	TCTGAAAGCT	GGGTAGTTCT	CACGGGCCCG	540
	CTCCAATTGA	TGCAAGGAGA	CGAAGGCTCG	AACCCACCAA	CAATAACCAA	GCCGTCAAAC	600
55	TTGTACTTTT	GGAAGTAGTA	GGCAATCATG	CCAATGTCTG	CATCTTCTGG	GACAGTTCTG	660
	TTGGTTCCCA	ACTCGGAACA	CCGCGAGATT	GCCAGCCAA	CATATCTTTC	CAGTTCAACG	720

1580RP

	GATCCGTGTC	GACAAGTTGG	TCACGTATAT	ATGGCGCGTG	TTCGAGCGCG	TCTGCGTGTA	60
	CCCGCCGAAC	CAGCAGCGCT	GCCATCTCGA	AGACATCATG	CTCTTGCGTG	TGTACTGCGG	120
5	CGAGGCGCGG	GGGCACCCGC	TCTTGCTCAT	GGCGATCGTT	CAGGCGGTGG	CGGCACGCTA	180
	CGGGGTGCAG	ACGCTCCTCT	GCGAGCAGGT	ATTGATCATC	ATTGACCGCA	AGTTGCGCGG	240
	CGGACAGTCA	TACTTGATGA	TCCCGCTGCG	AGGGAACGCA	AAGCCGCGCA	TCTTCACGCG	300
	GCGGCGCTTG	CTCGACACTA	TGCGGCACAC	AATACCCAAC	ATTGCCGACC	CGCGGAGCCT	360
	GGCGCTCGCC	CGGTTCTCTA	CTCCGCTCAC	GAAGCGCGCG	GGTGCTGAGA	AAATCTTCAA	420
	AGACTGGTCC	ATCTACTGCG	ACAAATCCAT	ATGGCGGACG	ATCCCTGATC	ACTCGCCCAA	480
10	TGGCATTCCTG	CGCTACCTCC	CGCACTCCTG	CACGCCGATG	GACGAATCCA	TCTTTGAGTA	540
	TTTCATCGTC	TATTGGAAAA	CCGCAACAGC	AAACCACTCC	ACGAACAACA	TTTTCCACAC	600
	CGTCTTCTCT	AAGCAATTCTG	AAACGATCTT	GGTCAAGAGT	ATCCCGGCGA	CGCATCCACT	660
	TTGTGCGATTG	CCGGGAGCAG	CTCATGGACT	CCATTATCGA	GATGTCTTTC	GCGAGTCC	

1580UP

	GATCCTTTTC	ACCAACAGCT	GTCTGGGCCA	GCTGCGGCCT	GGGATGAACT	ACAACGAGGC	60
	AGTGAAAGCG	CTGACGAACC	TGGCGCTGGA	CAGCTTTACA	CTGCCGGGGG	ACGGTGGGGT	120
	TTCCGCTGAA	CAACGTGTAC	TCTGTGCCGG	TAGAAGACGG	TGCTCAGATG	GAGCTGCTGA	180
20	AGGGGTACCT	GCAGCAGTTG	CGGCAGGAGC	CGGCCACGCG	GCTGCTGGAC	CGTGTGTATG	240
	GGGCGGAAAA	GGCACAGCCC	TCGAAGTTCT	GGCTGGCCTT	CACAAGGCGC	AAGTTTATGA	300
	ACAAGGCGCT	GTAAGGCGAA	ATAGGTACGT	AGCTGGCGGC	GCCAGGAAGT	ATTTACAAAG	360
	TTGGCTGTAT	CGCTACGAGG	TTTTGGTGGC	GTGTGCCCTT	TTGGAGCGCA	CGAGGAGTTC	420
	AACGGCGGAA	GCTCGGAGCT	GTTCCGCGTC	TTTCACGATC	GCGTTCACGT	CAATGCTGAG	480
	TTCGGTGTTC	TTGGCGCGGA	AGCCTTGGAT	CCGCGCCTGC	AGGTCTGTCA	GCGCCTGGAG	540
25	GACACGCTCA	TAGTCTGCAT	CTTCTTTTAC	GCGCTCTTTG	TATGTTTGGA	AGGACTGAAC	600
	GATGTCTTCG	ATACCGGGCT	CGACTCTGCT	GATCATCTCG	ATGCGCTGGC	GCAACAACCTG	660
	ATCGCGGTCG	CTGTTGGCGT	CGCGTCCCTA	ATCATCTGCT	GGATT		

1581RP

	GATCTTAATT	TAAAATTTTA	ATTAACATTT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACT	TAAGATAGTA	AGAATAAAAT	TAGTAAAAATA	120
	AATAGAAAAC	CATAAGTTAA	TTGATTCATA	AAGAAAAATG	GAATTATTTG	TGGCATCTTA	180
	ATTTTTATTA	TTTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATATAA	240
35	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAATTTAA	TTTAAATATT	300
	AAATATACCA	TTTTTATTTA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
	ATTTAATTTA	TATAAATTAT	TTAATTTACT	TCATTGATAT	ATATAATTAT	TAAATGTACC	420
	TTTCATAATA	TTTATTTTTA	TTAGTCTAGT	AAATTTTCTA	TTTAATAGTC	TACCCPTTAA	480
	TTGGATATTA	CTACCTACTA	AATATTTACC	TAATAATATA	TTATTAAGAA	TACTTAAATC	540
	TAATAATTTA	TTATCTAAAG	TATATAAATT	AATTAAATCT	TTTTTATTAT	TATTCTAAAT	600
40	TATTATTAAT	TAGTAAATTA	TATTTATTTA	TTTTATTAAAC	ATAATTTTTTG	ATAATAATAT	660
	ATCAT						

1581UP

	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTTAATAATA	AATCTATTAA	TTATATAAAA	60
	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCATTCAT	TTAATACTCC	TCTAATTCAA	180
	TCTTAAATAA	TTCTTAATTA	TTAAATTATA	TAATAAAAGT	TAGTGGATAT	AGTTTAATTG	240
	GTAAAACATA	TGTTTTAGGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATTAT	300
	ATCATTAATA	TAATAACTCT	TTAATTAGAG	TGGTACCACA	AGAATGCTGA	AAGCATTAGG	360
50	GGTGTGTACC	TTAGCTCTCT	AATTAAAGTT	ATAAAATTAT	CTTAACTAAT	AAAAATAATT	420
	AATTAATAAA	ATAAATAATT	AATTAAATTT	AAAATGTTTA	AAAAAAGAAA	TAAATAATAT	480
	GTTATATTTA	AATAGATCAA	AATTTCAACA	ATTTCCATTT	CATTTAGTAC	TACCATCACC	540
	ATGACCAATF	GTTACATCAT	TTAGTTTATT	AGGTTTACTA	TTAACTTTAG	CTTTTACTAT	600
	ACATGGTATT	ATTGGTAATA	TTTATCCTTT	ATTATTATCT	TTATTAGTAG	TTTTATTACT	660
55	AATAACTTTA	TGATTTAGAG	ATATTGTAGC	TGAACCTIAC	TATTTAGGTG	ATCATACTTT	720
	AACTGTAAGA	AA					

1582RP

	GATCTCAACA	CGGTCGTTGG	AGAAGTGTGC	AACACACGAG	TACGTAGTAC	CCAAATCAAT	60
	ACCGACTGAT	TTAGACATGA	TCACTGATTA	GAAAACGAAA	TCTCTGGTTT	TCGGATAACC	120
5	GGGAGAAATA	CCAATGGTGA	TAACCGTACG	TAAGGCCAGA	GGTACAAAGC	TACTCCAATC	180
	TGAAGCTACA	CACGCCCAAC	CCTTTTATAC	AATTTCAATT	TTTTCTCTCC	CAAACGAACA	240
	TGGCAGATAG	TAAGAGTCTT	CGAGCCCAAT	GCCTGTTCCG	TTTTTTTTTG	TTCTGGAAAA	300
	TTCTACCATA	ACGTATGTGG	CCGTTGAAAA	CTGATCAAAC	GGGTCTCGAA	GATCTTAGAA	360
	TAGAGGCTCC	GACAGAAAGG	GGGAGGCCGA	TTCAAAAAAG	ACCGCATGAG	CCTCACTCGT	420
	GCTTCGAGGC	GGGAGAGCCC	ATAGGCTTCT	TTCCAGCGGC	CACCGACGGT	TTCTGGAAAG	480
10	GAGCGAAAAC	AGAGAATGAA	CCGAGGCGGT	TGATCTGCAT	CTTGGACTTG	GCGTAGGCC	540
	GTTTCAACTG	AGCGGGAATG	CGTGATGCG	AAACTACGCC	GTCCGCACGC	ACCTCCCACT	600
	TCCGTACCAC	CGCACGCATG	TTGGCCGATT	TTCGTAGCGC	GCCTTGATGA	AAAGCGAGTA	660
	TAGAGCCAGC	ACAATCCACG	AGCGGCGGCG	ACAA			

15

1582UP

	GATCTTGTTT	TCCGCATCCA	GATACTGGTC	GAAGCGCGAG	TTCATCTCGT	CTACAATCGG	60
	CTTCCACGAG	TCGGTGTTAT	CTATCGCGTC	CCCGAAGCCC	GGCGTGTTCA	CCACCGTCAA	120
	CTTCAACACC	ACGCCGTTCT	CCTCGATCTC	CGTCGTGACG	GTCTCAATCT	TCACCTTGTT	180
20	CTCGCGTCC	TTGGCCCGCG	ACTCGTCGCC	GTCCCTCACCG	TCCTCAAGCT	TCAACGCGTT	240
	GAAC TGCTCC	GGCGTGTCGT	CTTCGCGCGT	GTATAGCTCC	TTGTTGAACA	ACGTGTTGAT	300
	CAAGTCTGAC	TTCCCCAACC	CCTTGCGCGC	CACGCAGAGC	AAATTGAGGT	TGAACCCGCG	360
	CCGGATCGAC	TTGCGATGCC	ACTGCTTGCG	AAGGTTTGCG	AACCCACAGT	ACCCGAGAT	420
	CTTGCGGTGG	ATGATCCGCA	GGTCTGGCTG	GTCTGGCAGC	ACCTGGCCCC	CCGCGAGCTC	480
	GCCACCCAGT	GCCGTCGCCA	CATTCTCCTT	GTGCTCCGGA	AGGTCCAACC	CCATCTCCTC	540
25	CTCCTTCACG	TTCAATGTCCG	AGCTTGTTGC	CTTCGCGCTC	GCCGTCCCGT	TGCTCATTAG	600
	TGCGCCCCCG	TGCTGGTTGT	CACGCCTCCC	GCCGTCTGTT	CACTGTTGGT	GTTTGCCGAA	660
	TCCTCCTGCG	AGCCTGTAGG	TAACATGCTT	GTTCTGATTT	GGTAGTC		

1583RP

	GATCAATTAC	CCTGGCGCCA	ACCATATTTG	GATGAATATT	TGCATTGTTG	CCGATAGGGG	60
	TTCCCTCATC	GTGTATGTTA	TAGACCTTCA	CGTCTTTCATT	AAAAGGGCAT	GTGATGACTT	120
	TCTTGCTGTC	GGCAGAGAAG	GTCAAACAAA	TTACAGATTG	TTCTGTACCG	GCCAAAACCT	180
	TATAAACCCCT	GAAGTTGTTT	AACACGTCAT	ATATGAATAC	CTTACGATCG	CTGGAAGGGT	240
35	CAGTGGATGC	ACTGGCCAAA	TACCGACCAT	CTGGTGAGAA	TTGGAGGTAC	CAGATTTTCA	300
	CTTTATTTTC	CGAAAGAGTC	TTCACATGAC	TGAAATTGAA	CATGCACATA	GAGCCCAACG	360
	TATCTTGAAG	CAAGTTATAA	GTGGTTTTCT	CTCCAGAACG	GTTTCCTTCG	TGGTTGTGAG	420
	GATCGTCGCT	GAAGCTTAAC	AGGTCGCTGG	ACCGCTGGAA	CTGTATAGCC	TGTTTTAACA	480
	ACGTAATGAG	CCTGCCCCGT	GGAACCAAAT	CATTCCGGTT	GATATATTGT	GAAATCTGAT	540
	CAAGCGCCAA	TTGCCGCGAG	GCTGCCAGAG	ACCCTCCCCA	TATTTTGTGT	GCCTCTGCGG	600
40	ATTCCGCGAG	ACACGTCAAA	ATAGTCGTCA	CTGCAGAAGA	GCTGTGTCCG	GAGTCATAGC	660
	CCACTCTCCC	TCGGGCTCCT	CCACCATAGA	TATGGTCTGT	ACAGCCACAG	CGAGTCC	

1583UP

	GATCGACTGG	AAGTACACGT	CCAGCGACCG	GTCAAGGCC	ATGTCCTGGA	CGGACTGCTC	60
	GAAGGTCTTC	ACGAGGTTCT	TGGCGATGCG	GAGCATTTGGT	GTGCGGTCTG	GGGCGGGCGA	120
	CGCTGCGGAG	GGCTCACCGA	ATTTGCTTGT	GCGTGTTGGT	ACGTGACACT	TGGGCCGCTG	180
	GCCCCGCGCG	GCCCCGCTGG	CCCCGGAATGG	CTGCCCGCGC	CTGGCACGCC	GTTCTTGCAA	240
	TCACATGATT	CATGATTCCG	CTTTTGGGGG	GGATCACTGC	GAGCCCGTTT	TTGCTGCTTT	300
	TAGCCTCCCT	GACACCCTCG	GCTGCGTCTG	GACGCAGGTC	CCCGCCGCGT	GTCCGCTGCG	360
50	TGGCTGTACG	TGTGGGGTGA	CGCCATTTTG	TGGGACAGCG	GCGACGCATG	ACGACGAGCT	420
	CGGAGGGTCC	GCCGTTGACG	ACAGCCCCCT	AAAGGAGTTT	CTTTTATTTC	ACGCGGCCCC	480
	TCAAAACACTA	TATATGAGCA	AAGGCAGGAT	GGAAGGTAGG	CTAAAGCAAG	AAAAGACCTC	540
	GACCAACGGT	ATCGAAGTCT	AAAATCTTAG	CAGGTACCAG	GATGTCCTTC	GAAGATTTGC	600
	ACAAGGCGCA	ACGCGGGAAA	GTCGAGGAGG	CAGTGACGCA	AATATGTAAG	GATTTTCGAG	660
55	TGACGGAGGA	CAAACCTCCG	GAGTTGACCG	CGTACTTCAT	CGAATGTTTG	GAACAG	

1584RP

5 GATCCAAAA GCCTTCCGGG CGCGGGCACA TTTATCACAC CCGCTGTGCT TGACGGCCTC 60
 GACAATACAT CCTATGACAT GCGTAATCCC TCCTATGTTG TTCCGACGCG GCGCAAACTG 120
 GCCAGCGTCT CGAAGGCTTC GCGCGCGAGC AAGAGTTCTT CGCCCTTGA AGAGGAGGAG 180
 AAGCCATTTA AATGCCAAGA ATGCACCAAG GCCTTCCGCC GCAGCGAGCA CTTGAAGCGC 240
 CATATACGCT CTGTGCACTC ATCGGATAGG CCGTTTCCGT GCACCTATTG TGATAAGAAG 300
 TTCAGCCGCA GCGACAATCT GTCGCGAGCAT CTCAAGACAC ATCGCAAGCA TGGCGATATA 360
 AAAGACACGC CACCAACCAC CAAGAAAGGC TGACTTTCCAC ACATCTATGC GAATACCCGA 420
 TGTTCATTA AGAGATACAT ACAGCGCATA CAAGCTGACA CAACGTCCCG TACGCCAACA 480
 10 GAGGAGATGA TAAATACTAC ATACTCAATA TATCAATACC TCCTACTTPT GGTAAATCATA 540
 TATAACTGTT TTCTTTCGCA CTGTTCTGGT AACGTTGTCA TAGGTTTCCC TGTTCGTGCT 600
 AGCTGGCCAG GATTCCTTA ATGGATGAGG TCCGGCGCGC AACCAGACAA AAGTTGCGCA 660
 GCTTAAGATA GTTGAC

15

1584UP

GATCCCATTT TGTCTTCTTC GGCTACCGGG ACGGCCAGTA GAGCATCCAG AATAGATGTT 60
 CACCAGTAGG CTTGCCAAGT GCTCATTAGT TGCCGTCACA TGGCTGCCCCG TGTACATGAC 120
 20 AGTGACACAC CATGTTGTAT TCATATCGAA GGTGGAAGGC CCCTCGATGC GCCCAACGCT 180
 CAATCCAATG GACGGAGTTG CATCGGACTG GGTTTTGGTG TGGAAGCTTG GAAAGACTAA 240
 TATTCGGAAC CTGAATCATG GGGACGTGGT GATCTTCCG TCACCCATGA ACCCAAGAA 300
 AGTATACTGC AAGCGCATCC AGGTAAAGCA GTATGATACG GTGCGCACGC GGTATCCTTA 360
 TCCGAAGAGT ACCTGCGAAG TGCCAAAGTC GCACATATGG GTGAGGGGGG ACAATGTCAC 420
 GCAGTCGGTG GACTCGAATC ACTTCGGGCC GATTTTCGACG GGGCTTGTGG TAAGCGAGGT 480
 GACACGGGTC ATATGGCCGC CATCGAGATG GGGCGCAGAC CTGCACGAGG GCATGGGTGCG 540
 25 ACGCGCAGTT GTTGCTTCAT GATTGCGGGA GCCGGGGTAG GCGAACCTAC CGCTACGTGT 600
 ACATAGCTGA AAGACTAGAT ATTATATAAT GTCGAACAAAC GTGCTGCACT GCGGCAGAAG 660
 GATGGCTTAA GAATCGTTGT CCTCCTCCTT GACGATCTCT GGGAAA

30

1585RP

GATCCCCGTT GTTGTGCACG TGTGATTCAA TATATACATA CTGCAAGTCT GTACATGTGC 60
 TCTATTATAT ATGGTGCTCA TGTTCGCGTT ACATTCTTTC TTTATACAGT TCATGTCCCT 120
 CCGTCGTGGC ATACCCAGTG ATGCCCGTCA TACCTGGTAA CCACAGTTTC TATAATCAT 180
 CAGGCTGAAC TGATCAATGG AGCTGCGTTT GCCGAATTTG ACGCAGAGGT TTGTATACAC 240
 35 ATTGATGTCC GCCCTCGTAA AGCCCTTGCT AAACGTGCAG AAGCAATTCT TCCGTTTGGG 300
 ACACGAAGTG CAAGGCTTGA ATGCTATCAA CTTATCCACA TGCTTCAGCA GCGTCAGTTC 360
 CTTTGTGAGC AGCGCCTGCC TCACCTCGTC TGGAACTCTGG CTAAGCCACT CGTTTGCCAG 420
 CTCAGACACA TTTACCGGTG CGTGAAGCAT CTCGTTGAAC GAGCCTGTGA CCGAGGCGTC 480
 CTGGAACAGT ATCGTGATCG TGGCGTCACA CTTAATCTTC TTGGAGCGGC AGATGTCGCA 540
 GCTGGGGCCC GTCCGCTGAC GCTTGTACTT CGACGCCGTG ATAACGGTTG GCTCCTGTAG 600
 40 CAGCGAGTTC GGTGGCGAAC AGTGCGCTGC ACGTCCCCCG TTGGAAGCCC GAAGCAGATT 660
 CCGACATCAG CGGCGACATC GACACGCCGC GCGCGGACTC TGGCGAGCGC GCGTGT

1585UP

45 GATCACTCTA CGGGGGACAG TTGATTGAGT CCAGTGACGT GAATGTCAGA GAGTCACCAT 60
 TTTTCAACCT ATGACCCTCA TCGGCCAGCA TGAGTCCAAC CTTGCAGCCT TTTAAATTTT 120
 CTACATTTTC CCGCAGAGTC TCATAGGAAA TAATCAATAC AGGCTTGACT ACATTACGGC 180
 CCTGGGCAAT CGCCCACTGC CTGACGGACT GTGCAACCGA GCCGTTGAA AGGGAACTTT 240
 TACGTCCATC GATAGCCAGT GGCAGAAAGG CATCGGGTCC CAACCACTTC ACAATCTCAT 300
 TAGCCAGTT ATTAACGAG GACGAAGGGC AGACAATGAT GCACTTTCA ATTGTAGGAC 360
 50 GACCTTGGGA GCCCTGCCGT AGTAGCGTCC ACATTAACGC TATACATTGC AGCGTTTAC 420
 CTAGACCCAT TTCATCAGCC ATAATACACC CATAAGCCCC CCTATTTGAT TCTCGAGTCA 480
 TAGCTGCATT GGCATCCAAG ATCTCAGGCG AAGGCGTCCG CGTCGGCGTA AGAATCGGCG 540
 TCGGCGTCTC CTCAAGCACC TCCACAATA TTGGCTCACT ATCTTTACTA CCCGGATCCT 600
 TACCAGTGCC ATCGTCTTGC ACCTCGCCCG CTGCCAAGAG AGCCTGTGTA TCCAAAAAAT 660
 55 CCTTCATCGC CAGACCACTC ACACAGCGGT ACAGGAATCT TACCCCTTCC ACTTGATGAG 720
 GCGGTTAAAT CCGCGCCAGA

1586RP

	GATCAGGCGT	AAGGGCAGGA	TATGAACTAT	GGAGACGTCT	ATTTTAAACT	CAATGGCATA	60
5	TAAACACCGC	ATATTTCTTG	TGGTTATGAT	AACTTCAATT	ATCGAATCAG	TCGCAGCGTA	120
	GAGGGTTGGT	GAGAGTTTAC	CACGATATCC	AGTTGTTGCT	GCGCCCGCAG	CACCAAATAT	180
	AACTGAGAAT	TTAAGTTTCT	CGAAGAGAGT	ATGCAACGGG	GGCTTGTCCA	CTACGATTAA	240
	AAGAGCACCA	GCTTTCTCAT	GCCTTCAACT	ATGTCAATAT	AAATATATTG	CAAAAGGCTT	300
	AAGCTCTGTA	TTGAGCCCCG	GAAATGTTTT	TAGCAATGTA	GCTCTCTCAT	CTTCACATTA	360
	GGCTGCGAAT	GTGCTGACCA	ACTGCAAAAA	CCCAGTCATA	TCGTAAATAG	TGATGATAGT	420
10	CAGCGCGATA	TTTAACCGCG	GGTGCAAAAA	ATTGATTTTCG	CCCAGGATCG	AACTGGGGAC	480
	GTTCTGCGTG	TTAAGCAGAT	GCCATAACCG	ACTAGACCAC	GAAACCAACC	TTGAAGAACG	540
	CACGCCGCGA	AACCGACCAA	CACAACCGGT	GCAAACCACG	TGCCTGACGA	CTCTTTAGGC	600
	GTGTGCTAGG	GGGGCGCCCA	CTCGTACTTA	TTTTATAAAC	CTTGGATCCA	GGTGCGTCCA	660
	TATACAGGGC	GATCCGCGCC	ATCTGCAGCA	GCCAGGAACG	CA		

1586UP

	GATCAACAAA	GTCAAATCCA	AAATTGTGCT	GGGAGAGAAA	AAGATTCCGC	CATCATTTGGG	60
	CCTTTTCTAT	AGCCATCAAT	TCAACAATCG	GTTAAGCGAT	TTGAAGCCTT	CAGCCCTTTA	120
20	TGAGGGTGAT	CCTGAGAAAC	AAGATGGGAC	TGCTACCGAT	GGAAGCAGCG	GTAGTGTCCA	180
	TGGGTATGCC	ACTGATGATG	ATATCATTTG	CACAGGCGAG	AACACCGTTT	ACAGCCTAAG	240
	CCAAGGGATT	GCATATCATA	TAGATGAGGA	AGGAAACTAT	TATTATGCTG	GTATCGATCC	300
	GTTTACTGAT	GCATTGGAAC	AAGAGGCAGA	TTGCTTATAT	CATGAAAGTG	AGGTAGAAAG	360
	CGTAAATGTC	AACAACTTGG	ACCATCTTTC	TTCCGATATC	AAGGAAGAAA	ACATAGACCT	420
	CGATGGTAAC	ATAGAAATGT	ACGATTCTGA	CTTTGACCAC	ACTTCCCTCG	ACCAGGTCCC	480
	GAAGGCTACA	GAAACAATCG	AAAAATACAA	TAATAACCAA	TACTACAAGA	TGAACACGCT	540
25	AATCACTGAC	TCATCAAATT	GCCAGGGCAA	CACGTGTAGCG	CTCTCATCTG	ATTATGGAAC	600
	AACTTCCGTG	CATGTTGAAA	ATGTCCTCTAA	TGAGAATTCC	TTGGGGTCAT	CAGGCTACAA	660
	GGAGATATTC	CTGAAAACCTA	TGATGACTAC	CTTTACGAAG	GGGACGAAGA	TGATTTTCGAT	720

1587RP

	GATCATCGAG	AAGGAGCTGG	AGGGCGTGCG	CATCCGGCTG	AACAAGTCGC	CTCCGGACAT	60
	CATTGTGAAG	AAGAAGGAGA	AGGGCGGTTT	ATCGATCACG	AACACAGTGC	CGCTGACACA	120
35	TTTGGACCAC	GACGGGATCC	GCGCGGTGAT	GAGTGAGTAC	CGCATCAACA	GCGCGGAGAT	180
	TGCGTTCCGG	TGCGACGCGA	CAGTTGACGA	CCTGATTGAC	GTCCCTCGAGG	CTCCCAGCAG	240
	GCGTTACATG	CCGCGTATCT	ACGTGCTGAA	CAAGATCGAC	TCGCTGTTCAG	TGGAAGAGTT	300
	GGAGCTGCTG	TACCGGATTC	CGAATGCTGT	GCCTATATCT	AGTGGACGGG	AGTGGAACTT	360
	AGATGAGCTG	TCGAGGTTCA	TGTGGGATCG	CCCTGAACCT	GTGAGAGTTT	ACACCAAGCC	420
	CAAGGGGACC	ATGCCCCACT	TCAATGACCC	GGTTGTGTTG	CGGTCAGACC	GTTGCACAGT	480
	GCGGGATTTC	TGTAACCAAA	TCCACAAGTC	TCTGGTTGAG	GAGTTCCGGA	ATGCTTTGGT	540
40	TTACGGTAGC	AGTGTGAAAC	ACCAGCCTCA	GTACGTGGGT	CTTGACACAC	CTCTAGAGGA	600
	TGAAGACGTT	GTGACAATTC	TGAAGAAGTA	ATGTCCTGGC	ATTTATGCAT	GGTTTCAATG	660
	CACACGTTCT	CGCGCTGC					

1587UP

	GATCCTAATA	AAAGCTTTTT	TGCAATTGCT	CTACCTACGC	CTGGAAGGTC	GCGTAGGGCA	60
	CACGTTTCAA	ATAGATGTGC	AGGAGATACG	ACCTGCGTAT	CACCCCCCTT	AATTGATTCT	120
	TTAGTGCAAA	CCAGATAGCC	ATCAGGTTTC	GCACGTTTGA	AAGCCAACCG	GGCTAGAACT	180
	AAGGACGGTG	CGCACCCAC	GCTTACCCTG	CAGCCGCTG	TGCGCTCTGC	TACTTCTGAT	240
50	CGGATGCGTA	TACACAAGTT	TTGACAACCT	AGTGTATCGA	GCGGCATGTC	AATAACACAG	300
	ACAGCCTCAT	CCACCGAAAT	TGGATACACT	GCGTCGAAAG	CCTTTAAACC	CTCCAATACC	360
	TCGTAGAAGG	CATTGCAAAAT	CGTTTTCGTAT	TCATCGTAGG	TATAGGGGAG	GCAAACCAGT	420
	TGGGGGCACA	AGTTCTTTGGC	TTTGAGAGCC	CACATGCCAT	TTTGTATTCC	ACATTCCCAG	480
	GCAGCATAAAT	TACAGGAGGC	AACGTCCGAA	GATGAAACCC	CATGACACAC	TGCCAACGGT	540
	ACTTCGGCCT	TGCTTTGGATA	GCCCCCCTTG	ATGCCCTGAA	TAGTCGCAAA	AAAGCAATCA	600
55	AAATCCACGT	GGAAGACGTG	TGCTGGTGGG	GCCCCGAAAT	CATTTAGCGC	ACCTTCATTC	660
	ATCCGGAGAT	GCCTGTTCGAG	AAACTCTCGC	GTAGAGCCCG	CT		

1589RP

5	GATCATTCAA	GCATATTTAT	TAATTAGATG	ACATTAAACT	ATTAGACCTT	GGTTTGGGTT	60
	GCTGGACTTA	GGGTTGTGGT	AGTCCGTGGG	TTATATATTT	TTTGTAGACA	GTCACCAACA	120
	CACTTGATGT	ATTTCTTTGA	GCTGTGTGCG	ATAGGCTCGC	ATTGGATGCG	GCACTGCTCA	180
	TTGGCATCCT	GCCCCTCAGC	AATAACCATA	GCGGCGCCCG	CTAGAAGACC	GAAAAAGTAG	240
	GTTAGCTTCA	TCTTGTGATA	TTATTCTGTG	TTTAATTAAA	TGGAACTTTA	GTGCTCTGGT	300
	TCTCTGCCAT	AGAGATCAGG	ACCTTGGTTA	GATATCCGTG	CCCTTATATA	CACTGCTGCC	360
10	AAGGATCGAT	GGACTGTAGC	CGAGCACCTT	CCAACTCAAA	AGATCCGACA	TCAATGTATT	420
	ACTGAGAGCC	AGTATACTTA	CCGCTTATCA	CACTAAACCC	CATAGCCATG	GTTACGAAGA	480
	TGCTGATCTA	TCATCCCA	CAGCTCGCCA	CTGTAAACGG	ACTTGAGGTG	GGCGACAGAA	540
	GGCCACTACA	GGATGAGCGT	AAATCTCCAA	CAGCTAGCAA	CACATGCCAT	TATTCTATAC	600
	GAACAGTAAC	GTGCTTGATA	TTACAGAATA	CCGATTAGGT	TTTTTCCTGC	CAGACCAAAT	660
	GCTATTGGTC	AAACTCAAAT	TTAGTCAGGC	TTACATTACC	TGCGTACCTC	GAAGGTAGCA	720
15	ATGTTAGGCA	CTCTGGCAGT	A				

1589UP

20	GATCTTCTTG	GCCATTATTG	CAGTAGCGGT	AGGCGGGCAT	ATGAAATGAG	ATCGCGGACG	60
	TCCTGCGCTT	GAGCACCTGA	AAAATGGCAG	TAAAAAGAAA	CGATCCCCGC	AACATTTGTT	120
	CGAGTGACTT	TTGAGGCAGA	AGTACAGGCT	TCAGCCCCGC	GCTGCTTTGC	TGTGGATTCA	180
	GACCACCGGT	GGTGAAGGTG	GTGGTACACT	GGGGTCAGCT	ATGCTCTCAC	GCTGCAGTCC	240
	AGGACAGACA	TACCGCCAC	TATAGCAGGC	CGATCACATA	CATAAGTAAG	AAAATTAGCC	300
	CCAGTAGATT	ATTGTCGGGG	TCATGCAGTG	CTGCACCATT	GCGTGATGTG	GTGTTGCCGG	360
	GTAGTCTGCC	ACCATCGTGA	TACCCGGAGC	CGCCAGATCC	AACCGGAGGT	ATAAAAACTG	420
25	GTAATGGGAC	AAATCCGGGG	CCGCCCGGC	CGCCGCCTCC	GCCCCGTAA	GAAGGCAACC	480
	CCGGCCTTTG	CGCTCCTCCA	TTCGAGTCTT	TTGGGCTGTT	CGGTGGCGGC	TGTGCTCCGC	540
	CGTTTGGGCC	TTTAGGGCTG	TACGGCGGCG	GCTGTGCCCC	CCGTTCGGGT	CTTTCGGGCT	600
	GTACGGAGGC	GGTGCGCCTT	TCGGATCCTT	CGGGCTGTAC	GGAGGCGGTG	CTCCTTTCGG	660

30 ATCCTTCGGG CTGTATGCCG GAAGAACACC CTGGG

1590RP

	GATCATAATG	ATTTGTCTTA	ATTCTTTTCT	TAATTATTCA	TAAATAATT	AATTAATATT	60
	TTATTAATAA	AAAATATTKA	KAKKKATGTT	CGTTTATGAT	AAATTCCTAA	ACTTTGSARC	120
5	ACGAACTGAA	GACAACTATG	TAACGCCTGT	AATTAATTAT	AAATTATTAT	AATTAATATAT	180
	TCAAAAAATG	GTAAGATTTA	TCGAGGATTA	TCGAATTAAA	TAACATGTTT	CACTGCTTAA	240
	GTCTGTAACC	GTCTATTGTT	TTGATTTTAA	TTATTGCTAA	CGTAGTCATC	AGGCGGAATA	300
	CTTTAATTTT	CATTTAATTT	ATTCTTTAAT	TAATAAAAAA	TAAATAGGTA	TTCATTGTTT	360
	ACTGCTAAAA	CTACTCGGGT	ATCGAATCCG	ATTTGCTACT	TTAGCCTTCG	TTCCTCAATG	420
	TCAATTAATA	TATAATTTAA	ATTTTCACCT	TATAAGTCTT	ATTCATATAA	TTATTATTTT	480
10	ATCTTTACTT	GAATAATTCT	TAAATTATTT	TTATTAATTC	TAATTATTAT	TTTAAATAAT	540
	CATTCTACGA	ACCCTTTAAG	CCATTACGAT	TAACGCTAAC	CCCCTTTGTC	TTACCGCAGC	600
	TGCTGGCACA	AATTTTGGTT	GGGATTATTT	AATTATATAT			

1590UP

	GATCTATTAT	TAGAGGTAAT	ACATTTAAAC	TATTATCTAA	ATTCTTCTTC	TTCTTATTTA	60
	TTCTTAACTT	TATCTTATTA	GGTAAATTAG	GTGAATGTCA	TGTTGAAGTA	CCATTTATTT	120
	TAATAGGTCA	AATTTGTACA	TTTATTTATT	TTGCTTATTT	CTTAATCTTA	GTACCTATTA	180
	TTTCTATAAT	TGAAAATATT	TTATTTTATT	TACTAAATAA	AAAATAATAA	TTAAATAAAT	240
20	AATAATAATA	TTCATTAAAT	ACTTTAATAT	TAATATTTAT	ATATTATACT	TCTTTATCAT	300
	TTATGAGGGT	ACCTCATATT	GCTGACTAGC	AATAGGGGGG	TGAACCCTAC	GCACCTAAAT	360
	GATAAGAGTT	TATCATTAAA	TTATATACTA	TATATTATAA	GTAAATTATC	AAACCATATA	420
	TAAAGGTATAT	ATATTAAGAA	AGTTTGACTG	AGTGGTTTAA	AGTGTAATAT	TTGAGCTATT	480
	ATAAATCTTT	ATGATTTTCAT	AGGTTTCAAT	CCTATAACTT	TCGTATTAAA	TAATTATTTA	540
	AAATAATTAA	AAATAGTTAA	TAATAATGAG	AACATGATGT	TGGTTTCAGAT	TAAGCGCTAA	600
25	CTAAGGACAT	TACACATGCG	AATCAAACGT	TAATATTATT	AATTAATAGT	ATTAATAAGT	660
	GGTGTACTCG	TGAGTAAAAA	TTAAGAATAA	TGAACCTAAA	TTTAACTAAA	TAT	

1591RP

30	GATCATAAGC	ATCTTTAGCT	CCACTATCCA	TGCTTGAAAT	TTGCAGCTGA	TAATAAAGTG	60
	GTGTGTGGC	CGAGCGGTCT	AAGGCGCCTG	ATTCAAGTGT	ATGCTTACAG	CTGTTACAGT	120
	TGGACACTCA	GGTATCGTAA	GATGCAGGAG	TTGCAATCTC	CTCGCAACCA	ATTATTTTTT	180
	TTTTTTGGAG	TTCCAATGCA	ATATCAATTC	TACTGCTGCG	AAAAGGTCTC	GTCAGCAGAT	240
	AAAAGAATAT	AGAATATGTA	TATTTATATA	CAAGAAGCGT	TTACTGACTT	TTTATTGTTA	300
	TAATGCCATT	CGAAGAGATA	TCGCTTATTA	ACAGCAATAC	CCCCCTGCAG	GTCCCCGCCA	360
35	ACCGTTGTCC	AGTGATGCAA	AATATATACC	TCGCATGATA	AAGAAGGCCC	TTCATATCAA	420
	ATGGCCCAGG	CATTAATATC	ACCGTTTCGG	CGGCCTTCAA	CCAAGTAGCC	ATCTTTATAT	480
	CTGACATATT	CCACGGCATT	CTCAGTATGC	TCATCACCGC	CGCAAAACCA	ATGCTTCTTC	540
	TCTTGCCGGT	TGTAAACCTT	CACTGTACCT	TCCTGGTTAG	CGACAACTAT	CTTATTCAAG	600
	TCAAACCTGCA	AACATGTAC	CGGGTGTTCA	TACGAAAATG	TATCAGCCAA	TGTACCGGTA	660
40	CGTAGATCCC	AGATCTAATG	CTGTTATCCA	AGGAACCAGT	CACAAGGTTT	AGAGAATCAA	720

1591UP

45	GATCCCCAAT	GATCCCTCTC	CGGGCTACAA	CATCGAGCAG	CTCGCTAAAC	AGTGCAAGAA	60
	CAAGGACAGG	CTGGTGGAAC	TGCCTTATAC	TGTGAAGGGG	ATGGACCTCT	CCATGAGCGG	120
	TATTTCTGCC	CACATCGACT	CGCTCGCGAA	GGACCTATTT	CGTCGAAACA	CGAAGAATAA	180
	CAAGCTCTTC	GACCGCGAGA	CCGGCAAGCA	GCTCGTCACC	GTAGAGGACC	TGTGCTACTC	240
	CCTACAGGAG	CACCTGTTTG	CCATGCTCGT	GGAGATTACC	GAGCGTGCCA	TGGCACATGT	300
	GAACCTAATC	CAGGTGTTGA	TTGTGCGCGG	TGTGGGCTGC	AATGTCCGAC	TGCAGCAGAT	360
50	GATGGCGAGT	ATGTGCCAGA	GCAGGGCCGA	CGGCCAAGTT	CATGCGACGG	ACGAGCGCTT	420
	CTGTATTGAC	AACGGTGTC	TGATTGCACA	GGCTGGTCTA	CTTCAATATC	GCATGGGCCA	480
	TATAGTAAAA	GACTTCTCAG	AGACCGTTGT	CACGCGAGGG	TTCCGGACTG	ATGAGGTTTA	540
	CGTATCGTGG	CGCGACTAAG	TGTGTACCAA	GTTTTAATGA	AGTTTACCAG	CCCTAATATA	600
	GCTGTTAACC	ATCAGTGGCC	TGCGATCAGC	TGGTCCAGAA	CAGTAGTCGC	CGGTGGCTGT	660
	CACCAGCCTA	CGGGCCCAGC	GCCAGGTATC	CTGTTTCG			

1592RP

	GATCAGGAAC	TCGCAGACCT	TGGCTCTCTG	GTCCGCCCTGC	AACTGGATGA	TCTCGCCCAT	60
	CTCGTCGTCC	TTGACCATGT	TGCCGTTGCA	GCCAAAGTCC	TTCCGCAAGA	CCTTCCAAGA	120
5	TGCGCTTGAG	GTCGTACTCC	TCGGGGATGC	CCTGCACGGT	GGTCAACGTT	TTTCTGCCGT	180
	TTCTCTGCTG	GATACGGATG	TGGATGTAGT	TGGAGGAGGA	GGCTTCGTCTG	TCGCCGGTGT	240
	CAGCAAAGGG	GTCGAACGAC	TTGAGGTTTT	CGATAGACAT	GGTGGCGGTG	GGGTGTGAGG	300
	TACAAGGTAA	GCAGAGAAAA	TTTTTCAGCTG	TCCTTTTAAA	AGCGCGCACC	TCGCGTCTTG	360
	GAACGCATTG	GCTTATTTGT	GAACCATATT	CTTATCTGTA	TAGGTGTTAA	CCCGCATTTC	420
	TCTGCAATTG	CCCGTCTTTT	TTTGGCGTTG	GGACAACGCT	TCCTTTTCAA	CACACTTTCC	480
10	AGGAACCTCT	TTGTTTTCCT	GGGTAACACT	GTTCTTCTTC	GCTGTTTATC	TCCTGTTAGT	540
	AAGGCAGAGG	CTGGGATTAC	AATGAGACTC	GTCACACATA	CTTCACCTAG	CAGAACACTG	600
	CAAATCGCCT	GGATTGCTTG	AGCTGTTTCT	TCAATACYTG	ACATTGAGT	TGTGGGGAGC	660
	GAGGAAAGA						

1592UP

	GATCCACTTG	TTAACGTCGG	CGCCGCCAAT	CCTCATCCCT	CCATATGTAA	CCACAAGTGG	60
	TTTGATATCCC	AACAATTGCA	GCTCAATTGG	CATCAAGTAC	GCGTATCCCC	CGCCTAGAGA	120
	ATGGCCAGTT	ATAATTACCT	CATAGTCTGG	ATGAGCATCA	TGTACTGGCT	TAAACGCGGA	180
20	ATAGATATCG	TTGTACGCCA	ACTTAAATTG	CTCATATACG	CCCGAGTGTA	CAAAGCAATC	240
	TCCCGTACAC	TTTCCAGCGC	CACTAAGTGG	CTGGTATGGA	ACCCAGGAA	AAATGAAATC	300
	CACATCCAA	TCTTGAATTG	TTACCGACCC	TCTAAATATG	ATCGAAATCT	GCTTAGCCGT	360
	GTCATTTATT	GCTATCATGC	TATAACAGGA	AAACTGCCCG	CGGGTCATGT	CCGGATCAAA	420
	AACTTTAACT	ACTTGAGTCC	CTGTTGTTCC	ATGTACCACT	TACCGTCATG	AAAAGGGTCA	480
	GTGAGTATTA	AAGTATTCAC	GCAGTAAACG	CTGTTAGTGA	GATATGACAC	ATATTTCAAT	540
25	GTATCAAACA	TCTCATCAGA	GAAAGAATGG	ACATGAAGGA	AAAAAGGC		

1593RP

	GATCGAAATA	GACAACTCTG	CAACGGTGTC	CAAATGGCCC	AGCAACTTCC	AGGAATAAAC	60
30	ACAAGTAGAC	CATAGCATCC	AAGTACCCTAT	GCTCCTCGCC	TTACTATGTC	TTTGGAATGC	120
	AAAGGACCAA	ACGTGCTGCA	AGACGGAGGG	AGAATTCTTC	AGAAGAATTA	CATTATACAG	180
	GCTCGAAGGT	GTGACAGCGA	ACCTATCATG	GTCCCTCCTTT	GTCGGTTCTG	CCAAAAGAGA	240
	AGACCAGACC	TCTTCAAGGG	TGACTGCAAT	TCGTGTCTTA	AGGTCGCCAG	TGACACGAAC	300
	AACCGCTTTT	CTGGGCAAGT	CAGCGAGTTT	TATCGTACTA	GTAACCCGGT	TATTTCCAC	360
	TAGGAGCAAT	GCATTCAAAT	AAGCAGCCCA	CAGTTCCCAA	TCAAATTCAC	TGGCATTCCC	420
35	ATCTGGAGGA	ACATTATATT	GGATTAAACG	ACTTTTGTTAC	ATTTCCAATA	TAGTAACGCA	480
	TGTCCTCAAA	AATAGGGCAT	GTAGTGAAAT	CCACTTACGG	GAGGGCATGT	ATCCATCTTT	540
	GGTCAATATT	GTTACAGTAT	TAACGGCACT	TATAATATCT	TCCTTGGTAA	ACCGCGTAAT	600
	GTTAAATACA	GATGTTAAAA	TAGGATCATT	GGCGCAATCT	TCCACAACCT	GTATAAATGA	660
	GCTGCCATGT	CCATATATTT	CTTCCTACAA	TTTGGGCTAA	AGTTGCCAAT	ATAGTACC	

1593UP

	GATCGATCTG	TTGTAATTTG	GACACGGGGA	GCTGCAAGCA	GGGTAACGTA	TGAGGCGTGC	60
	TGTGGGGCCT	GGCGATGGCT	ATAGATAGGG	TCATACCACA	TCATCGGTTT	GGCGGGGTGG	120
45	TATAGCATTT	GGAGGACAGG	TTAGCCCCGA	GCCACAGCAT	AGACAGGTTT	ACGAGGCTTG	180
	CAGCAGAGGA	AAAGATGGGC	AAGCCATTTG	ACTGGCAGCC	GACGGGGAGG	CTCGTGCGCG	240
	GCCGGATTAT	CCGGGCGTTT	TTGCCCTTGA	AGCGGCACCC	GCAGCAGCTG	CTGGACAACC	300
	CGAACTACAC	GAACCTGTAC	CCGGGGGATG	AGGTGTACAG	CTTTGAGGAG	ACGGCGGACG	360
	GGCGATGGTG	TCGCGTGTAC	CAGGTGGTCC	AACCGCTGCC	GGAGGACTTT	ATCTCGACCA	420
	TGAAGCGGTT	CTCGGACAAG	CTGCCGGAGG	AGCAGCACCG	CGTGGTGGTG	TGCCCCGAAGG	480
50	CGTTTGTGCA	CTGGTATGAC	GACGAAGTGG	TGACCTTTCC	GTTCCTGGAC	CTGCCCGACG	540
	AGCGGGAGGT	GAAGCGGGAG	GTGGCGGAGA	CGGACGTGCC	GAGCCTGCAC	GACCTGCTGC	600
	ATAGGGACGA	CTTGGGGGAC	CTGGAGCTAT	TCCGGCAGCT	GCGGCGGACG	CG	

1594RP

	GATCAAGACT	GCCGAACGTC	TAGTTTCCTG	CTTCATGAGG	TTTGAATCT	TGTCCACGAT	60
5	GCGGGCGTTC	ACCAGGCGGT	TACGCAACTC	AAAGTCGTCA	TTAAAGTCGC	GAGCAAACCA	120
	GTAGGAGGAT	TCTAGAAGAC	TGGTAAGCCG	GATGGCGTTT	TTGAAGGGTA	TTGCGTTTGC	180
	GAAGTTCTCA	TCCGCAAAGA	GCTCGCTAAG	CGACTCTATC	ATAAGCAGCT	GCAGGACACA	240
	TTTTACCACG	ATGGTATTCT	TAATACTTAC	ACGGTGCCCC	ATCTCCTCGC	TGCTTTTTCGT	300
	GCGCACGAGT	CGGCTCATAG	GCTTATCCTC	TTCAGTACTG	GCGTTGCCAA	CATCCTCGCC	360
	CTTCTCCTCG	CGTTGGGCAC	GCTCGACTTC	CCGATCAACA	TCACTGGCAC	ATGATTGGGT	420
10	TTCAGCAGTA	CCGTTGGTGT	TGATTGTGGC	TACTGATGGC	TTTCTTCCAC	GCTTCAATGG	480
	ATCTGACTCA	AAAAGTTCTG	TGGCAGTGGT	AAGCTCAAAAT	AACCGGGCAA	ACGAGTTGGT	540
	AACCTGCTCC	CAATGCGTTG	TCCCGAACTT	GTGGGTGTTT	TGGATAATCA	ATTGCTGCAG	600
	ACAAGACCTA	CCAATCCTGG	CAATGGTGTC	ATTTTCTCTGA	CAGATGCAAG	AGACTAACAA	660
	AACCAGGAAG	CCATCCAACA	TTTCGTTTCAG	TGAATCAAAG	TAATGCGTAA	CAGGGC	

1594UP

	GATCTGAATT	TAAACGTGAG	ATACCCGTTT	TTCTGACAGA	GATATATTTT	CCTATATCTC	60
	ACATGAAATC	TTCTACTCCA	CATCAGAAGA	GGTATTTTTT	GAGTGTATATC	CAACGACTAT	120
20	GCAATGACCC	GAGAACCCTA	ATTGAATTCT	ACCTAAATTA	TGACTGCGAC	AGTAGTATGC	180
	CTAATATTGT	CGAGACTGTT	GTGGATTATT	TGACGCGACT	GGCGCTAACA	CGTGTCTGTA	240
	TACACGCATC	ACAGCGTGCG	TACTATGATG	AACAAGTGAA	CAAACCCCTT	GCAACGTWTA	300
	ACCTATCGCA	GTTGCGCTTTA	TTATCCATAT	CTAATGTTAG	CAGTATGTCT	GTTGCTCCAC	360
	AGCAACTCCA	ATTCCCCTGG	GAATTTGCGC	TAAAAATGAC	CTCGTTGAAA	TGTATGTTGG	420
	CCGTGCTAAG	ATCACTAAAT	TCTTGGGCGG	ACAAGGCGAC	GGCTCCAAAT	GGCAGATTAA	480
	ACCACAATAG	GGCATCTGTT	GGCTCCAGTA	CGATTGAAAG	GAAGCACTCT	TCGGCTTTTA	540
25	GCTCTTTTCA	TCACACTATG	AACACAACAC	CTGTAGGAGA	CCAGAAATAGT	GTCCAACAAT	600
	CGGAAGCGAG	TGAGGATATT	GATGATCCCA	CACAGTTTGA	AAATTTGAAG	TTAAGGAAAA	660
	CAGAACTGCA	AAAATGTATT	CGGTTATTCA	ACTTC			

1595RP

	GATCTTGCTG	CTATCCAGAA	ATGGGAAGTT	CTTAGACAAC	GGGGAATTAA	GCCCCTTTTT	60
30	CAATATTTTG	AGCGTCGTTT	CATAGCTCGG	AAGACGCGAG	AGAAGCCCCC	CCAGTAGTGT	120
	CTGTTTATGT	TCGCTCATGA	AAGGTGTCTC	TATCAAATCT	AGCTCCATCA	TCGCAGAGTA	180
	GTTATTATCT	TTCTTCCAAG	ACAGACGCAC	ATGCCGCAAC	TTCGTCAGGA	TTACAGTAAA	240
	ATAATGGTAG	AACCGCGGAG	TCACAGAAGC	GACGACCGCT	CGAAATGAAG	TCGGCCCCGA	300
35	GAAGATCGTG	CGGCCCTGCT	TCTCTATCAC	AAGATGGAAC	TGCGAAAGTC	TGTTTCAGGG	360
	GGACACCGTG	CCCATAACGT	GCTTCTGTCAT	GAACAGCTGC	GGTACCATCT	CGCTCTTCAT	420
	CCGCGCGAGC	TCAGTCTCAA	GCTCGTTCGAT	CCGTCGCGAG	AGCTCCACAT	TGGGCGTCGA	480
	GCTGAACAGC	TCCCGTGAGT	TCACGTGCTG	CGTAAACTCA	GACAGGTACA	CACACTCGGG	540
	CAGGCCCTTC	CAATACATGT	AGAGCACTTC	GGCCGCGCCT	TGTTGCACTT	GACGCGCCGC	600
	TTGCGGCAGA	ACACGCACGA	CTTGCTGACC	TTCCGCTGG	TTTTTACAAT	CTTGCCATCG	660
40	GACTCTGCCA	TCCCGCCAGC	TTCAAGCAAA	ATGAGTAGGC	TATATTATT		

1595UP

	GATCGCGGAC	GTGGAGCACT	GGCCGGAGAT	GCGCGCGGCC	ATCCTGGTGG	TTTCTGCGGA	60
45	CCGCAAGGGA	CACGCCATCG	ACGAGCGGTA	TGCAGCAGAC	GGTGCACACG	TCGGACCTCT	120
	TCAAGGAGCG	CGTCGCGACG	GTGGTGCCCG	GGCGGTACGG	AGAGATGGCG	GCGGCGATCC	180
	GCGCGCGCGA	CTTCGCGACG	TTTGCGCGCC	TGACGATGCA	GGACTCGAAC	TCGTTTTCAG	240
	CCACCTGCCT	GGACTCATTT	CCGCCGATCT	TCTACATGAA	CGACACTTCG	CGCCGGATTG	300
	TCAAGCTGTG	TCATCTGATC	AACGAGTTCT	ACAACGAGAC	CATCGTGGCG	TACACGTTTG	360
	ACGCGGGTCC	GAACGCGGTG	CTCTATTACT	TGGCGGAGAA	CGAGGCGCGG	CTCTGCGGCT	420
50	TCTCTCTGTC	CGTCTTTTGG	GCCAACGACG	GCTGGGAGAC	CACGTTCTCG	ACGGAGCAGC	480
	GCGCCACCTT	CGCCGCGCAG	TTGACGAGT	GCGTGCGCGG	CAAGCTTGCG	ACGGACCTGG	540
	ACGACGAATT	GCACAGAAGA	ATTGCCCGCC	TCATCTTCAC	GAAGGTGCGG	CCAGGGCCCA	600
	GGACACTAAA	TCCCTCGCTCA	TCGACCCGAG	ACGGGCTGAC	CCCGCTGACG	CTATTCTCCT	660
	GCTATTTTCT	GCTCTGTATA	CCCTGCCAGA	CGCGCTATAT	ATATAGAATA	TGCATTGCGA	720
55	CGCTTACGCT	T					

1596RP

	GATCGACAAT	CTGAGCGAAA	TATTTAGCAC	GACATGCTAC	ATGGGCTCTA	CGGTGATAGT	60
	ATGGGAGTGG	AGCAACCGGC	TGTCCATACT	GGAGGCCAGG	CGCCAGGCGC	AGAGCATTCCT	120
5	GGGGCGGCCG	GTGTATGAGG	ACGAGGAGCA	GGGGTACAAC	TTTGCGCGAT	ATGCGCTGAA	180
	GATTCAGACC	GCAATTGACCA	GCAAGTCAGA	TGAAGGCGAC	ACCACATCAG	CGACTACCTT	240
	TGCTGCACCG	AGATCTGCGC	GCTTCGAAGG	GAAAGGCGGG	CCCCAATCCC	CAGTCTATGT	300
	TCAAGAGGGC	GAACAGCAGG	CCGTCAATGGC	ATTCAATAAG	CGAATGGGCA	CTCGAGCGTT	360
	GGCACATCAT	GTGCTGGATA	GCATCATATA	CTACACAGAC	AAGGTGGTGG	TGAAGGGGCT	420
	TGGAAATTTG	TCCGCGAGCT	TACCTTCCAA	GACCTCCTCG	GCGACAAGCG	TCAGGGGTCTG	480
10	TGTAAGGAAA	CGCATTTGGTC	TCGAAGGCGC	AAATGATGTC	TTTGTATACC	GCACAAAAGA	540
	CCTGGTATTC	GATAGTGATG	AAGATATACC	CAGAACCTAA	CTACTTGTGT	CGATATTTCT	600
	CACACCGCCT	GGTGCGGAAC	CGGGGGCATA	CATTCGTTTT	ACACAAGAGG	GGTTGATGCA	660
	TAAACGCGC	TT					

1596UP

	GATCTTCGTA	TCCATGTCCG	AAAGCTCCTC	CAAAATCTTT	TCGTCTCCAT	CATGAGAGGC	60
	TGCTACAGCT	TTTGAGCCGA	TAGAATTGGA	AATACCATTG	GAGATTGCTA	TTAGTAGGAA	120
	GACAATATAA	GTACCATCTG	TCGATGGGGC	AGAGGCTTTA	TCAAGAAGGT	CCATCAGCTT	180
20	GTTCTTGGAT	ACAGCAGTCT	CATTTAATAA	TAATGCCCTG	TCACCACTGG	GCAAAAATTC	240
	AGAAACATTG	AGCAGTTTCT	AGAGTGAGTT	CGACTCAAAG	TTTTCGGTCA	TTGTCTCTAA	300
	CAAGACAAAA	ACAACGTCTC	TCCTGTCTCT	ATGAACATCA	TAAGCCTTGA	AAACCTCGAG	360
	CAAAATAGTA	TTGTCTCTGA	TCACGTTCAA	AAATACCTCT	AGAATTAATG	CCTTCTCTCA	420
	CAATAAAGTG	TCAGATTTAG	GAGACAGAGT	GTGGATTAAAT	AATGATAAAA	TAACCTTCAA	480
	TTCCAATTCC	AGCAATGTCA	AATACTGAAC	CTTTATGAGA	ATGTAATACA	TCTGGCGCTA	540
25	CGAACCACAA	TTGCAAAATT	TTTGGATGAG	GAAATGTACC	TCAATAGCAG	CGGCACCGCC	600
	TTTGTTCGCA	ACAGAAATAA	CAGATCTCGG	TGTGTCAAAA	ATAATAATTC	ATAGTTCAAT	660
	AAAACCAAGT	CTAGGAGCTC	TAATCCATAC	TCCTCATTTA	TGCAATTGCT	ATCCAGCAAT	720
	GT						

1597RP

	GATCCATCAG	CGCGGCTACG	GAAATCCTGC	CCATAGAATG	ACTCTCCAAA	CCCCCTTGAA	60
	CTATCAGCAA	AAGCTCAACA	GCATRCACGG	GTCGCATGCC	CAGCAAAAAC	AGATCCAGCG	120
	TCAGATAAGC	GCTGCCARCG	CACCTCGATGA	CGGGAATACC	ATCACCGCAA	TGGTCCAGCA	180
	TTTGATGCCC	AAGAAGAAAG	ACCAGCCACC	GCAGCAACAG	GGACCCTATG	GCTCTCCGCC	240
35	AAACTCTGGC	AACAGCTCCA	CGTACGGCGG	CAGCCCTGCT	GCCACCGCGC	CGTCTGCATC	300
	CGTAAATGCT	CCC GCCCGG	ATGACGCGCA	AAACGCTGTG	CCACAGCCGC	ACAGCGCCCC	360
	TGCGCTATCC	GCTAACGGTA	ACACAGCCCC	TATGTGCGGA	AACTCGGTTA	GCCTTAGTAA	420
	TGGCTCATCA	GCAGGGCCCC	GTTTGTCAACA	ACAGTCAAAC	TCTCTGGACT	GGAAGCAGAC	480
	ACCGCCAAGC	AGTGCGCGAA	GCGTAACCGA	AAGAAAGCCA	AAGCTCGCTC	TATTCTGCTAA	540
	GAAAAAATAA	TATCATGCGA	CCTATCATTT	ACACATATTC	TAACGTTCCA	CCTGTGTTAG	600
40	TGTACTCATT	TAATTAATTC	ATTAGTGCTG	CCACTGCTGC	AGACATGTGG	CAAGAGGCAA	660
	AAATGGTTCC	TAGCGGGATC	GAACCGCT				

1597UP

	GATCGAGGCA	GCCGTACCGT	CTTTTGGTAC	GCATGCGCAG	AGTACTGCCG	GATACAGCGC	60
	AACATCTTAC	GCTGACTACA	GTTTCTGGAC	ACACCACCTT	ACAGCTTTGG	GCCTGCGTTA	120
	TTGGTGCTCG	AAGATATGAT	GTTTGGAAAT	TTTCACTCGC	CGTCCGGCCT	GATGAAACTG	180
	GAAGACAAGA	CCTACAGTCA	TCTAGCCAAC	ATAACGCCCT	GTAGTCGGGC	TCTCGAACC	240
	AGCGTAGAGC	GTAGGAGATG	CTCCACGCGC	CCCGGTGCGT	ACAGAGAAGA	ACAAGACCGC	300
	CGGCATTCTT	TTTATTTACT	TGATTAAACT	CTTGCCAGT	CTGGTTTCCA	CTGACAAAGT	360
50	GCCCCACCAGA	TGGATCGCGG	GCGCGGTGAT	CCTGCCCCGG	CGATAGCGGG	CGACCGGAGC	420
	TTGCGTGGGT	TTACCTTGCA	TCTGCACAAG	ATGTTGCTAC	GGCGTAGAAG	CAGCGGTGG	480
	GAGGCGCAGC	GCGCGCAAAC	AGGACGTCAG	TCTGACGCGC	TACTTCGCCC	GCGCTGCTGC	540
	ACCGGCTGAA	TTGGGCTCCC	GGCAAGTCCT	GATTGCTACG	TTGAGTCATA	GTCTCAGTAA	600
	TTATCGCATG	GTGTTACTGG	CGTTGCACGT	GACCACACTG	TGGCGTCCCT	TTGGCCCCACA	660
55	GATGAACCTG	CCATCAGCTC	TCCGCCAGGA	CGGTCACAAC	AGGCAGCAGT	AC	

1598RP

	GATCCTCATA	ATCATAGTAC	AATATCATTT	CCAATAAATG	GAATAGCACT	AAATAAATTA	60
	GTAATAACAG	TAGCACCTCA	ATGTGACATT	TGTCCATATA	CTAAACAATA	ACCTAAGAAA	120
5	GCTGCTGCTA	TAGTTAAAAT	AAAGATAATA	ACACCAACTG	TTCATACAAT	AACTCTAGGT	180
	GATTTATAAG	AACCATAATA	TAAACCTTTA	CCAATATGAA	TATACATACA	AATAAAGAAG	240
	AATGAAGCAC	CATTAAGATG	CATATATCTA	ATTAATCAAC	CTAGTTGTAC	ATCTCTCATA	300
	ATATGTTCTA	CTGATGAGAA	AGCTAATTCA	ATATTAGATG	AATAATGCAT	AGCTAAAAAA	360
	ATACCAGTAA	GAATTTGAAT	AACTAAACAT	AAACCTAATA	AAGAACCTAA	ATTTTCATCAA	420
	TAATTAATTG	ATGATGGTTG	AGGTGAATCA	ATAACATAAC	TATTAACTAA	ATTTAAATAT	480
10	AAATTTGATT	TTCTATATGC	CATATATTTT	ATTATTAAAA	TATTATTAAA	TTATTATTTA	540
	ATAAATATTA	GATTATAATA	TAATTCITTA	TAATAAATTA	TATTATTTAA	TTAATATATT	600
	AATTTATTAT	TTATTATTTA	TTAATATTTA	TATAATCTTT	ATAGGGAATT	GAACCTAATA	660
	AACCATTAA	ATTAAATTAT	TTAATTATTT	AATTTATTTA	ATTATTTAAT	TTATAAATTA	720
	TTAATTAGAG	AGATAAGGGT					

15

1598UP

	GATCTTATCG	TCTAATGGTT	ACGACATCAT	CTCTTCATGT	TGAAAAATATC	GGTTCAATTC	60
	CGATTAAGAT	TATTAATATA	TTTTAATAAT	TATTATAATT	AACAATATTA	ATTAGAGGGG	120
20	TACCAACATA	TTGCTAACTA	GCAATAGGGG	TGTGTACCTT	ATCTCTCTAA	TTAATAATTT	180
	ATAAATTAAA	TAATTAAATA	AATTAAATAA	TTAAATAATT	AAATCTTAAT	GGTTTATTAG	240
	GTTCAATTC	TATAAAGATT	ATATAAATAT	TAATAAATAA	TAAATAATAA	ATTAATATAT	300
	TAATTAATA	ATATAATTTA	TTATAAAGAA	TTATATTATA	ATCTAATATT	TATTAAATAA	360
	TAATTTAATA	ATATTTTAAT	AATAAAATAT	ATGGCATATA	GAAAAATCAA	TTTATATTTA	420
	AATTTAGTTA	ATAGTTATGT	TATTGATTCA	CCTCAACCAT	CATCAATTAA	TTATTGATGA	480
25	AATTTAGGTT	CTTTATTAGG	TTTATGTTTA	GTTATTCAAA	TTCTTACTGG	TATTTTTTTA	540
	GCTATGCATT	ATTCATCTAA	TATTGAATTA	GCTTTCTCAT	CAGTAGAACA	TATTATGAGA	600
	GATGTTCAAC	TAGGTTGATT	AATTAGATAT	ATGCATCTTA	ATGGTGCTTC	ATTCTTCTTT	660
	ATTTGTATGT	ATATTTCATAT	TGGGTAAA				

1600RP

	GATCTAAAAG	AATCCATGTA	TGTACACATA	TTACGGAGGG	TTAAGGTGAC	GAACGGTAGC	60
	TACAGGCCTA	TAAATCTGGG	TTCTTTTGCA	AAAGTTCATG	CAACTCATCT	GGGACGTTGC	120
	GCCAGTCTTC	GGCAATCCAT	TTCTTTATCC	TATCCTCATC	GGCCTGTGCT	AGTATATCTA	180
35	CTTCAAGAGA	GCTCCTGGCA	CATGTAAAT	TGCCAGCGGG	AGAGAGGAGA	GGCGAAGATT	240
	CTTGAGTGGG	GTAAGAAACT	TGTTTTGATG	GTATGCTGCT	AGCCATCTTC	TTCCGTCTGT	300
	GTTCTTACC	GTTGTTTAAT	GATACTCCGA	TATAATGTTT	TATTAACCTC	TCTGCGTATG	360
	GGGGCAAGTT	TTTGGGCCTG	TAGTCGCCCA	CATATTTGCA	CCTCCAGTAT	ACAGACCAAT	420
	GTAGTTCACC	ATATGCCGGG	ATGTTCTTAT	GTCTACCAAG	GTTAGGCACA	TAAACGTTTT	480
	TCCATTGGCA	ATTTTTATCT	TCAATCCTTA	TGCCGATGAA	CATCATTTCC	ACTATCCACC	540
40	AGGCAATGAA	CTGAAATATA	CTCTTTGTTC	CATGTCCATC	GTTCTTTGCT	GGCCGGATTA	600
	TACATCTCCG	GAAGGAAGGC	CTGGG				

1600UP

45	GATCAAGCAG	CTACTGCTCA	CCTGGAAGAA	GCAGGGCCAC	AAGGCCCTGC	TCTTCACCCA	60
	GTCCAGGCAG	ATGCTCGACA	TCCTGGAGGC	CTACATCTCG	CACAAAGATC	CCGAGCTGGC	120
	AGGCCTACAG	TACCTCCGGA	TGGACGGAAC	CACAAACATC	GCACACCGGC	AGGCCCTCGT	180
	GGACCGTTTC	AACAACGGCC	CGTACCACCT	CTTTCTTCTG	ACCACCCGCG	TGGGGGGCCT	240
	CGGCGTCAAC	CTCACGGGCG	CGAACAGAA	CATCATCTTC	GACCCCGACT	GGAAACCCCTC	300
	CACGGACCTG	CAGGCCCCGCG	AGCGCGCCTG	CGGCATAGGC	CAGAAGCGCG	ACGTGACTAT	360
50	CTACTGCTC	ATGGTTCGCG	GCTCCATCGA	GGAGAAGATA	TACCACCGCC	AGATCTTCAA	420
	GCAGTTTCTC	ACCAACAAGG	TCCTCAGCGA	CCCCAAGCAG	AAGCGCTTCT	TCAAGATGAA	480
	CGAGCTGCAC	GACCTCTTCT	CCTTCGGCCC	GGGCGCCGCG	AGCGACTCCT	TTGCCTCTGA	540
	GATCGAGCAG	CAGACCGCCT	CCCTCCGCGC	CCAGCCGGCC	GCCCACGGCA	CCGACGACTA	600
	CGACTCCGTC	CAGCGTTTTCG	AGGGCGTCTC	CAAGCTGGAG	GGCTTCTTCA	ACGCCA	

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1601RP

	GATCTTTTTTC	CCCCGCAAAC	CGCACACCTC	GTTCCAGGGG	TACTTGGGCA	ACAAAAAGGC	60
	GACGGAGAGC	AAGGTTCTAC	GCGATGTTTT	CAGGAAGGGA	GATGCATGGT	ACCGGTCAGG	120
5	CGATCTCTTG	AAATCCGACA	AGTACGGGCA	ATGGTACTTC	GTGGACCGGA	TGGGTGATAC	180
	GTACCGGTGG	AAATCCGAAA	ATGTCGCGAC	TACCGAGGTG	GAGAATCAGT	TGCTCTCGTT	240
	CAACAAGGAC	CTCTTTGACT	GTTTGGTTGT	AGTGGGCTTG	AAGATTCCAA	GCTACGAGGG	300
	TAGAGCCGGG	TTTGCTGTTA	TCCAACTGAA	TCCAGCGCGC	CGCGGACTGG	ACCATGCCAG	360
	TTTGTTAGAC	GACCTTGTGCG	AGTATTTGAA	ACATGCTCTT	CCTCGGTACG	CCTTGCCGCT	420
	GTTTCATCAAG	TTCACAAACC	AGCTGGAAAC	AACCGATAAC	TATAAGTTTC	CCAAGAAACA	480
10	GTACAAAAAC	CAGCAGTTGC	CTCATGGTGC	GGATGGGGAC	GAGACAATTT	ACTGGTTAAA	540
	AGACTACTCC	CAGTACAAAG	TCTTGACCGA	CGAGGACTGG	GAGCAGATAT	CAACCGGAAA	600
	GGCAAAGCTT	TAGACCAGAC	AATGCCGGGA	TTGACACCGG	TAGGGAGTTC	AAAAATAAAA	660
	AAATACCTGG	GAAGCCATCC	ATAAAAGCCA	TTATCAACTA	TAGAAATAGA	AAAGT	

1601UP

	GATCGCCCTG	TCCCGGGACG	GAGAGCGGGC	GCTGCGCTAG	CATAAAAGCA	CGCAGGTCAC	60
	TGTGCATGAA	ACTCGAATCG	AACGCCGTAC	TCGATGGTAG	AACTAAACGG	GCTCCGCTTC	120
	GAAGTACGCA	CAGTTGAGTG	AAATGTCACT	GTCCGGCGCA	CGCGCCCAAG	AGCAGAATAG	180
20	CATGGACATC	GAACAGAGGT	CATCGCAGCC	GAGTCGAAGC	AACAGCCATG	CAGGATCGCC	240
	GGGGTACGAA	AAAGTGCAGC	CGCTGTATGC	CGCAGAGAAC	GGTTCACCGG	AGACTGCCCC	300
	GACAGCCACC	GGGCTGTTTG	ATAGCTCGCA	CGTTGTACCG	GTGTCGCAAC	GGCGCGGACT	360
	GCTGAGTAGG	CTGGCGCTTG	TGCCCGAATT	CCGGGACGCA	CGTCTCTATC	CCCCGCGGGT	420
	CAAAAAGCTG	ATCCTGGTCA	TCGTGCGCTT	TGCATGTATT	CTGGGTCCCA	TGGGGACCAA	480
	CATCATCTAT	CCTGCGATCG	GGACTATCAT	GCAGGATTTT	GGCACTTCGC	GGTTTCTGGT	540
	CAGTGTGTCT	GTAGGCACCT	ACCTCGCTGC	GCTGGGCATC	TTCCCCATCT	GGTGGTCGTC	600
25	GCTGGCGGAC	AAAAACGGCC	GCCGAACAGT	GTACGTGCTG	TCGTTTCGCG	TGCTGGTGGT	660
	GTTTCAGCGT	GGGCACGGCT	TCTCGCGCAA	CATCGAGAC			

1602RP

	GATCCAAGCG	CCCGCACAAAC	CAGCGATGTT	TGCAACATAT	TCGGCTAGTA	TTCTCCGTTC	60
	GACTTTACCC	CTGCGTAGCG	TTGGCGTCAG	ACTGCTGAGC	CAGGAAACTC	GGCGGGCCAT	120
	TGAGGGCGCC	ATTTCTCTCT	CCCCAGTGGT	TCTGTTTATG	AAGGGCACCC	CAGAGTTCCC	180
	TCAATGTGGC	TTTTTCGAAGG	CCGCCATTGA	GATCCTGGGC	AGACAGGGCG	TGGATCCTGC	240
	GAAGTTTGCG	GCGTTCAACG	TGCTGGAGGA	TTCTGAGCTG	CGGAGCGGGA	TAAAGGAATA	300
35	TTCCGAGTGG	CCTACAATTC	CACAGCTCTA	CGTCAACAAG	GAATTTGTTG	GGGGGTGCGA	360
	CATCCTCACC	AACATGGCGC	AATCCGGCGA	GCTAACTACT	ATGCTCGAGG	AGGCATCCGT	420
	TCTTGTGCCG	GATACTGAGT	GATGCCGCGT	ACGGCTCCCG	ACTATATTTA	TAGGAATACA	480
	GCTTGTAATT	TACGACTTGT	ATTCTCATGC	CTTTAGACTT	GTAAATCATG	GTTGTTTAAAT	540
	TCACAAACTC	CGTTCTTTCA	GTTGAAAGAA	GTGAGAACAG	CTTGCTTTCC	GTCATGTGTG	600
	AAAGAGGCTT	CTGATGGAGG	AGGCGTGCAC	ACGCCAGCAG	AGAAAGTCTC	TCAAAAAATG	660
40	ACGTTCTAGT	GGAAGGGCGG	ACGCAATCAC	CCTTGAATGC	GCGA		

1602UP

	GATCGTGCCC	GGGCTTGTCG	TTGTGCCAG	AGTTGTGCTT	GTGCCCAGGC	TTTTGCTCGC	60
45	TGCTTCCGTC	GCTGCCCCG	GGGTAGTACA	CGCCGAACG	CTTCAGCCGC	AGCGGGCCGC	120
	GGAAGTGCAC	CGTCAGCTCC	TGGTCCAGCG	GAGAGAGACT	GCCCGAGAAC	TCCAATTTTC	180
	TCTGCTTACA	CTTGCACTC	TTCTCGTCCA	TGCTGGTGAC	GTCCAGGTAC	GTGCCGCTGT	240
	AGCCACATT	GGCATAACCG	ATATTTTCTG	CCTTCGAGCA	GTAGTAATTC	CCTCCGATGA	300
	AATCACAATC	GCCCAGCACC	TGCTGCGCAG	CGAGCAGGCC	ACCTGCAACG	ACTGTGACGA	360
	GCTTCATAAT	TTGTAAACGC	TTGTAAAAGA	ATGACTAGTA	GTTAGAACAG	ATAAAAGAGT	420
50	GCTTTGCTGT	GTGCGCTGTC	GCCCGTCCAC	GCCTTCCGAG	CTCACCCGCC	TTCTTA	

1603RP

	GATCCGGCAA	GATCGTCGTT	CAGTTGACCG	GCAGATTGAA	CAAGTGCGGT	GTCATCTCTC	60
	CAAGATTCAA	CGTCAAGATC	AACGACGTCG	AGAAGTGGAC	TGCCAACCTA	TTGCCAGCCA	120
5	GACAGTTCGG	CTACGTCATC	TTGACCACCT	CCGCCGGCAT	TATGGACCAC	GAGGAGGCC	180
	ACAGAAAGCA	CGTTGCTGGT	AAGATTTTGG	GTTTTGTCTA	CTAAGCGGCT	GCTATATAGC	240
	GTATCTAGCT	CTAATGTACG	ATACTCAGTG	TCTATTACGA	CGGCCGCGAG	CTCCACGCGC	300
	CACATACGAG	GCCAGCCGGC	GACGGCAAGC	GGGAATTGAG	ATGCGTTAAT	TAGCAGTAGA	360
	TTAGTAGTAT	ATATGTACAA	ACAGCATACA	CATGAACGGC	GTCGCCGATC	ATAATCTTCT	420
	ACCTCTTCTA	CCACCCCTTCT	TTCTGGTAGA	GTCGGATGGG	ATAGGAGTGA	CGTCCTCGAT	480
10	ACGGCCGATT	CTCAAGCCGG	ATCTGGCCAA	AGCTCTCAAA	GCAGCCTGAC	CACCTGGACC	540
	TGGGGTCTTG	GTCTTGGTAC	CACCGGTAGC	TCTGATCTTG	ACGTGCACAG	CAGTGATGCC	600
	GACCTCCTTA	CACTTGGCAG	CGACGTCCTG	AGCAGCCAAC	ATGGCAGCGT	ATGGAGAGGA	660
	CTCGTCTCTG	TCGGCCTTGA	ACTTCATACC	ACCGGTAAC	CTGGCAATAG	TTCTCTGCCA	720
	GACA						

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1603UP

	GATCTATTTG	TGCCGTCCGC	CATTAAGCAA	GCGGCAAGCA	TCGATCCAAA	TCATGAGAGT	60
	ACCCTCGGGC	TTTCACTTTC	CAAGCCTTTA	TCAACAAATC	TGGTACACGA	TACATCCATC	120
20	GCGACAGCAC	ATATAACCAGA	ACGGGAAAGC	CGACAAGATG	GCACTAGACT	CTGGTAGGTA	180
	ATCTGAGTTC	GACCATATCC	ACTTCGTAA	TGGTGATAGT	GGATAAAAAG	AAACGATACT	240
	GAAAATTTTA	ATGGTTACCA	ATCTCATCTC	ATCGCCATAC	TGAAAGAATA	TTGTAGGTCT	300
	CGCAGTGGA	CAAGGATCAA	GCCCAGGCTA	AGACAATAAT	GGTTGCAGCG	GAGGCAGTAC	360
	AGGAACTACC	CCCAGATGAA	GAAGAACTGG	CCTTGGCTAA	GCTAGTGTTC	GGCGACACAG	420
	CAGACTTCCA	TGAAGCGCTG	CGAAATGCAG	ACCTTAATTA	TGTTTCTTCA	GATGAAGACG	480
25	TATATGGCCA	GGAGTCGTCC	AGTGATGACG	AAGAGGGGAC	TGAAATTGGT	CACCTGAATG	540
	ATGACCAATT	GTTTTTTTGTG	GACGAGGGTG	CAGATACCGA	GGGAGGAGCA	GATGGAGAAC	600
	GGAGGCCATG	GAGGTGGACC	AGGTTAGCGA	GGAAAGCGAC	TCCGGAGAGG	AAAGCGGTAG	660
	CAGCGCTGCA	TGGTCAGATT	CGGATGACGA	ACACTTAAAC	GTTACAATAG	GGCAAACCAA	720
	T						

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1604RP

	GATCCCTATT	AGAAGAGGTT	ACTGGGGCTC	CAACCTTGGT	CAGCCACACT	CTCTAGCCAC	60
	GAAGACCTCT	GGTAAGTCTG	GTTCCGTCAC	TGTGCGTTTG	ATCCCTGCCC	CACGTGGTTC	120
	CGGTATCGTC	GCCTCTCCAG	CTGTCAAGAA	GCTTCTACAG	CCTGCTGGTG	TCGAGGATGT	180
35	GTACACTTCC	TCCACCGGTT	CTACCCGTAC	CCTAGAGAAG	ACCTTGAAGG	CTGCCCTCGT	240
	TGCCATTGGT	AACACCTACG	GTTTCTTGAC	CCCAGACTTG	TGGCCAGAGA	ACCAGTTGCC	300
	AGCTTCTCCT	CTAGACGTCT	ACGCCGACGA	GGCCGTTGCC	CAGAAGAAGA	GATTCTAAGT	360
	AGTGTGTGTA	CATACCAACA	GTTTGTCTCT	TTGCACGTGA	ACCGCCCGCC	TAAGCCTTTA	420
	GGCGCATGGC	ACACAGACTG	CCGTTGGGCA	GGAGATCGGT	TGCTTCCGA	CGCTGGTACA	480
	GGGCTGCGAT	GCGCGTCTGC	GGCTGGCGGT	GCATATCGGA	GATATGGCGC	CGTGCCCGTA	540
40	CGGCAAAGAA	TCAGCAAGAC	ACTAGCGTCT	GGCATTCTTT	TTCAATGCAT	TATTTAGCTT	600
	TTTTTTTTTTT	TTTTTTTTTTA	GTATAGACAC	ATATAAGT			

1604UP

45	GATCAGAGCA	TCCGATGAGG	TGGCACCGGC	CGCGTCCGCT	GTGTCTTTCT	TCGCGGTATC	60
	GGCTTCCGAA	ATACTTAGCT	TCTCAATACT	TGGGACTGCC	TTATCTTCAG	AGGAAGCGGT	120
	AGCATCTTCA	CTCTTAGGAG	CGCCCTCTGC	GCTGCTCTTA	GGCTCCTCCT	TTGTTGGCTC	180
	CTCCGCCCTTA	GCCTCTTCTT	TCTTCGCGAC	AGGTTTCTTA	GCACCAACTA	GCTTGATACC	240
	GGAGCTGGAA	GCCAACTTGA	GGGTCTTCTT	TGGTTTTGGA	GCAGTCGCAT	TCGGCACAGT	300
	TCCCTTCTCA	AAGTGTGTTA	GCGTCACCGG	AGCGGTGGCT	GACTGGCCCT	GTCCGTAACC	360
50	ATAGCTCTGG	TTCCCTTAC	GGTCCCCTG	TGGCTGTGAG	TTGTACTGCT	TGTAGCTCTG	420
	ATACCCACCT	TGCGCATGTG	ATTGCTGGTA	ACCTTGGTAG	CCAGCTTGTG	CTGGGTTGTA	480
	CTGCTGGTAT	CCCTGATAAC	CCTGGTACCC	GCCGGCTTGC	TGGTTGTATT	GCGCATAGCC	540
	TTGGTACCCA	CCTGCTGTG	GGCCATACGC	CTGGTAACCT	CCCTGAGGCA	CATACCCCTG	600
	GTAATCTTGG	AAGTTACTTG	GGTTGTAGTA	TTGGCCGAAA	TTTGCTGCC	CTGACCTTGA	660
	TTTTGACCTT	GATCCTTGGC	TGCGACTGG	CCTTGGTCTG	TGCCTTGCGA		

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1605RP

	GATCTTCTCA	AAAGTAGCAT	TTACAATCTG	CGTTAGCGTT	GCTTGTGCAA	TTCCCTGGTT	60
	GGACGAGCTT	AGTGACAGGA	TGAAAAATAT	ATAGATTTGT	CTGACGGCCT	TTAATAGTGA	120
5	TGCACCGTGA	CAATTGCAAT	AAGGCTCATC	TGTCAATATA	CAGCTTGCGA	GGGCGCGGAC	180
	TACCTGCAAC	TCGACCTTCC	CATCAGTCGC	TTCTCCATCA	AAACAGTCGG	TTATGGTATC	240
	AACGGCAGCA	TCTATCAGCC	GCATTCTTGG	AGGTGGTGTA	ACACCAGAGT	CTGGCAACGT	300
	CGTGCCCTGG	TCGTTTGATG	CTGCGGAATT	TGGAGGGTTG	ACTAAAACAT	TCTCGTCTAA	360
	CGCCTTAAAG	GCAAACAAC	TTGATAGACA	ATCAAGAGCG	CTAACCTGTA	TTTCTGGAAC	420
	ATTAGTTCTA	CAGCAAGCAC	GTAGTGCCCTC	AAAGACCAAC	AGAGAATCCA	AAAACCTTGG	480
10	ATCGTTTTC	GATTGCAGGA	GTTGCTCGGT	CAAGTTTTC	ACAGTTTTCT	CAACCAGTTT	540
	TTCAATTATTA	GGATGTTTGT	GCATGGATTT	TGCTGTAGT	ATACCCTCTA	ACCTTAGTTT	600
	CACAAGATGC	ACTGCGGATT	TCATCGTCCA	TGGACTACCA	GAGACATTGG	AATATGCCCT	660
	TGTGTGACGC	TTGAGATTAT	CCTGCGAC				

1605UP

	GATCAGAGCA	TCCGATGAGG	TGGCACC	CGCGTCCGCT	GTGTCCTTCT	TCGCGGTATC	60
	GGCTTCCGAA	ATACTTAGCT	TCTCAATACT	TGGGACTGCC	TTATCTTCAG	AGGAAGCGGT	120
	AGCATCCTCA	CTCTTAGGAG	CGCCCTCTGC	GCTGCTCTTA	GGCTCCTCCT	TTGTTGGCTC	180
20	CTCCGCCCTTA	GCCCTCTCTT	TCTTCGCGAC	AGGTTTCTTA	GCACCAACTA	GCTTGATACC	240
	GGAGCTGGAA	GCCAACTTGA	GGGTCTTCTT	TGGTTTGGGA	GCAGTCGCAT	TCGGCACAGT	300
	TCCCTTCTCA	AAGTTGTTCA	GCGTCAACCG	AGCGGTGGCT	GACTGGCCCT	GTCCGTAACC	360
	ATAGCTCTGG	TTCCCTTAC	GGTCCCCCTG	TGGCTGTGAG	TTGTAAGTCT	TGTAGCTCTG	420
	ATACCCACCT	TGCGCATTTG	ATTGCTGGTA	ACCTTGGTAG	CCAGCTTGTG	CTGGGTTGTA	480
	CTGCTGGTAT	CCTGTATAAC	CCTGGTACCC	GCCGGCTTGC	TGGTTGTATT	GCGCATAGCC	540
25	TTGGTACCCA	CCTGCCTGTT	GGCCATACGC	CTGGTAACCT	CCCTGAGGCA	CATACCCCTG	600
	GTAATTCTGG	AAGTTACTTG	GGTTGTAGTA	TTGGCCGAAA	TTTTGCTGCC	CCTGACCTTG	660
	ATTTTGACCT	TGATCCTTGG	CTTGCAGACTG	GCCTTGGTCG	TTGCCCTGCG	ATTGAATTTG	720
	ATCTT						

1606RP

	GATCAAGCAT	ATCAAATTTT	CGGCAATCTG	CGGCGTCATT	TTTTTGGACA	ACAGGCGTCT	60
	CCACAGGGTC	CATCTCCATC	AGCGGAGCTA	TACGTTGCGA	CAGTGGCCTC	AGCTTGGTAC	120
	TCTGCGAGAG	AATTGAGACG	CCCTTGGAGC	TGGCTGTATG	GTAAGTGTG	TCCGTGCGGT	180
	AGGTGGTCAA	AGACAGCGAC	TCTGAATACT	CGCATTTTCG	ATCCCGGTTG	CGCCGTACGT	240
35	ATCCGTCGCC	CGTGGAGTTG	ATGGCAGTGG	TGTCCGAGCA	CGAAGACAGC	GAAGGTAGTC	300
	TCAGTGGCCG	CGTCGGCGAT	ACGTCGTACT	CGAGCACAGA	CTCGTTGTGT	CCCCCTCCCG	360
	TCATGTTCTT	CGGCTCAGTT	CGCGACAACG	CTCCCGACCA	TGCCTGCCCC	CTCCCTTCTT	420
	TTCTGTGGAA	GCGCCCAAC	ATTAAATCTA	GCTGCTTCTT	CCTGGTACTC	TGTTGCTCTT	480
	GTTTCTGCCC	GGCGAGCCCC	TCGGATTCAA	TCTCTGTATA	GCGTTTATGC	CGCACTTGCT	540
	CGTCTTAATT	GGCTGCCACA	CTCCTGCTGC	TCGAACCTAA	GGCGTCTGTA	CCGAACGCTT	600
40	TCGTTGACTT	GACCGTTGGG	GCGTAATCTA	TTATTGGAAC	CTTGTAAGG	CGGGCTTCTG	660
	TACGCTATTA	GTTAGCCC					

1606UP

	GATCCGCTTG	AGTACTGAGA	TATTAAGTCA	ATACCAGGAT	AAGCTTTCAA	AGCACCGTAA	60
45	TCCTACTGTG	CAATGGTGGG	GACCTACTGA	TTTCTCGCAC	TACGTCTTAG	CGCCTGAAAT	120
	TTTATCATAC	GTGTGCCGAG	ACGAACCTGG	CCCTGCGAGT	ATCGATGAGG	CTTGGACTTA	180
	CATGGAAAGT	ACCACGGAAT	ACGGGTAAAT	TGTGGCGGAC	GAAGAGCCTC	TAGATATTTG	240
	GGAATTAGAA	TACGAAGAGA	AAAAGCTGCA	ACGGTTAGGA	TTAGGACCCA	AGTACAGCAG	300
	CATGACTTAC	AGAAAGCATC	CTGCCAGGGC	GTCGGCTGTA	TTAGATACAT	CCAAAAATGG	360
50	TTCTAAAGAG	CATAAGCGTA	AAGGAAAGCA	ACACAAATTA	AAAAAAGGAC	AGCAGTCTAC	420
	AAAGATAAGG	GTATCAAAAA	AAAGGCGACG	CGTACAACCA	CACAGCATAT	GCGATTAAATA	480
	ATCTTACAAT	CGTACTAAGT	AATACATACC	GCGCTTATAG	AATCTGCTGC	TGCACGGAAA	540
	GTTGTCATATG	CGAAAACATG	CTATGCAGTG	GATGATCGCG	TACCACTTTT	TAATCCGATA	600
	AAAGTGGACT	AGCGATAAAT	AGTAATTTCA	ATAGGGAATG	TGAATTTGAA	TTGAGAATTG	660
	GGATAATGCT	GTGGATTTCT	GTGATTATAA	TACCATAAAT	ATA		

1607RP

	GATCACACGA	CAGTGCCAGT	CGGGGCAGCC	GGTACCCGTT	GGCCGCATCG	TGAAGCTGAC	60
	TCCGAAGAAC	CCCTTCTACA	AAGTCCCCGA	GACGGAAGAC	CTGTGACGG	TCATGGGCAT	120
5	CCTTGGCTCC	GGCGTGACCC	GTGTGCGCAT	TGTGGACTCC	ACCTCTTCAT	CTATCCGTGG	180
	CATTCTGTCTG	CAGCGACGTC	TGATGAAGTA	CCTGTGGGAC	AACGCCCCGCC	AGTTTCAGCAA	240
	CCTGGAGGTG	CTGCTCAACT	CGTCGCTGCA	AAAGTTGGGC	ATCGGTGTGC	TGGATCCACA	300
	TACCCCTCCT	ACTTCGCGGC	AGTCGCGTGT	TATTTCCATT	CTCGACACAG	AGCCGCTGCT	360
	CGTTGCCCTG	CACAAGATGC	ATACAGAACG	GATATCCTCC	ATCGCAGTGA	TCGACCACCA	420
	GGGCATGCTG	CTCGGGAACA	TCTCTGTGAC	AGACGTCAAG	CAGGTTACGC	GCACCTCGCA	480
10	GTATCCGTTG	CTGCACAACA	CCTGCCGCCA	TTTCATCAGC	GTGATCCTCA	ACAACCGCGG	540
	CCTGGAGATG	GGCAAGGACT	CCTTCCCCAT	CTTCCACGTT	TACCCACCT	CGTCCCTGGC	600
	CCGCACGGTC	GCGAAGCTGG	TC				

1607UP

	GATCGGTGCC	CGCACCTCCG	CCCGATTCCT	CGCCAGCTCG	TTCCGAATGT	TCGGTATCGA	60
	CTTCTGCTTC	TTCATCCCAT	CCACCTCCGT	CCC GCCGCTG	TCCAAAGCTC	GCTTGGCTGC	120
	GCCGCCACTC	GTACCTGCCT	GCCGTCTCTC	ATCTTCAATA	ACTATCACTT	GCATCCCGTT	180
	AGTAGCTGCA	CGGTGCAGAG	GGCTGTAAAC	CTCCCCCTCAG	CCCTTCAAAA	CGCCCCACCA	240
20	CATACCTTCT	CGTCCCTGGA	TCATGATTGC	CCCTGGTAAT	CTTCACGCTA	GCACTAATTT	300
	GGTCACTAAC	TGCGCTCTTG	CGGACTGGAA	TTGGTGGTGC	AGATGGTGAA	GTCTCATGTC	360
	GTCCATTCTC	GCCGATGTTA	AAATATGGGT	TTCCGAAAAA	GCCCTGCTTG	CCCTTGACTG	420
	ATGCTCGACT	CACAGAGGAC	TCACCAGAGC	TTGAACCGCA	GCCAGGAAGC	ATTCTGTGTC	480
	TACCAGAAAG	GGCCACGGC	GAGAATCAGA	ATCGATGTTG	CATAGTCGGG	CAGCAAGAGT	540
	GCTCCAGCGC	TCGGGGTCCG	CAAGCGCAGA	TGCAACAAC	CCGTGCACAG	CATCACAAGC	600
25	GGTATAGCAT	GGCTTCCCCA	ACGATTTCCG	AGGTGCCGGA	CTTCAGCAAG	TATTCCCGAC	660
	CTGGCCGGTT	ACAG					

1608RP

	GATCAAAACC	ATCACCAAGT	TTATTCATGA	AGTGTCCGAC	GATTTCAAGG	TCATCATAAT	60
30	CGACGCAATT	CGTACTTTGT	CGCTAAAGTT	CCCAGATGAG	TGGAAGAATA	TTCTATCCTT	120
	TTTAATTGAC	ACTTTGAAAA	GTGCAGAGGG	TGGGTATACA	TTCAAAAATA	ATATCGTAGA	180
	TGCGCTGTTT	GACCTGATCC	AACATGTACC	TCAGTCAAGG	GAACAGGCTC	TGGAACACTT	240
	GTGTGACTTT	ATTGAGGACT	GCGAGTTCAA	TGAAATCTCA	GTCAGGATCA	TTTACTTATT	300
	GGGTAAGGAG	GGCCCTCGA	CAGAAAAGCC	TTGCTTTTAC	GTTAGACACC	ATTACAACAG	360
35	AGTTGTCTTG	GAAAATTCAA	TCATCAGATC	TGCTGCTGTT	AGCGCATTGT	CCAAGTTTTC	420
	CTCTCCGAAG	AAAGATCCGT	CGTTAGCTTA	TTCCATCGAA	AAATTGCTAA	AGGGTATCCA	480
	AACCGATGAG	GATGACGAAG	TGAGAGACAG	GGCAACCATT	CTAGTAAAGC	TCCTTGAGGA	540
	GAACAAGGAA	AAGCCTGGTG	TTGCCGATGA	ATTTATCCAG	CCAAAACATA	GTTACGATCT	600
	ACTTGCCCTG	GAAAAGTAAA	TTAACGAACT	ATCTCCACCA	TAATGAAGAT	GGCTTTGCCA	660
40	CACCATTGGA	CGCGTCGAGC	ATTCCAAAGT	TACACAGAAG	AGGAGCTCAA	GGCTATTAAT	720
	TTGAAGCAGA	AAC					

1608UP

	GATCTGCGCA	AGGATAAAGG	TGTTTCATCAA	GTCATTGTGA	ATGACGCCGG	CAGCCTGTGG	60
45	CGCCTTAGTG	CCATTTCTGA	TGGTCCATTC	TCTGACTTCG	TCGGGCCCCG	AGGTGAAGAA	120
	CGAGATCAGA	TCCAGCTTCT	GTCTCATGGT	GGTGATGATC	TTTGGGAAGG	CGGACTGGAC	180
	GCCGATCTTC	TGCACTCCT	CGACAGCCTC	CTCGGCGCTC	ATGTGCGACA	GTCTCTCCTC	240
	CAGGCACACC	GAGAAGGGTA	TAATTAGATC	GCCAGGGGAG	TACTTGTCGA	TCCACTCCTT	300
	GATCTTCAAG	AGGTGCTTGT	TCTTCTTTCT	AATGTAGTCC	CGCTCCGATA	GGTTGATCAG	360
	GTAGATGGAT	GGCTTGCGGG	TTAGCAGGAA	CATCGAGTTG	ATGACCTCCA	CCTCCTTGGT	420
50	GCTCCAGGAC	TGGTTTGCGA	CTCTCTGACC	CGACTTCAAA	AGCTCGATAA	TGCGCTTCAC	480
	CAGCTCGGCC	TCCTCCTTCT	TCTGTTTCAC	CTCCAGGGAC	TGGCCCGCTC	TCTTGGTGAT	540
	CTTCTCCACG	GCCTCCAGGT	GCTTCTCCGC	GAACCTCAATG	TCCTTCAAAAC	GCAATTCCGT	600
	GTTAATGATG	TCCAGGTCTC	TGACCGGGTC	GACGTCACCC	TCAATGTGGA	TGATCTCGGC	660
55	GTCGTGGAAG	CAACGCACGA	CCTGGTAGAT	CGAGTCCACA	GATCTGATGT	GCGATAAGAA	720
	GGC						

1609RP

	GATCAGACGG	TAATGGCGCG	CATGCTGGCG	CAGGTGGAGC	ACGTATCTAG	CGTCCATCGT	60
	CTCTTGCTGT	GGTGGCGGCG	GCGCGGCAAG	GGCTCGCTG	CGCGAGAAAT	ACAGTAGGGA	120
5	TCTGTGCGCG	CCGCGCACCA	GGGCACGCGG	GGCCGCGAAC	AGCGCCGTTT	GCCCCCTAAT	180
	CGGGACAAAC	GCATATAAGT	AGAGGCTTAG	GCGCTGCTCG	AGGGACGGCA	GAACACACAC	240
	AAGGACCAAT	GAACACGATT	ATCAACTTCC	AGGAAGGCAG	CGCGCAGGCT	CTCAGCGAGC	300
	ACAGCATCTT	CCCAGATGTG	CTGGTGTCCA	CTGCTGAAAA	CGGTCCATCA	GGACACCTTG	360
	TAGTGGAGTA	CCCGGGCGAG	TCTACAGCGG	TGACGCTGGG	GAACGTTATG	CCTGTGGAGG	420
	CTACGCAGAC	GGTGCCCAAC	CTGATGTTAA	TCACGACCGA	GCCCGGAATC	GTCAGGGAGG	480
10	GGGACCTATT	CACGCTGGCG	ATGACAGACC	CAGATGCTCC	CTCGCGGTG	GACCACAAGT	540
	GGTCGGAATA	CTGCCACTTT	CTGGAAACGA	ACATAACGCT	GGGCTCGGAT	GACGGGGTGT	600
	CGCACGTGGT	GCTAAAGGGC	ACCCCGCAGG	TGGAGCACAT	GGGCCCTGCG	CCGCCGGGCC	660
	GGCACAGGGG	CTCACCGGTA	CGTGTGGTTG	TT			

1609UP

	GATCGAGAAG	ATTTGGAGAA	GGAAAGCGTC	TTGGTGCTAG	CCTCGTGACC	CCCTCCCGGG	60
	CTGGAACTGC	GCGATATACT	ACATAAAATA	CGTTATCCCT	GGAATTTGTA	GCATTAAGG	120
	ACTTATGGAC	TATTCTGTAT	ACCTGCGCTT	CCCGCTGCCA	CCCGTAGCAA	TGCCAAACTC	180
	ACTCCGAGGC	CTCGCTGCTG	GCCCAACAAT	CGGACTCACG	CGGACCCGAG	CCCCGCGTTC	240
20	ACGTGCCCCC	CGCATTCGCG	CCACATCAC	TCCGCTTGCC	TCGCTTCCGC	ACCCCGCCAC	300
	GCGACTCCGG	GCCCCGCGAGC	CCCACGTGAT	TCTAGTTGCA	TAGGAAACTA	GGCTAAATC	360
	ACGTGACTGA	ATCGCGCGGC	CACATCATAC	CATGGGACAC	GACCCCGACT	ACCCCCCCCC	420
	CCCCGCGCCG	CGCGCTGCAC	AGCAGCCGTA	TACGGCGCAG	GCGCAGTCCG	GTGCGCGCGC	480
	TCTGAGAGGG	CGCATGGCCG	CCGATGCTGC	ATGGCTGCCT	CGGTGTTGCC	GAAGATGTGG	540
	AGGCACGTAC	GCGGGCAGCT	CAGTTACCCG	AAGTTACCCC	TTCTTCTGAT	TAAATTTGGA	600
25	CTGAAACTTA	AAAGCCGTCA	GCAGTGGCAA	ATCCACGGTG	AGAATAATTA	CAGGAAACAG	660
	CGGTGGACCA	GCTGCGGAAC	TAGACGACGG	GTTGGTGTTG	CACGCATAGA	AGGTATGTTT	720

1610RP

	GATCAATTTT	CTTTCGTATA	GTTGGCGTCC	CAGGCTCCGA	GATAGCCCCA	CATGATAAAT	60
	TGCTATCGCA	CATGATGTCC	TGTTGTTCAT	TGTTGTCCAA	ATTGCTCAAA	TCAAAAATGA	120
	AACTACCATC	ATCTGGTTTC	ACTTTTCAGTA	AACTATCGTT	TTTCTCTGTT	GCAGGGTCTGA	180
	AATCCATATC	ATCCCGTAGA	TATTCTATGT	ACAGCAGAAA	CGGAACCTTC	TCTGCTGAGT	240
	TCAACACCTG	AGCTTCGTTA	GCAGCAATAT	TTACAATTCT	ATGCAGCTTG	CCCTTCTTAT	300
35	TAGGCGGCAA	CAGTGTAGGG	ATATCTACCT	CAGCTGGCAA	GTCCTTATTC	ATGATAGAAA	360
	GCTCAGCTCT	CAATGAAGTT	AGGCGAGCTT	CAGTGGGAAC	TTGCGCCAAAC	TTCTTGATA	420
	TCGTTTCTAG	AGCAATCACA	AACTGCATCT	CGCAGCGGAA	GTAATTTGCC	TTCAAGATTT	480
	TGATTTTATG	TGTGGCTGAT	AAACTGGAGG	GCTCCAGGTT	ATAGATGTTT	GCTCCATGCC	540
	GAGATGTCTT	CCGTTTGTGG	CTCTTCTTTA	AATCATTTGA	CGGAGACTGC	GTGATGCTAC	600
	CACTTCCATG	CTGCTCCAAT	GATTGCTGAT	CCTTATACGA	GTGGAGTGAC	GTGCTGGATC	660
40	GAGAAATCAG	ATGCAAAATTA	GGCATAGAGT	TTGTGTATTCT	CTCTAGCTTA	GCACCATCGT	720
	TATCTTTGGG	C					

1610UP

	GATCGATCTG	TACAGAGCCG	TTACAACAGG	CACTTGTA	AAGCAATATC	GTTACTTTTT	60
	TGCATGTCAG	TTTTTTCCCTC	GAGCCTCGTC	AGCGCGAGGA	ATGAGTAATG	GATACTTTGA	120
	CGACAGAAAA	AGTGAAAAC	TTGAGCGGAC	ATCGCAACCT	GCTCGTTAGT	AGCACCTAAG	180
	CGCAGGTTAG	CACAAATGGCG	CCAAAGGATA	CGGCGGTGTC	GGAGACCTCT	ACGCGGTCTC	240
	GCTATATCAA	AAAGGGCAAG	ACTTTAGAGA	ATGACATTGA	GCTACAGTCG	GTGACGCCAG	300
	CCACCGGGGA	GTTCCCCGAG	GACCACACGG	AAGAGGGCGA	CTACCAGGAG	ACGGAGGTCA	360
50	AGAGGGCGCT	GAAGGCGCGG	CACATCTCGA	TGATCGCGCT	GGGCGGGACG	ATAGGCACAG	420
	GCCTGTTTCT	TGTGATTGCA	TCCCGCTGTC	GGACAGCGGG	GCCAGTGGGG	TCGCTGTTGG	480
	CGTACATCTT	CATCGGTACG	GTGGTGTACT	CGATCACGCA	GTCGCTGGGG	GAGATGGCGA	540
	CGTTTATTCC	TGTGACTCCT	CGGTGACGGT	ATTTTCAAAG	CGGTTTCTGT	CGCCTGCGTT	600
	TGGCGTGGCA	AACGGGTATA	TGTACTGGTT	CAACTGGGCG	ATCACGTTTG	CTGTCGAGCT	660

55

TTCTGTGGTT GGCCAGATCA TACAGTACTG GACGGACCGC GTGCCAATCG CGGCGTGGAT 720
TGTGATTTT

1611RP

	GATCCATCGT	GGTGTCTGTC	ATTACCTGTA	ATTCCATTGA	TATCCTGGCT	ATGCAGTGCT	60
	GGAAACGCTC	CTCCAGCGCC	TCTATTTTGT	TATTCAGCTC	CAAGTACTCC	GCGAGCTTAA	120
5	AGGTCAACGA	GAGCGACCC	GGATTGCACC	TGACGGCGAT	CTCAAGGACC	TTCTCGTGCT	180
	CGTTCTCGTC	CACAAACATG	GCGTAGTTGT	ACCATATCTC	CGGCGCAAAG	CACATGTGCT	240
	GCACAGCCTG	GCGGTGCACG	TATTCCACGC	GCTGGCGCAG	CACGACTTCG	GGCAGGTGCA	300
	GCTTGTTGTC	CAGCTCCAC	TGGATCCACT	TCGTCCAGAT	CTGCAGCTGG	TACTCATCGT	360
	ACTGACCGGG	CGCAGGCAGG	TTCTGCTGTG	TCGCCTGGTT	TAGCTTCGTG	GGCAGCGAGC	420
	GCCGCAGGCC	CTTCGTCAGG	TTGCACCACT	CCTGGTACAG	CGAGCGCGCA	TTCATGTAGC	480
10	TCGCCGAGAG	CTCTCCGATG	AACTTCCGCG	CCGTCAACTG	GTTGACCTCC	TGCTCCCACT	540
	GCGTGTATTT	CTCCAGTAC	CGCTCCAGCG	ACTCCAATGG	CAGGCACAGC	AGGCGCTTGT	600
	ACAGCTTGCG	CAGAACTCTG	ACCCGGCTCT	GCTCCTCCCA	CTTGCTCACC	GGCTTCCACT	660
	GCTCCA						

1611UP

	GATCTAAGGG	ATGGGTGACT	GCTGCCGGTG	CTCACAGCAG	TGGCACGTAG	CTAGTAATGG	60
	TGCGAAATCG	ATCAAAGAGG	GTGCGTCTGG	CGGTACAGGC	AGAAAGCACG	CCCGCCGATA	120
	CAAGTTCCAG	TTCTACAAGC	ACCTGCAGTT	CCAGGGTACG	AGGTACCAGG	TGGTGACTTC	180
20	GCGGCCGTAT	CTGATAGAGC	GGTACGGGGA	GCGCAAGGCG	GCGACGATCA	GGTCGTTTGT	240
	CAAGTGCAATC	CATCGGAAAA	TCAACGACGA	TGTGACACGG	ATCAGCGACG	AGCGGGTGAC	300
	GCACGGGGTG	TCGAAAGTGG	AGAAGTCGAA	GCTGTTCTTG	CTGCTGGTGA	CGCTGTCGCA	360
	GCGGGGCGGG	CCGGAGTACT	GGCTGGACAA	GACGAACGGG	TGCCAGAGCC	GCGCGGGCGG	420
	AGACGGCGCG	CGGAAGAGCG	ACCAGGTGGA	GGAGGGCGGG	AGCCGGCGGG	GCCAGAGGCT	480
	CGTCTGCACA	CTGGTGGAGC	AGATCATGCG	CGAGAACATC	ACGGAGGACT	ACGACGAGAG	540
	CGTGACACGAC	GAGAACTACG	TGTTCTCGTC	GATATGGGCG	AACTTCATGG	AGGGGTTGAT	600
25	AAACCACTAC	CTAGAGAAGG	TCT				

1612RP

30	GATCCATGCG	ATAAATCTCC	TAGTGGTGTG	GTTTCACACG	AAGCAGCTTC	CGTCGTTCTC	60
	GTGGTTTTTC	CTGCAGCTCT	GTTTCGAGCTT	GATTTTGGTG	TTTTTTGGGA	CGTGGACCAC	120
	GAGGTGGCGC	GAGCTTCGCG	ACACGTTTTT	TGAGGGTCTC	ATAGATCAGG	AACCTATTAC	180
	GGGTGGGGCT	GAGTCTCCCT	ATCATGGCAG	TTCTCAGAAC	AGACAGCAGT	TTGAGATGAA	240
	GGACTTGGAG	GCACAGAAAT	AGCCTACATT	ATAAATACGC	TTGAGATCAT	TCTAGCGCCA	300
	CGGTGAGACT	GATCATTCGT	AAATAGCATT	TTAATAACGT	AATATATCAT	ACGCTGGTTA	360
35	TTTCGGATGC	AGGACTCCGA	AATAGTCTGA	CAATTATGTA	CTGTTAAGTT	ATTTATTTTC	420
	AGACGGCGTA	TCTCGCTTGA	AACCTGTTCC	AGTGCACAGC	AGATCCAGCA	GCTCGAATAC	480
	TGATTTTTTC	GTATTGTTAC	CTGGTCGACA	GATCTCCAAG	CCACCCCTCA	ATCGCTGCCG	540
	CAGCTGCAGC	ATTGCTACCG	TAGACTCCAG	CCTAGTGACA	AGATGATCCA	ACAAGGATAT	600
	CCAATCGTAT	TCCGTGTTCT	GGCTCAGCGC	TTTATCAACC	TTTTTATCAC	GAGTCATATG	660
	TGTGGGTAGT	TGTAGGACAC	TATTGTCTGAT	TTCGATCAGA	CCGCCGTT		

1613UP

	GATCAAATAG	ATGTGCGCTG	CCACATAGGA	CGGAGTCGCG	GCTAAGCTGT	GTGTTTTACC	60
	TGGAGGCAAC	TGTTGGACTC	CTGTGTCAGC	AATCGCGCCC	CGACCTGCCG	AACAAGCGAC	120
5	TATATAACAA	GCGAGGAAAC	CACCTTGTGA	TACGCACGGG	GACCAACGAC	ACAGCAACGA	180
	CACAGCAACG	ATGGCGGACC	TCGGGGCTCT	TATTGACTTG	ACGCGGATAT	CGGAGACGCG	240
	GTATGAATCG	ACGAACCATC	ATAGGATGAT	ACACGGCGGC	AAGGCGCTCT	ACGGGGGTCT	300
	GCTAGTGGCA	CAGGCGATAC	TGGCGTCGTT	CTACTTTGTC	CCCAGGGACT	TTATTCCGCT	360
	CTCGGTGCAC	TGCCTGTTCA	TGGTCGGCGG	AGACAATGCT	ATCAAGACGC	AGTACGAGGT	420
	TGAACGGCTG	CGGAAGGGGA	GCAACTTCGC	GCACCTGTTG	GTGCGCGCGT	ACCAGAAGGA	480
10	CAAGGAGCTG	TTACAATGC	AGATCATCTA	CCGGCGCGAC	CTCGGCAAGC	AGCCGGACAC	540
	GCTGCACCGC	AAGGACAACC	TGGGCCCTGT	GGACCGGTCC	CACCTGGAGG	ACGCTGGCAC	600
	GCTATGCAGG	CGGGATCTAC	TGTCCAACCG	TGAGAACCTG	CAGGCGGTGA	GCGCGTCTTC	660
	GAGACGGATA	AGGGCCTTAA	TAACATTCTG	GAGGGGTTCG	ACAACACGTC	GTCCGAGTAC	720
	AGGCTGCCTG	GC					

1614RP

	GATCGCGGCG	ATGGACCCGT	GCTTCGACCG	CCTTCTGGCG	CACCGCGCGG	CGTTCCTCGC	60
	CGCGGTGCAG	GAGCAGGTGC	AGCGGGACTA	CGGGGCGATG	GAACAGTTCC	ACAAGTTCCC	120
20	CGACACGATC	CGTGTGACA	AGTTGGTCAC	GTATATATGG	CGCGTGTTCC	AGCGCGTCTG	180
	CGTGTAACCCG	CCGAACCAGC	AGCGCTGCCA	TCTCGAAGAC	ATCATGCTCT	TGCGTGTGTA	240
	CTGCGGCGAG	GCGCGGGGGC	ACCGCTCTTT	GCTCATGGCG	ATCGTTCAGG	CGGTGGCGGC	300
	ACGCTACGGG	GTGCAGACGC	TCCTCTGCGA	GCAGGTATTG	ATCATCATTG	ACCGCAAGTT	360
	GCGCGGCGGA	CAGTCATACT	TGATGATCCC	GCTGCGAGGG	AACGCAAAGC	CGCGCATCTT	420
	CACGCGGCGG	CGCTTGCTCG	ACACTATGCG	GCACACAATA	CCCAACATTG	CCGACCCGCG	480
	GAGCCTGGCG	CTCGCCCGGT	TCCTCACTCC	GCTCACGAAG	CGCGCGGGTG	CTGAGAAAAT	540
25	CTTCAAAGAC	TGGTCCATCT	ACTGCGACAA	ATCCATATGG	CGGACGATCC	CTGATCACTC	600
	GCCCAATGGC	ATTCTGCGCT	ACCTCCC CGA	CTCCTGCACG	CCGATGGACG	AATCCATCTT	660
	TGAGTATTTT	ATCGTCTATT	GGAAAACCGC	AACAGCAAAC	CACTCCACGA	ACAACATTTT	720
	CCACACC						

1614UP

	GATCCTTTTC	ACCAACAGCT	GTCTGGGCCA	GCTGCGGCCT	GGGATGAGCT	ACAACGAGGC	60
	AGTGAAAGCG	CTGACGAACC	TGGCGCTGGA	CAGCTTTACA	CTGCCGGGGA	CGGTGGGGTT	120
	TCCGCTGAAC	AACGTGTACT	CTGTGCCGGT	AGAGGACGGT	GCTCAGATGG	AGCTGCTGAA	180
35	GGGGTACCTG	CAGCAGTTGC	GGCAGGAGCT	GGCCACGCGG	CTGCTGGACC	GTGTGTATGG	240
	GGCGGAGAAG	GCACAGCCCT	CGAAGTTCTG	GCTGGCCTTC	ACAAGGCGCA	AGTTTATGAA	300
	CAAGGCGCTG	TAAGGCGAAA	TAGGTACGTA	GCTGGCGGCG	CCAGGAAGTA	TTTACAAAGT	360
	TGGCTGTATC	GCTACGAGGT	TTTGGTGGCG	TGTGCCTTGT	TGGAGCGCAC	GAGGAGTTCA	420
	ACGGCGGAAG	CTCGGAGCTG	TTCCGCGTCT	TTACAGATCG	CGTTACCGTC	AATGCTGAGG	480
	TCGGTGTTTT	TGGCGCGGAA	GCCTTGGATC	CGCGCCTGCA	GGTCTGTTCAG	CGCCTGGAGG	540
40	ACACGCTCAT	AGTCTGCATC	TTCTTTACAG	CGCTCTTTGT	ATGTTTGGAA	GGACTGAGCG	600
	ATGTCTTCGA	TACCGGGCTC	GACTCTGCTG	ATCATCTCGA	TGCGCTGGCG	CAACAGCTGA	660
	TCGCGGTGCG	TGTTGGCGTT	CSCGTGCTA	ATCATCTGCT	GGATTTCTGT	ATCGGTCAAG	720

CCCGAT

1615RP

	GATCATTTCAG	CTGGACGTCA	GCCGACTACT	GTTGGACCCC	ATATTTCACGG	TCCCCGAGGT	60
	GCAGAACGAC	ATGGTGGAGA	TTCTGCGCCA	GTATATGCTG	GAGTCGGGGC	GGCCGTACAA	120
5	GCAGGGTTTC	CATGAGCTAT	GCGGCATGTT	CTACATGCAG	CTTTACCGCA	ACGGCTACCG	180
	GGACGGCATC	CAGCACACCA	CGCTACATAT	GTTCAGGAG	TTCATCGCAG	AGGTAGCTGT	240
	GACCTTCTAC	GACGAGGGAA	ACCTCATCGA	GTGGACGAAG	AACACGTTTG	AACCGATACT	300
	TCGACACGCG	TTGCCAGGCT	TGTACGAGCA	GCTTCTAATG	CACCATGAGC	TGGACAACCTC	360
	GATATGGCTC	ATCCGCTGGA	GCAGGCTGCT	CTTTCTCCGA	GAGTTCGAGC	TGGAGTACAC	420
	GCTTTGCTTG	TGGGATCACC	TGCTGACATT	TAGATACCCA	GTATCCCAGC	TCGTAGCAGC	480
10	CATTATCGTT	GTCTGTCTGA	CACTCATTTGT	ACAAGAACTG	CATTCTCTGTG	AAGACCACGG	540
	CGACCTGATG	TCTATTCTAC	TGCACCTACCC	TCCTCGAAGC	TGCTGAGCGC	CCCCAGATGA	600
	TCCGCTCCGC	CCGGACGCTT	CCTGATCTGT	GGCTCGCCGA	ACAATATGAA	GACATGCAAC	660
	TCATCTGCGA	TTCACTAATT	AAGTCGCACA	ACGGCGCCTG	GTTC		

1615UP

	GATCTCGTTA	TTCTGGACAA	CATTGCGTAT	AGGGACTGCT	CCTGCTTTGT	GTGAGGAGAC	60
	GTGTGCTGAC	TTTAAATAAG	TACGATGAAA	CGGTCAGCCT	ACGGTGGGGC	CCCGTTTTTC	120
	AGTTTCGCAC	GGAGAGGGTA	TCAAAGGAGG	TCGAACACAG	CTACGTTATT	GGTTCGTATA	180
20	GCATGCTTTT	GAAGCCCCTA	GCTTCACGAG	CGCTCCGACC	ATCCCAGCCA	CCGCGCCCCT	240
	ACGCCCAAGG	CCAGCTCCCG	CAATACGGCA	GCGCCGTGGG	CCCCTTTTCG	TAAGTATATA	300
	TGGCGTGGCC	GCGCCGCGCG	GCCGAGGTCG	CGCGGTGCAC	AATGGCTTCT	CGACTTGACA	360
	AGCTCCCGGA	GGCGGTCACT	CGCCTGCAGA	GCCTCAGCCA	TAGACAGCTG	CTCCGTCTGG	420
	CGCAGGGCGT	GTGCATCCCT	GCCCTGTCCC	CGTCCCTGCA	CAAGGGCCAG	AGTGGACGCG	480
	TGTGCGTCTG	GGGGGGGTCT	CTGGAGTACA	CCGGCGCGCC	GTACTTCAGC	GCGCATGCCG	540
25	CGGCGCTCAT	GGGCTCGGAC	CTGGTGCACG	TGCTGTGCGA	GTGGAACGCT	GCAACGCCGA	600
	TCAAGGCCCTA	CTCGCCGGAC	CTGATGGTGC	ACCCGCACCT	GCGCGACAGT	AGCTCCCTGG	660
	CGCGCGGGCT	GGAGCCCGCC	ACAGAAGCCG	TGCGCGCGCT	CGTGGA		

1616RP

30	GATCTGCTTC	AAGAGCTCCT	TCTGGTAGGA	CGAGCCCAGG	ATGAAAATCT	TGGAGACGGT	60
	GACAGGGTCC	AGGAACGGCT	TGAACAGGCG	GAATGCGGCG	GAGAAGCCGA	ATGGCGCGTT	120
	GATCATGTAG	AACTTGCCCA	TGCGCTCGGG	GTAGTAGTTC	TGGCCGATGT	TCGAGGCCTC	180
	GCGCACGTAG	CTGAGCACCT	GCGCGGCTGC	GGAGATGGAG	ATGCCCTTGA	GGTCTAGGAT	240
	GGTGCAGGAC	GTCTCGACGA	GGCAGTCCGC	CTGTCTGGAG	CTGGCCGGCA	AGCGGTACCG	300
35	CGAGAAGGAC	TGCTACTCCC	ATATCAAGTT	CTTCAGCATG	CGCTCCTGCG	TCGTGATCTT	360
	GTACATCTCC	GTCACTTTCA	CCGCGCCCAG	CTCCTCGATG	TACACCGGCC	TCCCGTCCTT	420
	GTCCGTCTTG	TGGTAGTACT	GCGGGTAGAA	CTTGGCCACC	AACGGCTTTT	CCTCGTAGTG	480
	GAAGTCTCTG	AAGATCGTGT	CCACGCCGTT	TTCTTTACGC	CACCTTCTCGC	AGTTCTCAAA	540
	CATTGCCCGC	GCAGCCGCCC	ACGTTGGAAC	TTGCGCGCCC	GCAGAAACCG	CAAAAGCGTC	600
40	GAGTCGTCCA	GACGCTTGGT	GAATCCGGCC	TGCTTCAGCA	CCTTGCGCAG	CTCCTCCAGC	660
	GCCGCTCCG	TGCTCCGCTC	CGTCAGG				

1616UP

45	GATCACCTTT	TGGCAGGAAC	GCCACAGAAA	ATCCATTACG	CGATTCTGCC	CGTTCAATTC	60
	TGTACGAATG	GGGAAATGAC	TCGTCGCCAT	GGCACAGGTG	ACTATCGCAT	TTCTGTTTCGG	120
	GGGCGTGATG	CCCAGATTTT	CTTGCAGAAA	GCCGCCACCC	TGCGGGATAG	GGCTTTACCT	180
	CACATGAGGC	GCAAAGCGAC	AATAATCGCA	GAGCTGCTTC	TTACTTTCATT	CTCTACCCCA	240
	CTAACGTAACT	CGATCGGACA	GGCACAGTCC	TACGGTAATC	CTCTGAGATA	CCAGATTCGG	300
	TTGCATAATG	ATCTCGCCTA	CAGGGCCGTG	TTTGTTTCGAG	CCCATATCTC	ATGCAAGATC	360
50	GCGATGCCCC	TGACGATCCA	CCTTCACCAT	TTACTCGTTT	CTTTTTCATG	TTTTCAAAAA	420
	GAAACGAAAA	GGTGAGATAA	AAAGCAAACA	TTACTACCGA	CATTTAAAAT	AGGTGATGTC	480
	CAGGACTGTA	CCTCATTGTG	GGCGCTAACA	GCACCAGCAA	TGTCTGTGTC	ACCCCTTGTG	540
	CTGTTTGACT	TTTCAACAGA	CAATCCGAAC	ACACTGCCCC	GGGAATACGA	CCTTGCAGTG	600
	GCCCGAATCT	GTGTGCTGGG	CCACGGGGGC	AGTGGCAAGT	CATCACTCGT	TGCTCCGATG	660
	GCTACACGGA	CTGGAGAGTG	GCCTG				

1617RP

	GATCTTGACA	CCAATCGACT	TCCGGAACGC	CTGAGTCAAG	GCCTCGGTCT	TGGATAGCTC	60
	CAACGAGAAT	ATCTCTGACC	CTGCCATCGC	TGTGAAGGGC	ACATCTGCGC	CCAGTGACTG	120
5	CGACAAGCCC	ATCGCCAGCG	CCGTTTTGCC	GGTCGACGGC	GGACCAGCAA	CCAACACGGC	180
	CCGCCCGGCA	ATCGTACCGT	TCTGCACCAT	TTTGAGAATC	ACGCCGTGCGG	CCCTCCGCGC	240
	CTGTAACCTGG	CCCACCATTC	CCTGCGAGCT	CGGCTTAGGC	TGTAGGTTCT	CGTCCAGTCC	300
	CAGGCCAACA	ATGTGCGAAT	GTGTGCGCAAT	TAGCGACAAG	GACTTCAGAG	ACATGTTCATG	360
	CGCCTCCTGT	GTTTGAATCG	ACATATTATA	GATCTTTGAA	ACTTTGAAAC	CGTCAAGAGA	420
	GTCCAATGGC	CTTTGTTCGAT	GACCGTCTAA	CTGTTCAAAC	GGTTGTGCAA	CATACCAAAT	480
10	TTTGCCGGAG	CCTGAGGACT	AAAACGCATG	TTATACGAAG	TCAAGAAGAA	GCATCGTTTG	540
	AGCTGCTAGC	AGTTCCCTGA	CTCTCAACTT	GGTGCGAGCG	TGCGGTGTGA	TGCTTCGCAT	600
	GGGAGAGTAC	ATATGTGGTT	GCAAGCCACT	TTGGAACCTG	TGGGCTAACG	ATGTACGCAT	660
	CACCGTGAAT	GGGAAGCGGT	ACTTGGTGAC	TGGGCTCCTC	AGT		

15 1617UP

	GATCAGTTCG	TCGAAGAATT	CATGTCATGC	AGAGAAATGG	GAAGCAATTT	ATGCTCAGCT	60
	CCCTCCCCCT	GTTCTCTTTC	TACCGCCAGG	CCATGCAGGC	ATGTCAGGCG	CTCAACACAC	120
	CTAGTGACAA	ACTCGCCGTT	GTCCTGACAG	CCTATGCGTT	CGTAAATGTT	AAGGCCATCC	180
	GATGTTTCGAA	GAGGTGACAG	AAATTCCCGC	TGTAAATTCT	CAAAGAAACT	GTCCAAGGGC	240
20	GTATCCTTTCA	CAAAGTCGGG	GCGCCGCTGC	AGCACATCTT	CCAGCTTCCT	CTGTTCCCCC	300
	GAGGCGTTGC	TCATGCTCGT	GGCGATTGCA	CTTGCTCAGC	TCGGCCTCTG	CAAGTACGTA	360
	ATTTTAGCTA	TCGAAAATTT	TCCCTCCTGG	CGATGAGCTC	ACGAAGTCTA	CATACCGATT	420
	GACTAAGACA	CTTGCCACCC	GTTTGCGCCT	CATGCCACTA	CACCAAGGAC	CTCTGGACAT	480
	CGAGGATCAA	CTTGCCATCA	TTGCCGACGC	CCGCATAGGC	GATCTTGACA	GCCTCAAGCA	540
	AATCTTTTCC	GAGCTCATCG	ATCCAAAGCT	CCTGCCATCG	TGCAGCGACC	CAGACACGCT	600
25	CTGCACGCCG	CTGCACATGG	CTGCCGCCAA	CGGACACGCC	GACGTCGCCC	GCTAACTGCT	660
	CTCGCTGCTC	GAGCCCGCCG	CGGGACGCCA	CTGGGG			

1618RP

30	GATCCGGCGT	CCGGAAGAGC	AGCTTATGCT	GAAGGGCTAC	CTAAGGGACA	CAATCCCCCC	60
	CCCCCCAAA	AAAAAAAGCA	TGAGACTCTG	TATCAGTAGG	AAGTCTATCG	CATCTTCTTA	120
	TTTAGCCTGT	ATATGTCCCT	TCCGCGTGTA	GACAKTGCGT	TGGACGAGTA	TGCTCGATGC	180
	GGAAATAAAC	GTACTTTTTT	GAAGAGTAAT	ATGGACTTTC	GACCTGCAAA	GTACCGTCTG	240
	CCGTTGCGGT	GTCAGACACT	CATCGGAACG	CAATTGTTGC	GGGATCACGG	TATGCTTCTG	300
35	TTGTATGCTA	TGGTAGCTAT	AGGGTCTGGA	CGGCTATCCA	GAGAGATATT	ATCCCATTAA	360

1619RP

40	GATCAACAAT	GTGCCGCGGC	TGCTCCTGTT	CCGCCCGGGC	GGTGATCTGG	ATAGCTACGA	60
	GCCTCTCGGG	ATTCCGTTCG	ATACAGGCGG	CGCACGGGTG	CGGGCGATCA	TCGACACCCT	120
	CAAGAGTTAC	ACCGGCATCG	AAGACTTCGA	GTACCACGAA	CCAGTGAAC	GGGGCCAGTA	180
	TGCCGCTATC	CTCATGATGG	CCGTCCCCGT	AGTAATCATG	CTGCGCAACT	ACTGGTCCGT	240
	TGTGGTGTCC	ATCGCCCTTT	TCCGGCCTCT	GTGGGGGTTT	TCCTGCGTGT	CGATCGTCAT	300
	CGCACTTGTG	AGCGGCGCGA	TGTTTCAMCAA	GATTAAGGAC	ACTCCCTACG	TGGGCTCGTC	360
45	CGGTGATGGC	AATTACGTCC	AGTACTTCGC	AATCAGGCAG	CAACAGGTTT	AGTTCCGGGT	420
	GGAAACTCAA	ATCATCTCCG	TCATATATGG	CACCTTCAGC	GCAGGAGTCG	TACTACTTGC	480
	CATTGGCACC	AAAAGCATCA	GAGCTTACTA	CATCAAGTAC	AACTATAGCA	TGCACGCGGT	540
	GGTGCACTTG	TTGTTGTCCC	TCGCCGCAAT	ACTGCTTATC	TATATCTCCT	TCGCCGCCCT	600
	GCTCGCAGTC	TTCAAACCTGA	AGAACTTTGA	GTATTCA			

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1619UP

	GATCGCTTGC	TGGAGACCAC	AGATTTTCTA	GCGTTGTCCG	TAAGGGCGAG	ATGGCGTCGA	60
	CAACCACGGA	GGAAAAGCTC	ATGAAGCTGA	ATCCAACAGC	TACAGATGCG	AACAATTACA	120
5	TTAATACTGA	TACCACTGCG	AGCAAGCCGG	CTCCACCTTC	GTCAACAGAG	GCTGGACAGG	180
	CAATTGAACG	AGAAAAAATA	CTAGACCGGA	GGCAGACTGA	GAAGGACAGT	GTAGAGAGCA	240
	GCAAGGTTGA	GCGCCCGGTA	GTAGATGCAT	CGTACGTAGG	GTGGAAGCAA	ATCGGCGGGT	300
	GGGAAGAGCG	CGACCGACTC	ACCGAAGATG	ACCTGCACTG	GGAGCTTGAC	AGAGAAACCT	360
	TTTTAAGCCA	TGTGCTGCCT	GCTGCTGCGT	ATGGCGACTG	GTATCACTCC	GTGGGGATAT	420
	TCTTCCTCGG	CGGATTTTTA	TCGTTTGCCT	TGGGCTACTT	CAAGTTCAGT	TTATCACCTG	480
10	TATTCTTCGT	AATGGTTTIG	ACGGCTTTGC	TATACCGTAC	ATCGATTTGG	AAGTACAGAG	540
	GGTCGATAAG	GGAAGTGGTG	CAGAAGGAGC	TCACAGTGCA	GAAAGTAGAG	GATGACTACG	600
	AGAGCATGGA	CTGGCTCAAT	AACCTCTTGG	ATAAATTCTG	GACCAGAATA	GAGCCCAACA	660
	TTTCCGTGAT	GGTTGTGGAT	CAGGTGAACC	ATGAATTGGC	TAAGAACCGT	CTGTGCCGGG	720

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1620RP

	GATCAAACCTA	TTTCTTTGTTT	TGTTGGTGGA	AGCATACTTT	CGTCAGTACT	AACTTCTTCG	60
	CTCCACTCCA	TAAATTCGTA	TTCCCTATTG	GGATTAAATT	CCGGACCCAA	GGTAACGACC	120
20	AAAAACATTA	GAGCAATAGA	TCCCCACACA	AAATAGGCCA	TAACCTCTACC	ATAATCATAC	180
	AATTCCTTAT	TGCCATTATC	GAGTGGAATA	TTTCTTGCAA	GGCTGCTTTC	AAGCAACGAT	240
	GAGGGGCTAG	ATGCCAAGTT	TCCCAATTGA	TATGCCACGC	CCACGAAAAA	GGTTTTCGTG	300
	TCTGAGTTTG	GAGCTAAGCA	GTGTAAATGA	TGTGGGACAA	GGCCCCATGC	TCCTTGAACA	360
	AAAACTGTAT	GGAAGAACAC	GGACACTATA	ATACTTCTAT	CATGTACAAA	TCCCCACGGA	420
	TAAACAAGAC	AGGCAGCCAA	CAAAATACAC	ACGAGGATAA	CAACTCTTCT	AGAGCTTATG	480
	CTGGAAAAAC	GTGAAATGAA	AAGTCCACCT	ATTATAGCAC	CAACGTTGGC	TGCACAATTT	540
25	GTGACGGCTG	ACTGATTGGG	AGAATAACCA	AGTTGTTTAA	TGAGCATGGT	TGGAAAGAGA	600
	TCCTGAGACG	CATGAGAAAA	GTAATTATAA	CCCGTCATAA	GCAATATCAT	GTAGATGACA	660
	ATGT						

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1620UP

	GATCAAATAA	AAATAGAAAT	TAGCTTAATG	GTAGAGCATT	CGTTTTACAC	ACGAATAAAT	60
	TGAGTTCGAT	TCTCAAATTT	CTAAATAATA	ATTAACAATA	ATTTAAATTT	GGGTAAAAAT	120
	TAATAAATAT	TAACGTATAT	AATAATTATA	TACTTTATAA	AATTACTCAA	TGTTATTAAT	180
	AAATTTATTT	CTTATCATT	ATAATGATGT	ACCTACTCCA	TATAATATAT	ATTTTCAAGA	240
	TTCACTACTA	CCTCATCAAG	AAGGTATTTT	AGAATTACAT	GATAATATTA	TATTCATAT	300
35	GTTACTTGTT	TTAGGTTTAG	TTTCTTGAAT	AATAATTATT	ATTATTAAAG	ATTATAAAAA	360
	TAATCCTATT	CTTTATAAAT	ATATTAAACA	TGGTCAAATA	ATTGAAATTA	TTTGAACAT	420
	TTTACCAGCT	ATTATTTTAT	TAATAATTGC	ATTTCCATCA	TTTATTTTAT	TATATTTATG	480
	TGATGAAGTT	ATTTACCACG	CTATAACTAT	TAAAGTTATT	GGTTTACAAT	GATATTGAAA	540
	ATATGAATAC	TCAGATTTTA	TTAATGATAA	TGGTGAAACT	ATTGAATATG	AATCTTATAT	600
	AATTCCTGAA	GAATTATTAG	AAGAAGGGTC	AATTAAGAAT	GTTAGATACT	GATACTAGTA	660
40	TTGTTATTCC	TGTTGATACT	CATGTAAGAT	TTATTGTTAC	AGCTCCTAGA	TGTTATTTCAT	720
	GAATTTT						

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1622RP

	GATCCGTGTA	TTTTTTATTT	ACATTATTTA	ATTAAAAATA	ATGATTTAAA	TAAATATTTT	60
	TTATAAAAAA	TAATTAGTGC	ATTGTTACAT	GTTCAATTAAA	GAATGATTAT	TATCAAAACC	120
5	ATCAACTAAT	TGTTATATAT	TTATTAAATA	TTAATTTTAC	TTAATTAAGA	ATTAGGAACT	180
	TTATCTATTA	GTCTGGGCTG	TTTCCCTTTT	GATTATTTAAC	CTTATCGCTA	ATAATCTGAA	240
	ATATTTAAAT	TTAGATTAAT	AATATATTCT	GAGATTTAAT	ATTTTAAATA	AAATAAATAA	300
	TTATTCCTTA	AATAATATTA	ATAACTATAC	CATATATATC	TAATATTTAA	ATAATCATAC	360
	TAACATATGT	TTTCGTAGAAA	ACCAGCTATT	TGCAAAATCAG	ATTTGACTTT	CTCTACTTAC	420
	CATTATTCAT	CAGATAATAT	TGCTACATTA	ACCTGTTTCAA	TCGTTTTTAT	ATTTTATTAT	480
10	ATTTTAAATA	TAATAAATAT	ATATTTTAAAT	CATTTGATAA	TAGTAAGATC	ATCTGCTTTC	540
	GGGTAAATTA	ATATTTAACTA	AATTTAATTT	ATTTTAAATTA	ATTTTAAACAT	TGTTAAATAT	600
	TTATATTATT	TTTAATATCA	TTTTTTATTT	TAATATTATG	CTAATATTAA	TTACTTGCTG	660
	ACCCATTATA	CAAAAG					

1622UP

	GATCCAGTTA	CTTAGTAGAA	TGATAAAATT	AATAAATATT	ATTTATTAAT	ATTTGGTTAA	60
	CAATAAAAATT	CAATAATTTA	TTTAAATAAT	GATTAAATAA	TCTCAATATA	AAATTATTAA	120
	TATAATGAGA	TATATATTTT	TAAAAAGAAT	ATATAATTAA	ATAATCCCAA	CCAAAATTG	180
	TGCCAGCAGC	TGCGGTAAGA	CAAAGGGGGT	TAGCGTTAAT	CGTAATGGCT	TAAAGGGTTC	240
20	GTAGAATGAT	TATTTAAAAT	AATAATTAGA	ATTAATAAAA	ATAATTTAAG	AATTATTCAA	300
	GTAAAGATGA	AATAATAATT	ATATGAATAA	GACTTATAAA	GTGAAAATTT	AAATTATATA	360
	TTAATTGACA	TTGAGGAACG	AAGGCTAAAG	TAGCAAATCG	GATTCGATAC	CCGAGTAGTT	420
	TTAGCAGTAA	ACAATGAATA	CCTATTTATT	TTTTATTAAAT	TAAAGAATAA	ATTAAATGAA	480
	AATTAAAGTA	TTCCGCCTGA	TGACTACGTT	AGCAATAATA	AAAATCAAAA	CAATAGACGG	540
	TTACAGACTT	AAGCAGTGGA	ACATGTTATT	TAATTCGATA	ATCCTCGATA	AATCTTACCA	600
25	TTTTTTGAAT	ATTTAATTAT	AATAATTTAT	AATTAATTAC	AGGCGTTACA	TAGTTGTCTT	660
	CAGTTCGTGC	TGCAAAGTTT	TAGAATTTAT	CATAAACGAA	CATAACTCTA	AATATTTT	

1623RP

30	GATCACAATC	GCATGGTATG	ATCGTTTTAG	AATCAACGAA	ATATGACAAA	ATGAAGGAAC	60
	ATATTGCCAT	AAGGACTTCA	GGTATTACAG	TCGCAGATAT	TCTATCGAAG	TCCACTGAGT	120
	ATGGTTTAGT	ACCTATACCA	AAAGAACAAT	TTGAACAGAT	TAAAATGGAA	TTAGAGCATC	180
	CAAAGTTTAC	TAGAGAGATG	ATTGTTGACC	ACGCTGGTGA	CTTCGACTTA	ATTGCAGTGG	240
	AATTAAAGGA	ATACAATCGC	CTCAAAAAGC	AATCGCAGTT	CTCCTTTGGT	GACATTTTCG	300
	ATAGCATTAA	CACTGACGAG	GAAAGTGAAG	CATCTGATTT	TGAATATCAT	GATGACGAGA	360
35	TAAAGCAGCT	TAACAAGACA	GCCAAACGCT	TTGGGTTATT	ATGTATTCCA	GAAGCTGCGT	420
	TTATCGCTAC	TTCCGTCGCT	AGCACGCCTG	ATGTCGATAA	TGTCGTCTGT	CTACCAATAA	480
	GCTACTATAA	TAAGTTGATT	GCGAATGAAG	CAAAGAGCCT	CGAAAAGCTG	ACTGACTGGG	540
	ATCTTCAGTC	AGAAGCTAAA	AAACGTGGCT	ATCATATAAA	TTTCAGCTTC	CAGAAGGAGG	600
	ACGCCCCACC	GCCGCCCTCA	ACCCATATGC	CTCCACGGAT	GCCGAAGTTT	TCCCCAAAAC	660
	CGTTCGACTT	TGTCAC TAGA	CTCAAAAAC	ACTAGAAGGG	CGTTTAAATGA	GGCTGCTACT	720
40	GTGCGCCGAC	AGAGCGAATT	TGAACAG				

1623UP

	GATCAGCGCA	AAACACATCT	GTATTCCCAG	CAGCATGTCC	TCCTCCACCT	GCCGCATGGC	60
	CTGGCTTGCA	AAGCCGTCCA	CCTCGCCGTC	AAATGAAATG	CTGTCCGGAA	TATTCTCCAG	120
5	TTTCGCAACC	ACAGGGTTCC	CGTGCTCGTC	GTACTCCTGT	TCCTCATCCT	CCTCACCTGC	180
	CTCGTCTCCG	CCGCGCACGT	CCCACGGCCT	AATGCTCAGC	TGCGGAGCCT	CCTCGGGATA	240
	CCGCTCCGGC	AGCGTAATGT	CCACCACCAA	GTGCTGCTCC	TTGCTGATCG	CAGCCGCCGT	300
	GAATGAAGAG	CTTGCCAGCG	GGATCAGATC	CAGTTTTAGG	TCCACTTCAA	ACTGGATTTT	360
	CGGGTACTCC	CCGCACACCA	CCGTCAAGTC	ATCGGCATAG	ATGGACTCAA	GCACTTCCAG	420
	CTCCTGCTTT	TGCTCCTCCT	GATAGTCCAT	ACCTATCCGC	TCGACCAACT	ATGAGCCAC	480
10	GCGCAGCTTA	GGGCTAGACC	GTTACAGCTG	CAGGTGACCG	TCCGGGGGAC	GATGCGCTAT	540
	CGCTGGCGAA	ATTTTTCGCC	TATACCACCA	CTTATGTTAC	CCGGTCTATA	GTGCTGCTCT	600
	CCGACCTCAC	TGATGGTGCT	GTCCCGCGGG	GACTGCTGCC	TCGTGCGGGC	AAATCCCCAC	660
	CGCTCTGAAC	GCTCGTTCCA	TCTGCGTCAC	GGGTTGACCG	AACGGGAATT	GCGCGCGCCG	720
	AGAAATCTTG	GCGAACCATG	CTGCACTTAG	CCTTACTG			

1624RP

	GATCGCACGT	CATTTTACCT	ACAGGCTGGG	CTTTTGAAGA	AGACGCCTGC	ATGGTACAAT	60
	GTCGTAGCCA	GGATCCCAAC	TGTGACCAAG	TTCGCCAGAG	AACCGAAGCT	GCATGACCCA	120
	GTTAGCGGCA	AGTACAAGGG	CGAGCTGGAT	ATAATGACGG	ATAGATTAAA	CAGAAACACA	180
20	TGCACGTACA	AGACACGCGC	TGGGAGTTCC	GACCGGCAGA	CGGCCGCGGT	GCACAAGCCT	240
	TCTAAGCTGC	GGTTTATCGA	GGACAAGCTG	CGGTGCGTGT	TTTTCCAGCA	GCATCCTTGG	300
	GAGCTGTGCG	GGCCGAAGGT	GCTGGTGGAG	AACATGGGAA	ATGAGCAGTA	CGACTGGTCG	360
	CGGATGTTGC	AGCTAGGCAA	GCCGCTTGAC	GGTGAGTCTG	TGGTGCAGCG	GACGCTGTAT	420
	CTGCTGAAGT	CGGGCGCGCA	CCGGGAGATG	CTGGCGGCAT	ACGACCAGGC	GCGGTTTGAG	480
	TTCTATCGTC	TGAGGATGCA	GCAGGAGCTG	GAGGAGCAAA	TAGCGTACGA	GGAGGCCACG	540
25	ATGGTTGGCG	CTGTGTTCAA	GACAACCGCT	GTGGAGCACG	GTCTGCAGCA	AGAGCAGAAG	600
	TCCCTCGACA	AGTGGAAAGG	GGACGTGGTT	GCGGGGTTGC	AGCTGATGTC	TGCGAAGAAG	660
	AACCTCTACAA	AGCAGTCGTG	GGCCGAAGCC				

1624UP

	GATCATATAT	CTTCCTGTGG	TAAGGTCTGT	GGGAAGCAGC	TCTCCTGCGG	GAATCACACT	60
	TGTCCCATGA	CCTGCCACGA	TGGTAACTGC	ATGGATCCAT	GCCTCGTTAT	AACTGAGCAG	120
	AAGTGTGCAT	GCGAACAGAG	GCGTTTCCTT	GTTCTTTGCC	AGTTCCCCCA	TTCCCCAAGT	180
	TGCACGTCAA	AATGTGAATC	ATTGATGTCT	TGTCGTGCGC	ATCGGTGCGC	TGAAAAGATG	240
	TGTTCCGGTA	GACCGCATTC	TGTCAAGCGG	AACTCTAGGC	GGCGCCGTGA	GAGTCCAGAT	300
35	GATGAATCTG	AAGTTGAGGC	CCAGCACGTG	TGCTTAAAAG	ATTGTAATCG	GGTGTGCTTT	360
	TGTGGTATCC	ACATGTGCAA	TTACAAATGC	CATGCAGGCA	AATGTCCTCC	CTGCTTAGAA	420
	TCAGATTCCA	ATGACCTTAT	CTGTCCCTGT	GGTAAGACAA	TCGTACCAGC	CCCTGTCCGT	480
	TGTGGAACAA	AGCTCCCTCG	CTGCACATCAT	CCATGTGCGA	ACTCGCTGCT	GGATACTTGG	540
	CCCTGCGGAC	ACAGTCCACC	TTGCGATAAT	TGTCATCCCT	TAGATGAACC	TTGCCCCCCA	600
	TGTACCATCA	CAGTCAAGAA	AACTTGTGCG	TGCGGTAAAA	ACGAGATCAG	GACATTCTGC	660
40	TACAATGATG	ATGTGTGCTG	TTCGAGACCG	TGTTAGAAGC	CATTGTCTCTA	TTGCAATCAC	720
	TTCTGCCAAG	TTCCCTGTCA	TT				

1625RP

	GATCAACTAC	GAGGACTTGA	CGACCGCACG	ACGGGAGCTC	GCGGCCGCGC	TGGCCACTTT	60
	GGAGAATATG	TAGCGCACAA	CATCAGCAAT	GTTACAGTAC	AGACGTCTAT	CCGTGGGGTA	120
	CGGCTATGAT	GAATAGAAAT	ATATACACAG	CTGCCTGCAG	GCAGCTTAGA	AGCGCAGAGG	180
	CTTGGGCTTC	TCCCACGAGT	ACTCCTGGTT	AGTGAAGTGC	CCGTACGAGG	CGGTAGGTAG	240
	GTAGATGGGC	TTGGCGAGGT	CGAGCTCTTT	GACAAGAACA	CCTGGTCTGA	GGTCGAAGTT	300
	GTTGCGGATG	ATCTCGATCA	GCTCGTCTGC	GGACTTGTTG	CTGGTACCGT	AAGTCTCGAC	360
50	GTGGATGGAC	AGCGGCTCGG	CAATACCAAT	GCGGTAGGCA	AACTCAACCT	GCACACGCTT	420
	GCACAGGCCG	GCGGCCAACA	GCGCACTTGG	GACCCAGCGC	GCAGCGTACG	CAGCCGACG	480
	GTCGACCTTC	GAATAGTCCT	TTCCGGAGAA	CGCACCGCCA	CCGACCGCGG	CGGCACCGCC	540
	GTACGCGTCA	ACAATGATCT	TTCTACCGGT	CAGACCTGCG	TCACCTTGTTG	GCCACCGATC	600
	TCGCTGCGGG	CGCTGGCTGC	AGCTAATGAT	TCGCTGTTTC	GTCTAGCATG	TCGGCAGGCA	660

55	TGACCTTGCC	TACGATGCGA	TCGCGCAACG	CGGAACGCAG	GTCTCGGTG	GAGATGTCTG	720
	CCGCG						

1625UP

	GATCTGGCTC	TGCGCCATCC	CAAACAACCT	GGGTGTTGAC	AAGAAGTACT	ATGATGAGCA	60
	CAAGAAGGAA	TGGGCCATGT	ACCAGGAGAT	GATGAAGCAC	TATGCCAACG	AGGACCTTGT	120
5	CGACACCAAC	ATGCAGGGCG	GGTTTATCGT	CGCGCCGCCA	CTCCACGAAA	TAGAGCTGGA	180
	CAACTTCCAG	CTCGGCGTCT	ACAAGGAGCT	CGTAACTAGC	ATGTTCCCTT	GACTTCATGG	240
	AGTCCAGCAT	CGCCCATGTT	TTATGCCCAA	TACTTTTGAG	ACTATACTTA	TATTATATAC	300
	TGATAAACAA	TTTCCCGCGC	TCTCTCACGC	CCACTACTTG	TTCTCCGCGT	AGAAGAAGTT	360
	CACGGCCATC	AACTCGAGGT	TCTTCTCGCC	CGCAAACCTG	CCCACACCCA	CAGGGGGCCG	420
	CTTCTCGGTG	TAGCCCCAGT	TCACGCGACT	CTGCAGGCGG	GTGACCTCCT	CCTCGCTCAG	480
10	TTCTAGCCGC	CCGGGCTGCC	GAAACAACAA	CCACACGTAC	CGGTGAGCCC	CTGTGCCGGC	540
	CGGCGGCGCA	GGGCCCATGT	GCTCCACCTG	CGGGGTGCCC	TTTAGCACCA	CGTGCGACAC	600
	CCCGTCATCC	GAGCCAGCG	TTATGTTTCGT	TTCCAGAAAG	TGGCAGTATT	CCGACCACTT	660
	GTGGTCCGAC	CGCGAGGGAG	CATCTGGGTC	TGTCATCCCC	AGCGTGAATA	GGTCCCCCTC	720
	CTGACG						

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1626RP

	GATCCGTGGG	GACCATGCGC	AGATGGCGCC	CTTAATATAA	GCCCCTCCTC	GCAGGCATGA	60
	CGTCTGCCAA	CTCCGACCAT	TCTAAATGGC	CAGCTGCTGC	TTTGATGGTA	GCGTCCGCGG	120
20	CTGGCGCAGA	AGTAAATATA	GCCATTAAAT	CCCCCTCTAA	ATATACATTA	CATACCAGCG	180
	CTCCAGAGGC	GCTCCCGAGG	CGCTCCCGAG	GCGCCCCACG	TCTCGCCGCA	GCGACGCCGC	240
	TGCGAGCTGG	CCCTCTGGCC	ACGCAACAT	GCGCGCCGAG	GCGCCCCAGT	TATATACAGC	300
	CTGGCCTGTC	TCATATGCAG	ATGGGTCTGA	GCGAAAGAAG	TTCTCTGCTC	TCCGAGAAGC	360
	AGTCGTCTGT	ACCCTCGCGC	TCCGCGCCCA	ACCGCGCAGC	AGAGAATCTT	CCAGCGCTTC	420
	CCGCCGACCC	GCACTCGGCG	TACCCGTGCA	GCTAAGGATA	CTTCGCGGCC	GCCGCGGCAC	480
25	CACCGCCCTC	AGCCTGACTT	GCGCAACGCG	CATACGCAGA	GGACCCGCCT	GCTTCCGCGC	540
	TTTCGTGCCT	GTGCACGTGA	TCTCACCGCC	TGCTCAGCC	GCCCTCGTCA	ACGATGCGCA	600
	CCAGACCCTC	CAGAGCGTGC	CTTCGTGCCC	AAGTCGGAGC	CCA		

1626UP

	GATCCATGCA	TATTTGCGAA	CTTACGAAAA	AAGGCGTGAA	GAGGCGGAAC	GTAATCTAGG	60
	TTTGGAAGAA	TTAATGAATG	ACAACATAGA	CCTTGTTACA	GGAGAAAATA	ATGAAGAACG	120
	CCAGCTGAAA	CAAAAGAAGT	TGTTAGAGGA	GCAGTTGGCA	AAGTTGGAGA	AATCAAAGGA	180
	AAGACGACAA	GCACGCAAGG	CCGCGAAGGA	GAAGAGCAAA	GATGGCAAAG	TCGTGAAAGT	240
35	AAAAAACACC	ACGCGACGCT	GCGCAACATG	CGGTGCGATC	GGGCATATCA	GAACATAATA	300
	ATCCTGCCCC	ATGTACAATG	GTGGCGTTTG	AGCAAAACGCA	AACGCAAACG	CGAATGCGTC	360
	GAGTGCAGCA	GTGTCAGGTT	CTTCAGGGAT	GGCCTCAAAT	AATAGCGCTA	CCAGCAAGTC	420
	TATAACTCCT	AATGCCAGTA	TTCCGCCGAC	TTCATTTCAG	TAGCTCGCAG	TATAATATAT	480
	ATCTAATATG	TACCAATTGT	ACTTCTTTTC	ACTGCTATAG	AACTTTCTCC	TCTTCTTGCA	540
	TCACATGTGC	AGCACTGCAG	CACCGTGCGC	CTCGCAATAC	TTATGGACCG	CGGCACGGTC	600
40	GGCCTCGTAT	CCAGCGTACG	CTATGTATCC	TGCGGGACCC	TTATTCTGTG	GCGACACGGG	660
	ATAGTGCACA	GACTCCACAG	AAGTGTCTC	TACAATGCAG	AAGA		

1627RP

45	GATCTTCCTT	GAATTTACTT	AGCAGCTCGT	TAATTTCTCT	CTTCTTCTGC	TCTCTAAGCT	60
	GGAATCTGTA	AAAGTCCTGC	TTGGCCTTCT	TGTCCACCAT	GCTGGGAGGC	TTCTCCTTCC	120
	GTGTATGCTT	AAGAAGTGGA	TTGCGGTTCA	GAATCCTACG	CCTTATGGAG	TTTAACGATT	180
	TTGTGTTCTT	CCCTACTACA	AGTGTGAACC	CGTCCCTCGT	CACAATACTC	GATTGAACCT	240
	CATCCTGCGC	AAGTTGTTCC	CGTTGCTCAA	ATAACAACAT	ATGCTCGTGA	ATGTCGCTGC	300
	GCAAGTACTC	AAGGTCGAGT	GGCTTATAGA	AGCTCTGGAA	GGTCGCTATC	GAAGGAGACT	360
50	GGAACGCCCA	CTCCACCAAT	TCCTTTTGT	TGTGCGCGTA	TTTGCGCAGA	GCAGCCCAGC	420
	AGTTCTCCAG	AGATGCCTGG	TCCACAAACT	TCAACAGAGC	ACTGTTTCTC	GGTGTATACC	480
	TTCTGTCTTC	CGCATCCCCG	GTGTCTCTGA	AATCGGACGT	CAGCGCACCC	AAATCCACCT	540
	CGTGCAATCC	GAATCGTTCG	TGATGTAGCA	GCTCTGCCAC	ATGCGCCACA	GTCTCGTACT	600
	GCGCGCAAAT	CCTGCCAAAG	CTCTCCTTGA	TAGAGTCGAC	CTGTGTCAAC	AGAGGTAAAT	660
55	TGACAATAAA	CAGGCAATTA	GCCTCCGATT	CCACCTTCGT	CTGATGCTTC	CTC	

1627UP

	GATCTTTGAG	ACGCGGCCTG	GAGAGTTTAG	AGCAGATTGT	TGACCAACGC	ATAGCAGATG	60
	CTAGACCCTGA	GTCATACACC	CTCCGTCTTG	TTGGAGACAC	GGAATTGCTA	AATTCAAAAA	120
5	TAAAGGAGGA	GGCAGATGAA	GTGATTGAGG	CTATAACGCC	AGCTGAACTA	CAATGGGAAG	180
	TTGCGGACTT	GCTGTATTTC	CTCATGGTTA	AAATGAGGAG	CAATAATGTG	ACTTTAAAGG	240
	AGGTGGAAGC	CAACCTAAAC	ATGAAGCACA	TGAAGATTAC	GAGACGGCCT	GGAAACGCGA	300
	AACCAAGTA	CCTACCCGCG	CAGGAGTGGC	AGAAGAACAA	GGAAACTCCT	GTAGATATTG	360
	CACCATCTGC	CATTTACTTG	AACGTCGTAT	CCTCAGATGA	TGAGGCCGCA	TTGAAAACAG	420
	CAATTACAAG	GCCAATTTCAG	AAAACACTG	ATATATTAGG	TCTTGTGAG	CCTATAATAA	480
10	AAAAAGTGAT	AGAGGAGGGC	GACAATGCGT	TGACTGAAT	AACAGCGAGG	TTTGATGGAG	540
	TAAAGATAGA	AACACCAGTA	CTAGAGGCTC	CTTTTGCGCA	CGAGTATTTA	AAAGGATTAA	600
	CGGAAGACGT	CCGTACGGCC	ATAGATATTT	CGATGGAGAA	TGTCCGTAAA	TTTCATGCCG	660
	CACAGCTGAG	AGACGATATT	CTCAAGGTCTG	AAACGCAACC	GGGGGTGGTA	TGTACGAGAT	720
	CCCAGGCCA	TAGAGA					

1628RP

	GATCTGCCCC	TTTAAGCAAC	CACATATTA	GCCGCTGACA	CACAGACTGT	CAGCGCTTAG	60
	AAATACTTCG	GTGAGTGTTT	AGAAGCCCCG	GCGCTCGGAG	TTATTCATGA	TCACGTGATG	120
20	GGTATTGACC	TTGCGATCCA	CAGACAGGCG	GAAATATGCA	TATATGTAAG	CCAAGATGCC	180
	GGCAACCAAT	TGGTCTAACT	GTAATGCATA	ACACTGTATT	CCGCGAAGCG	GCTCTGAGCA	240
	TGTATGGTAT	TCGGCGCTAG	ATTGTCAGCC	CACGTATATT	TCCACGTGAC	GCCCTGATGC	300
	TATTTACAAC	ATAATCACTA	TTGACGAGCA	AGGATAGTGG	TCGCACGTTA	CGAAAAAGAA	360
	ACGTTGAAAA	ATTTGGATGG	TGGTGATGAG	TAGAGAGATAT	TAACGTTAAT	GGCGGAGCAC	420
	GAATTTGGTC	GAAGTTCTAT	ACTGCCAACG	ACGTTTCGAG	ATTGCTGAGT	TGATGGGTTT	480
25	CAAAAGTATT	AAAAAGGCGG	TAGTCCCTAA	ATTATCGGAA	AAAGCCAAGG	AGGAAGAGTT	540
	GAGCACTTCG	GGCTCCTCTG	ATTCTACTTT	AGAATCAAGT	TCATCTTCCT	CGTCGGAGGG	600
	CAGCTCCAGC	AGCAGCTCTA	GTTCTCCGG	ACAGTGAATC	GAGCTCGTCG	GACAGCGGCT	660
	CCAGCTCTTC	TAGCAGCAGC	TCGAGCTCCT	CCGGCGAATC	GGGCTCC		

1629RP

	GATCTCCAC	ACTAGGCTGG	GTCTTACTGT	CCATGAATAG	CATTCTGAAGA	ATGGAGGAAT	60
	CGGTCTTCAA	GTCAGCGGGG	AAATTTTCAG	GGCAATATAA	TGGTTCCCAA	GTATTTAGAA	120
	CTTCTCGACT	GTCGTACAGTA	CTTGGCCCCCT	TTAAATCGGC	TGTTCCCTTT	GAAGATATAC	180
35	ACCATTCATT	CCAGTGATATC	GTACCCGAAA	AATTAGCAGT	AATGGCACTT	GGAACATCAT	240
	CCGGAATCGT	GTAAGCACTT	GCAATAACTG	AAAGCTTTGT	AAGAGAGGTA	AAAATCGGTG	300
	CCGCGGTTCC	AAAAATTGTCC	AATTGTGAGA	TTTGTGTGATC	TTCATTAGGC	CTACTGGCCA	360
	GTTCCACTAG	TGATCTAACG	GGGCTTATTT	CAGTGGTTAG	AAATTTATCC	TTCTCAGTTT	420
	TCGACTTACA	AGCAAACCTCA	GTGAACAAAG	GGGGGTATCG	ACGAGCAGCT	CTTGTGTAA	480
	CTGCTGAGGT	TTTCCCCTGT	GAAATAACAT	GTTCTTTAGT	TTTATGTAGG	GCTCCAAATCC	540
40	ATGCCGTTAA	CTCTTTTATAA	CTGGTTGCTT	GGAAAATTAA	AGTACCAGAG	TTATTAGAAT	600
	ATTCTTCCTG	AGGTGAAGAA	GTTAATGGAG	AAGAGATAGT	CATTCTGAAAG	CAGTATTTAC	660
	GTGCTCTTTC	TGGATGGTGC	ATGGCACTGA	GTAATAATAC	TCCAAATCTG	TCCGTTTCTT	720
	CGACTGCAGT	TTT					

1629UP

	GATCTCGGCT	CGCTGCTCGC	GCTCGAGCCC	TACTGGGCAG	AGCGCTACCC	AATAACAAC	60
	GCCCTAATCG	GCGGTGCAGA	TAAATTGCAC	AAGCTCTACT	CAACCGATT	TGCGCCCATC	120
	GTCGCGCCCA	GGACTTTTCG	CTTGAACCTC	GTCGACAAGC	TTGGACCGCT	GAAAGACCTC	180
50	ATAATGGCAA	AGGTGAGCGG	CCCAAATTAA	TAGTCACGTG	TACATAAAGG	TTTTCTTAAT	240
	AGCTATACAG	CTTGCCCGCG	TCCTCAGCTT	GCAGCGCGCA	ACCGGCGTGC	AGCCATGAGC	300
	GTCCTACTGG	AAACTACCAT	TGGCGACCTT	GTAGTAGACC	TGGACTACAA	GACATGCAGC	360
	GCCGAGAGCT	CAAACTCTGC	CAAACCTCGC	AAAACCTCGT	TCTACGACTG	TCAGTGCATC	420
	TACGACCTCC	ATCCTGAAGG	CTCAGCACGC	CTCGGCGATC	CACAGGTGGG	CTTTGCATTTC	480
	CGCACGGATT	TGCTGTGACA	CAATACCTCG	ATCGAAGGCC	TGCGCGACAC	ACGGGCGGTC	540
55	ACCCCGAAGC	TCATTGGAAGC	CTCCGTGCGC	GCTCAACCCG	CAGAGCGCTT	CGGACAGGTC	600
	CGCGGCTTAA	TCATGCGGCT	CTGCGGCTTC	CTGCGGCTTC	TCATGCGGCT	CGCGGCTTAA	660

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CCCGAACTCG GCCCCACATC AACACAGTGC GCTTCGCGCA GGTCATCGAC GAGTCGCTGG
CAGTTCTGCA GCAGCTCAGC GA

720

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1630RP

	GATCGACTTT	CAAACATTAT	TATACAGATG	GAGGGCATCT	CACATCTTGC	ACAGCAAGAC	60
5	GGCAATCCAA	CAGGTTCTGT	AATGCAGCCT	AAGAGGCGAA	GGGTTGAAGA	TGGAGCGTCT	120
	AGTGATGGAG	AAGTACGAGG	AGAGATAAAG	CGCAAGTATG	GTATTGGCGC	GCAGTTGATG	180
	GCCAAGATGG	GATATAAGGA	GGGCAGCGGT	CTAGGGAAAG	AAGGTACGGG	ACGCACGACG	240
	CCGATATTGG	TATAGCAGCG	GCCGCAGGGC	ATGGGGCTTG	GAGCCAACGT	CTCCATTTCC	300
	TCTGACTCAG	AGCAGAGTGA	GGTGGAGCTT	GTGACTCGCG	AGGCAGTGAA	GTTTGAATCG	360
	AAAGGTGTGG	AGACTGACAC	AAGCAGAATA	GCAGACAAGA	TAGCAAAGCT	GGAGATCGCA	420
10	GGAGTGCAAG	TCCCCGCAGA	AGTGATGAGT	TTGCGTTCTG	GGACAAAGAC	GCTGGGTTAC	480
	CAACGGGCTG	CAGCGATGGA	AAGGGTGCTC	TCCGAACTGC	TGCAGGTGGG	TGAGCAACTT	540
	CGGACCCTAC	AACTACGCGA	AGATCAGCTG	CAGCAAGGGC	TAGATGCGGC	CATTCAGAGT	600
	AGTGACCTGT	TGAACAAGTT	CTCAACGCGC	TGCAACAGCC	GACTGCGCTG	CCGGAGCGGG	660
	TAGCGGCATA	TTGGCCTTGG	AGGACCCAGA	AA			

1630UP

	GATCGTCGCC	TCATCGGTGA	GCTGCGCCCC	ACGGGCGAAC	CTGGCAGCCT	GCCCCGCGAC	60
	CCGCGCGCGG	TGGGCGACCC	GCGTCCAGTC	GGCGAGCCCC	GTGGTCCCCG	GACCATGGTT	120
20	ACCGTATCGT	CCCCGACAAA	TGGCGAGGGG	TAGATGATGC	CCTCCTCCGC	CTCCGGCGTA	180
	CCGCGCGGCT	CCGGCGTGTG	CGCCTCCTCT	GTCCGGCCTG	GCCGCGTCCC	GTCCCCAGAC	240
	AAACGGTGGC	CGGCGCGCAC	CCCAACGCGC	AGGCCCTTCCG	CGGGCGGTGG	CGGCGGCGCG	300
	CGGCTCCGCG	CTCCGCCAAG	GCCCTTGCCC	TGACCCAGTC	CTGTAGGTCTG	CTCGTGGTCA	360
	TCGAAGGGCG	TCCAAGCAAT	TCGTGTACGA	TGATCTATGC	CAGCCGCAGC	CTTCGTCAAC	420
	AGCGGCGGCA	GCTGCGGCAG	CTTGGGTTTG	GTCTCGTCCA	TATCGTGGTC	TGGGTCTCTG	480
	TAGGCATCAT	ACATCTCCCG	CTATCTTTCT	CTTGCGCCTG	CACCGGTACC	GTGCATTGGA	540
25	AACGCTGCTC	CTGCCCAGAG	GCAGTTCTAT	AACGTTGCCA	GTGAAATCG	TGCAGTACGG	600
	AACAGTAGCT	CATCGCGCAC	CAGGCGAACA	CATAGGCAAC	AGCTTCGGTG	TAGCGGGCTG	660
	CGGGCCCCGAC	CACGATACTC	ATGTTACATA	GACTCACATG	ATCAGGCAGC	AC	

1631RP

	GATCTAATTT	ATTTACATTA	ATTAATAATT	AATAATATTT	AATAATATTC	AATAATTTAT	60
	ATATTTTATT	ATATTTAATA	ATTATATAAA	TACTTTTAAT	ACATAAATAC	TTTAATTAGA	120
	GAGTTAGGGT	TCACCCCCCT	AATGCTTATC	AGCATTATGA	GGTACCACCT	TAATTAAAGG	180
	TAAATATATA	TATTTAATAA	TAAAAGGATA	TAGTTTAAAT	GGTAAACTA	TTGACTTCAA	240
35	ATCAATCATT	AAGAGTTCAA	ATCTTTTTAT	CCTTGTTATA	TTTTAATAAT	ATAAATTAAT	300
	AAATAATAAA	TATGATAAAT	CATAATATTA	AAGATATTGA	TTAATATTTT	TAATTAAATTA	360
	AATAATATGC	AATTAGTATT	AGCAGCTAAA	TATATTGGTG	CAGGTATTTT	AACAATTGGT	420
	TTATTAGGAG	CAGGTATTGG	TATTGCTATT	GTATTTGCAG	CTTTAATTCA	AGGTGTATCA	480
	AGAAATCCAT	CAATGAAAGA	TACTTTATTC	CAATTTGCTA	TTTTAGGTTT	GCTATTAGTG	540
	AAGCTACAGG	TTTATTCTGT	TTAATGATTT	CTTTCTTATT	ATTATATGGT	GTTTAATTTT	600
40	ATTAAATTAT	ATAATAATTA	ATATTCAAAA	TAAGTTATAT	TAGCTTAATT	GGTAGAGCAT	660
	CCGTTTTGTA	ATCGAAAAGG	TTAGGAGTTC	AAATCTCTTA	TGTAACAATT	TAATTAAATT	720
	AAATAAAGA						

1631UP

	GATCTTAAAA	TAAGATAGAA	TGGTAATAAA	TATCATTTCAG	GTACAATAGA	TGCTGGTGTT	60
45	ACTAAAGGAT	TACCTGGAAT	ATAATTATCA	GGATGTCCTA	AAGTATTAGG	TGAAAAGAAT	120
	ACAAATAATG	AAAAGAAAAT	TATAAATACA	AATACTGTTA	CTAAATCTTT	AAAAATAAAA	180
	TAACCATGCA	TTGGTAATCT	ATCTAAATTA	CCTGTAATAC	CTAATGGATT	TGATGAACCA	240
	TGTACATGTA	ATAGCATTAA	ATGCATAATT	ACTATTGCTG	CAATAATAAA	TGGTACTAAA	300
50	TAATGAAATA	GAAAGAATCT	TATAATAGTA	GGATTACTAA	CACTAAATGA	TCCTCATAAT	360
	CATAGTACAA	TATCATTTCC	AATAAATGGA	ATAGCACTAA	ATAAATTAGT	AATAACAGTA	420
	GCACCTCAAT	GTGACATTTG	TCCATATACT	AAACAATAAC	CTAAGAAAGC	TGCTGCTATA	480
	GTTAAAATAA	AGATAATAAC	ACCAACTGTT	CATACAATAA	CTCTAGGTGA	TTTATAAGAA	540
	CCATAATATA	AACCTTTACC	AATATGAATA	TACATACAAA	TAAAGAAGAA	TGAAGCACCA	600
55	TTAAGATGCA	TATATCTAAT	TAATCAACCT	AGTTGTACAT	CTCTCATAAT	ATGTTCTACT	660
	CTAATCTAAT	CTAATCTAAT	CTAATCTAAT	CTAATCTAAT	CTAATCTAAT	CTAATCTAAT	

1632RP

	GATCTTCGCG	CCGTTGCGGC	CCAAAACCCG	CAGCTCCCAT	ATACCCGTGT	TCAGGTTGAA	60
	GCTGATGCTA	GCGTGCTGCC	GCGACACCAC	TTTCGCAGGC	CCCAGGTGCA	TGTGTACTGA	120
5	CCGGTCTCTG	GGAGACGTGT	TCCGCCCGAT	ACTCGTCATC	ATGTCCTTCA	CGTAGTACGT	180
	CCAGTCTCGT	CCCAGATATCT	TGGCGTACGC	CTGTACTTCC	GTTGCCGTGT	TCTTGTCTGT	240
	CGAATATACT	TGCGACACTG	TCGTGCGCTC	CTTCGGCGCA	TCCAGCACCG	AAATCACCCG	300
	ATTGATCACG	TCCTGTCTCC	GTTAGTACTC	GGTCTCGTGC	CGCCCGTCTC	GCTCCTACAT	360
	ACCTGCTGGT	GCTGCTGAGA	CGCAAATGGG	TAATTCATCT	CGTCGCCTCA	ATTTTCGCTCC	420
	TCCACTGGCT	GCCCCAGGGT	AACGTCGGAC	TTCCGTTGCT	GTGGAAGGGG	TGGTCGCTCA	480
10	GCGTAGCTCG	GTACAGCTGA	TCTCGGTCTT	AGTATCAACA	AAGCAAAAAT	AAAAATAATA	540
	ACAATAAGCT	TTTCACTGTG	TGTGAACGTC	CCAGAACTG	ATTCCAACGC	TCCAACACCG	600
	CACCTCTTGA	AGCAACCTCA	CGCACCCCTC	TGAATGACAG	ATCACCCCTCA	CTAAACGG	

1632UP

	GATCGAGACT	GTGATATAGC	TGTATAAGAA	GGTTTGAAA	CCTTAGTAAA	TACCCAACTT	60
	TTTTAATTCG	AACCTTGTTAC	AGGTTTTTATA	CTCAATTGTA	GCTTTGAGTT	GCAAATACCC	120
	GAGGCATAAA	ATCAAAGCGT	ACTTAAAAAC	AATCACTACA	TACAGTCCTC	CACACCCCTG	180
	CAGAGTGGAA	TAACATGAAG	AATAAATATT	AAGGACAGTA	ATGCTATAAA	TACATGTGCT	240
20	TCAAATAAAT	ATATGCTTGC	TAAGGGTTTT	CAAATTCGGT	TTGCGGCAAA	GAGTACGCCA	300
	TAAGTGGATC	TTGGGAAAGT	GATGGGGGCA	GATAACGACC	AAACAAGTGA	GTTTCCACGT	360
	TACCTATATC	TTCTCTTGGG	ACAAAACCTG	CACGTGTTGAC	CATTGTTGTG	CTAGGTGTTT	420
	GATGTATGGA	TGGAGTATCA	GCACGTCCGG	TAGAGGAAGT	GGGAATTAGT	GAACTAACG	480
	TCCCGGAGAA	ACTGGATGCC	ACACGATTGT	TTGGTAGTGT	GGGGGGCGTG	TTAGGATTTT	540
	TAATGTTGGT	TACTGGGGTG	CCTGATGGCA	ACGATGGGCC	AGAAAAGTAT	ACTTGCTCCT	600
25	GTGCTTTCAA	AGATGGGTCA	ACAGCCCAAT	TGTGAAAGAA	ACTGGCATT	CTAGTCTCAG	660
	GGATGCTAAT	AAGCTCTTGG	ACAGAGTTGT				

1633RP

30	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTTAATAATA	AATCTATTAA	TTATATAAAA	60
	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCATTTCAT	TTAATACTCC	TCTAATTCAA	180
	TCTTAAAATA	TTCTTAATTA	TTAAATTATA	TAATAAAAGT	TAGTGGATAT	AGTTTAATTG	240
	GTAAACATA	TGTTTATAGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATTAT	300
	ATCATTAATA	TAATAACTCT	TTAATTAGAG	TGGTACCACA	AGAATGCTGA	AAGCATTAGG	360
35	GCTGTGTACC	TTAGCTCTCT	AATTTAAAGT	ATAAAATTAT	CTTAACATAA	AAAAATAATT	420
	AATTAAATAA	ATAAATAATT	AATTTAAATT	AAAAATGTTA	AAAAAAGAAA	TAAATAATAT	480
	GTTATATTTA	AATAGATCAA	AATTTCAACA	ATTTCCATTT	CATTTAGTAC	TACCATCACC	540
	ATGACCAATT	GTTACATCAT	TTAGTTTATT	AGGTTTACTA	TTAACTTTAG	CTTTTACTAT	600
	ACATGGTATT	ATTGGTAATA	TTTATCCTTT	ATTATTATCT	TTATTAGTAG	TTTTATTACT	660
40	AATAACTTTA	TGATTTAGAG	ATATGGTAGC	TGAACCTACT	TATTTAGGTG	ATCATACTTT	720
	AGCTGTAAGA	AAAGGTATAA	CTTAAGGTT				

1633UP

45	GATCTTAATT	TAAATTTTTA	ATTAACATT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAATAAAAT	TAGTAAAAATA	120
	AATAGAAAAAC	CATAAGTTAA	TTGATTCATA	AAGAAAAATG	GAAATTATTG	TGGCATCTTA	180
	ATTTTATTTA	TTTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATATAA	240
	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAAATTTAA	TTTTAATATT	300
	AAATATACCA	TTTTTATTAA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
50	ATTTAATTTA	TATAAATTAT	TTAATTTACT	TCATTGATAT	ATATAATTAT	TAAATGTACC	420
	TTTCATAATA	TTTATTTTTA	TTAGTCTAGT	AATATTTCTA	TTTAATAGTC	TACCCTTTTAA	480
	TTGGATATTA	CTACCTACTA	AATATTTACC	TAATAATATA	TTATTAAGAA	TACTTTAAATC	540
	TAATAATTTA	TTATCTAAAG	TATATAAATT	AATTAATCT	TTTTTATTAT	TATTTAAATT	600
	ATTATTAATT	AGTAAATTAT	ATTTATTTAT	TTTATTAACA	TAATTTTTTG	ATAATAATAT	660
55	ATCATTATTA	AATGGTTAAT	TTATTAATAA	TTATCTTTAA	TGATTTTTAAT	GATAAACCAT	720
	CA						

1634RP

	GATCCATCTG	CGGTTTGTGC	GACGTCTCTG	GAAACTCTAC	CAGGCGAATA	GAACCTCTGAT	60
	AGACGACTGG	CAGGTGTCTG	TTGAGTGGCA	ATAACGGGAT	TTGCATCATC	TATATGGGCA	120
5	TTCTTGGTAG	TATCTATCCT	TAGACTCGAT	AGGGACCCAT	GCTTTACAAG	TTCAGGTTTC	180
	GCTTGGCGGAG	CCACGACATC	CTTTTCTCGA	TTTAGGAATG	ACAAAATTGA	GGAGTTCCCTC	240
	CTATGCTTGT	GTTCAAACATC	ACCAGCAATG	CTGGCTCGTT	TATTGGTACT	CGCAGATACA	300
	TTCTTTGAAT	GTCCATAGAT	ACTCGAAGAC	GGCCTTCCAG	TGGGAGCTGG	AACGGCCAGA	360
	CTGTCTTGTG	CACCTAGCCC	TTCTGAATCG	TTTGGAGAGG	AAAGCATGGA	AATTCGATTG	420
10	AACAACTCCA	CAAACGAGCC	ACCCGATTTT	GTCTTCTTAT	GTCTCGCTCT	TATACTCTCT	480
	TCCGGAATGG	CCCTTTCAAA	AGTACGCTGC	ATCGGAGATA	TGCCAGGATT	ACTGTAAGGA	540
	TTTCCAAGGT	CTGGGCCATC	AGGCTGTTTC	TCCACAGCAG	GCTGCATAAA	TACTGTGGGA	600
	TAGATTGCTT	TCTCGAGGAA	GTGTAAGAAG	CTGGTGAGTT	TAGGGTTTGT	GGGCCGTGTT	660
	CGTAAATGGT	AATGTGCTGA	TTCTTGGCTT	GATTCTGCAA	AA		

1634UP

	GATCACAGCG	TGGCCAAGCC	CAGCATTTGTG	TCTAAGTTAC	ATGTAGAGGT	CGAACAGCAC	60
	GAGGGAATGC	TTTTTCGCTAC	GGCGGAATTC	GAGACCTTCA	GACTGACACC	GCAGATTTTC	120
	TGTGCGGCTC	ACCGACCCCT	AAATAGCTAC	AGCAACACAG	CTGCGCCGGT	GTACACTGAT	180
20	AGCAAAGATG	AACCGGTCTA	TCCATTTCGT	GGTGACTCGG	ATGGCCTCGG	ACGACGCCAG	240
	CAGCTTTCGG	CATGAGCGGT	CGACGTACTC	GGCGGAGTCA	GAGGAAACGC	TCGTCAACTC	300
	GTATGGGCCC	TACAGCACCA	CGGGAATCGT	GATGACATCT	GTGATGATGA	ACAAGGCCCA	360
	GCGCAAGGCG	GAAGTGTCCG	AGCAGTGGAT	GCGGCTCTTC	CTGGACAGCA	CGCCTGTCTGA	420
	GGACGTGGCG	GTGCTGCAGC	GCGGGATGTC	GGTGACGGGG	CGCTGCCTGG	ACACGTTGCA	480
	GCGCATCTCG	CAAAGCATGC	ACGATACCG	CCAGATCGTC	CCGGGCTGG	CGATGTTCAA	540
25	AGAGGCATGG	AACCTGCAGT	GCTACCACGG	CAACGAGGCG	GACTTTCCGC	TGCTCGACGT	600
	GCCGATCAAG	GTCAACAGCC	TGACCACACT	GGCCAGCCTG	CTGGTCGAGC	ACCGCGTGTC	660
	CGGTTACAGC	ACGCCGATCG	AGCAACTCAC	CACGGTGCTT	CAGTACCTCA	ACAAGCTGCT	720
	GCAGGCGTCG	CGCGTC					

1635RP

	GATCCTAGGG	TGGTTTCATGG	CACCTGAGCGG	GACCGTGTTT	TTGGACCGGT	CGAACCAGCAG	60
	CAAGAGTCTG	AAGTCGCTGA	ACGCGTCGCT	GGAGCGGCTG	AAGCGCAATC	GGCAGGCGGC	120
	GTGGATTTTC	CCAGAGGGCA	CGCGGTCTGT	CACAACGGAG	ATGCAGCTGC	TGCCATTCAA	180
	GAAGGGGGCG	TTCCACCTGG	CGAACACGGC	GCAGATTCCG	GTGATTCCGG	TTGTGATGTG	240
35	CAACACGAGC	ACGGTGTTCA	ACCCGCGGCT	GGGCATCTTT	AACCGCGGCA	CGATCACGGC	300
	GAAAGTGTCTG	GAGCCGATCG	ACACGGCTAA	CATGACCAAG	GATGACGTGG	ACAAGCTTGT	360
	GAGCGACGTG	CAGGCCAAAA	TGCAGGCGGA	GTTCGAGGCG	CTTGGCTACG	CGCCTGCGAT	420
	CGTGGACACG	AGCCTACCCG	AGGAGGCGCT	GCGGCCGGAG	TTTGTGGACT	GCAAGGAAGA	480
	CATCACGGAG	GTAACGCGCC	TCTTGAAGTA	ACCCTGGTTG	GTATCATATA	AACGTTGCGA	540
	CGAGTTATGT	ACATATAGCG	CTGCTAAGTA	GGCATTCACT	CCCACGAACT	CATACCTGCG	600
40	TGAGCTCTAC	GCCCCGCCGA	TGTGGGCCAG	ATACTTGTCG	ACCTCGCCAG	CGGACCCGAG	660
	CCAGATCGAG	GACTTGTCGT	GGATGTGCTC	GGGAGTAAGG	TCCAGAAATG	CGCTCGCCCG	720
	GGTCGTTTAC	GGCCTTG					

1635UP

	GATCGGACTG	ACGGTGAATA	GGCCACCGTA	GCATGCGCCG	CTGAGCGCGC	TGGCGAGCGA	60
	TAGCAGCGGT	CCGTCCGAGG	CTCTGGTGGC	CAGGACAACG	ATCCACTGGC	CCACCACGCC	120
	CAGTAGGAGG	ACTGCCCACT	GGACTGACAT	CGTCGACACA	CCGTTGTGGA	TGCAGAGGTC	180
	AATTATCAAG	CCCGACAGGA	AGCGCGAGCA	CGTCGAGGCA	ATCGCAAATT	CTGGCAGCAC	240
50	CGACGCCTGG	CCCAACAGGC	TGCACAGCGA	GCCCATGTTG	GTGAGGAACA	TCTCCATCGG	300
	GCCCAGCGAC	AATAGCAACA	CAAGGCCAT	GAAGTACGCC	GCTGGGTCTG	GGAAGAAGTT	360
	GCGCAGCCGG	CGGCGGATGT	CCTGCGGCAG	CAGCGGCTCG	GTGGGGCTCT	GCATGCCGGC	420
	GAAGGTCAGT	GTTGCGGCCCT	TGACCTTGAG	CATAGTGACG	ATGCTCGTCG	CAAACCATAT	480
	GCAGAGCTG	ATCAGCGTAT	ATGCCACAGC	AAGAGTCCTG	AATACACGAG	AAAGGTCAAG	540
	GTACGGCGAG	CCATTTTCGAA	ACCATGGTAT	CTTCAGCAGC	TGCGACCCTA	GCACAGACGC	600
55	CTTGGCGGCT	CTTGGCGGCT	CTTGGCGGCT	CTTGGCGGCT	CTTGGCGGCT	CTTGGCGGCT	660

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TGATGCGGTG AACAGCGCAC TGAAGT

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1636RP

	GATCTTCTTC	TGCTCGATGG	ACGAGCCAGT	TGTATCTTGG	ACTCTACGGA	TAACCCACAC	60
	CTTTTCCTTC	AGCGACAGGA	ACTTGGCATC	GGTTGGGTTA	TTCGGGTATA	GATATAGCGC	120
5	TACGANCGCT	ACCACAAACG	TTAGGCTGCC	GATTATAATT	GACAGAATTT	TCCAATGTGA	180
	GATAGCTGGG	TTCTTTATCA	GCAGGATCAA	GTAGGAAAGG	ACGCCCATTG	GTATGGATAC	240
	ACTGACCGTC	GCGATAACAA	AAATCGGGGC	GGTCGCTGCC	TTTTTCATTCT	CTGTTAAGAA	300
	CATCAGCATT	GTGTTGTTCA	ATGCAGGAAT	GATAATAGCC	TCCGTGAAAC	CTAAGCAGAG	360
	ACGAAGAACA	TATACACCTT	TGTAATCCGT	CATTGCACAT	TGTACCATCA	TAATGATGCA	420
	CCATATCGTC	AGGAGGACGA	TAACAACGTT	CTTCAAAGGA	AACTTCTGGA	TAAACAGCAA	480
10	GTTGATCTGT	CCGGTAATAT	AGCCAACGTA	GAATAAGGTA	TTACATTTGT	TGTAACGATT	540
	CAAGGACATG	TTTACATCTT	CAAAAAATCC	TAACAGAGTG	CTGTAGGACA	ATTGCGCCTT	600
	GTCTATGTAG	GTGATGAAAT	TAATGCTCGC	CGTCAGTCCC	ACGATGTACC	ACATAACCTT	660
	TCGTGCAAGC	TTCTTTTCCT	CGGCTTCTGT	GATAGGAGGG	ACATCCTTGT	CTTGCTTCAA	720

1636UP

	GATCCGCAAG	ATGACCGAGG	GTAAGGGCCA	CCTGCTTTTCG	CACCACCGCT	TAGTTTCCTT	60
	TGGAGGTGCA	GGTGGTCAAC	ATGCAGTTGC	AGTGGCACAC	TCATTGGGCA	TAGAAACCGT	120
20	CCTCATGCA	AGGTACTCAG	CAATTTTATC	TGCGTATGGA	ATGCTTTTGG	CGGATGCGGT	180
	AAAAGAGGAG	CAAGTGCCAT	GCTCCATTTT	CTTGCAAGAT	ACATCTTCTA	AAGACCAGCT	240
	AAATGAAATA	TTCCACCAAT	TGATTACCAG	TACCTCAATT	AGCCTTCTTA	AGCAGGGATT	300
	GGCCGACGAT	CGGCTTGAAT	TCGAGAGATA	CCTGAACTTA	CGTTATGAGG	GTACTGAAAC	360
	AAGTCTTATG	GTTCTACAAG	AAGGAGACTC	GTGGGATTTT	GTAGAAAAGT	TCACAAAAC	420
	CCACAAGCGT	GAGTTTGGCT	TTGTTTTTCG	CGAGAAGAGG	ATTTTAGTGG	ATGATGTCCG	480
25	TGTGCGTGCT	CTAAGTAAGT	CTATGGTGCG	GAACAGGAGC	CTGTTGATCA	GCAGTTATCC	540
	CAGGTCACCTC	GTTCTACAGC	TGACCCCTTC	AAGGATGCAA	AGTTCTTTAA	GGACGTGTAT	600
	TTCGTTCGATG	GGTTTATTAA	GACCACCTAT	TTACAGGTTA	GATAGTTTAC	CGGTAGGTAC	660
	CTGTATTGAA	GGACCTG					

1637RP

	GATCTGCTCA	TACTGAGCGG	CCAAC TGGTC	GTACTCCGTA	TGCAAAACAT	CTGTGGTTTC	60
	CTGGAAGTGC	GCCACCTTGA	GCGATATCTC	ATTAAACTTG	GTAACCAGCT	CTCCCAACTG	120
	ATGATTGACT	GCACTGGTTT	CCGTCAGCAG	GTCCCTCCAGT	TCGCCAGTTC	TGGTGTCCAC	180
35	TTCCGCCACG	TATCCGCTGT	ACAATGTATA	CTCGTCGTTT	GCAGACCCCA	GAGCAGAAGC	240
	TCGCCGCCAC	TCTGGCGCCA	GCAGTCAAT	TACCTGAGGT	TCAATCTCTG	TTTCAACCGT	300
	TGCCAACAGA	GTGTCTACTT	TTTGGCGTAA	CGAACTATCC	CCAAAAGCG	GAGGCAGCTC	360
	ATCGTGAGAG	GAGGCACCGG	GATTTGCCGC	TACATCCTGT	ATGACTGAGT	TCTTCCGGCT	420
	CCTAGGCATG	GTGCAAGTGC	TGCCCTCAACG	GCTTCTCTCC	TGGTGCAGGT	CTGCAGTGGT	480
	TCGTGCTTAT	GCGCAAGCAG	AATACCATGT	TGAGCCGCGG	AAATCTCATC	ACGTGATCAT	540
40	CATCTTGCAA	CGGCTCGGAG	GACGCTGATG	CACTGTTCCA	TAGGCTTAGG	GCGCAATTAT	600
	ACGCTAGCTA	GTTATATTGA	TAATATGTAC	ATGATGCCCT	CGGCACGACA	GCGCACTCAG	660
	TGCTCGGCCG	CCGCGCCGCG	CTCCGGCAAG	CTCTTGCTCT	AAC TTGGGCC	TTCTCGGCCT	720
	CCACGT						

1637UP

	GATCTTGCCG	TCCTTCTTGT	CCAGCTGTAG	GTCCGGATGA	GGGTACGCCT	CGCTCAGGTA	60
	CTCCAGCCGC	AGCTCGCCGC	TCTCCATGGA	CGCCTCCAGG	ATCGAAGGCG	CCGGCACAGC	120
	CTCGGAGGGG	AGGGGCGGCT	GCAGGAGGGG	CATCTCCGTG	CGCTCCTGGT	GCATCTGCAG	180
50	CGCCGACGCG	CTCGGCTCCA	GCGCCGGGTC	GAAGTACTTC	ACATTTCGTCA	GGCCCGACTT	240
	GTACAGATTTC	AGGATGCAGC	CCTTGAGCTG	CGCACGGTGC	AACCGGTACG	CAGTCGCGAC	300
	ATACTGGTAC	CCGCTCGTCC	CCCCTCCCGT	GAAGTGCGGC	CGCTCCGATC	CGATCGAAGA	360
	CAGTGACGCT	GTTGGCTGGT	GGCTGTATCG	CCCCTCGCGC	GCCGGCGCTG	CGCCCTCGCG	420
	CTTGTTTACC	CACCCGAGCC	GAAACACAGT	CCCGTCGTAC	GTCTCCCCGT	TCAGCCCGCC	480
	TCCACGTCGC	ATCCGGCGAGC	CCGCCGGCTG	CGAGCAGGGC	GACACCTGCT	CCTCGCAGCG	540
55	CGCACCCGCC	TTCAATGTCT	CACATGTTCG	CGTCCGCTTG	TGCGCTTGCC	CCGTCCGGCAC	600
	CTGCTAATCTG	ATCCGGCGCTG	GTGGCTGCTG	CTGCTGCTGC	TGCGTGTGCT	GTTGCGGTTT	660

GCCTGTTGGC CTTGTTGTGT GTA

1638RP

5	GATCCTGTGCG	CTGGAAATGT	CGCGGACGAG	AACAGACAAC	CGTCGGGGGC	GGGCGGATCT	60
	GCCGGAAGCT	GTCCGAAGGA	GACCAAGAAG	GAAATTGTAA	AGCTGCAGCC	AGCGCCGATT	120
	CCACAGAACT	CTCCGTGGAA	ACCGGTGCAG	ATGGGGACGG	GGGCCGGACG	GGCCACCGAG	180
	GACGGCCGCT	GGCCTTCTGC	GCACGAGGTT	GCGACAAAGC	TTGCTGACGA	CGGCAGCGGG	240
	CGGGGGCGCT	CGCAACCGAT	GGTGACGACC	GGGAAGGAGA	AGTGGGTGCC	AATGAAGCCG	300
10	GCCATGCTTG	TGCCCCGGCA	GGGCTTGCGC	AAGATGCAAC	GCAAGAAGAA	AAACGGGCAG	360
	GCGGTCAACG	GCGGTGCCGC	GAAGCGCAAG	ACCGGAAACA	AGGCACCCCG	CAGCCAGCAA	420
	AAGAGAGCTC	CAGACTCCCA	CAGGAAGGCG	CATGACGAGG	CGAGCGCCGC	GAGCGCCACG	480
	CCATCTGCAC	CGGAGGAGCA	CGTGGAAACAG	CGCGAGCTCG	GCGAGCAGCA	GCAGGTCCCC	540
	GAGGCCGCG	AACAGGGTGC	GGAACACCCG	ACACAGCATA	TGGCGCAGAT	GCAGCCCCAG	600
15	CCCAGAAGAC	GCTTCTACGG	CGGCAGGCAG	CAGCACTCCG	CTGACGGACA	CAAGCCAGTT	660
	TGTGT						

1638UP

20	GATCTGAGAA	CTACTGTGTG	TCGGCTAGCG	CAAACCTTATC	AGAATTCCAT	CAACTCACCG	60
	AACCATAGCA	CATCTACGTC	ACCTCCCCCT	ACCGCTACAG	ATACCGGGAA	TGATCAATTT	120
	TTGCGTGTTT	ATGCTGTAAC	CATATCGCAT	GATGACAAGT	ACCTAATATG	CATGAGCAAT	180
	GACACGTACA	TTGATGTCTA	CGACATGTCA	GAATTATCGC	CTGATTGTGA	ACGCTCGCAC	240
	GAAATTAGGA	CTCCTAGACT	ATCTAGACTT	AATATTGGGA	AGCAGATGAT	GTCCATGAGC	300
	GGGCCAGTTG	GACCCGATGA	TTCGCTTTTA	CTAATCAGTG	TACAGCCACA	CGAGCTTCAG	360
25	CTATGGGATT	TCAAAAGGCA	GATTATGGTC	CAAAGATATG	TAGGACAGCG	GCAGGTGGCA	420
	TACATCATCC	GTTTCGTGCTT	TGGGTATGGG	GACAACCTAG	TTGCTGGAGG	TTCGGAAGAC	480
	GGGAAGATAT	ACATTTGGGA	TAGATATTAT	GGTAATATTA	TTGGCGTTCT	ATCTGGGCAT	540
	AACATGGAGA	GACCCGACGA	CTCCAGAAAT	AAAAACTTCC	CAATGACCAA	AGTTTGCAAT	600
	ACTGTAGCAT	GGAATCCCGT	CAATTCAAGA	CTATTTGCCT	CTGGAGGAGA	TGACGGTCTG	660
	GTGAAGATAT	AGAAAGTTGA	CCCTAATTGA	TGAATCCTAT	AGCATGACGT	TATTTGTCTA	720
30	TAGAACTTCG	AGAAATCCTG	CCGATCTGTT	GTTTCCTAAA	TTGTA		

1639RP

35	GATCCATCTG	ACTATTGTTT	CACGCGATTC	GGGGACCAAC	TGTGCAGTCA	GGCCCAGGAA	60
	CCGGGAGAAA	TAAGCCTTGA	ACGAGCGCTG	GTCGATATTA	CAGTTGTGCG	CACCTTGACA	120
	TCCTGCCTCG	TACAGGGTGT	CGTTGCTGAG	GAAGATTCTG	GCGCTGTCCA	AGAAACGCAG	180
	TGTTCCGTGG	TGCCACAGCT	CGTCTGGGT	ATGGTTGTAG	ATGAAGGCAC	AGCCTGCCAT	240
	GATCAGCCCA	TGGTTGTAAG	TCCACTGCGAG	CTTATTTAAG	TTGGTACAGT	TGTCGTTGAT	300
	GTCTGTACCG	TCGTAGACGA	CGTGCCAGTT	TGGCTGCACA	ATCGAGATCA	GCCCAACGCC	360
40	ATACATCCAG	TCGTAAACCC	GTTCCGCCCA	CTCTAAGTAT	GTGGCATTCC	CGGTGTAACG	420
	CGTTAATCGT	GCCGCCATGT	GGAACAGCGC	ACCGTTGGAA	ACGGAGTTT	TGTAGTGGTA	480
	CCCGTCGTTT	CAGCGGAAAA	TCTGCCATCT	GAGCCCGCCG	TTGCACGTCT	CCATATCCCA	540
	GCGCAGGGCC	ATGGTATTAA	ACACCGCCTG	CGCCAGCGCC	AGCCATTGCG	GCTGCTCCGC	600
	GGGCGGGTTC	GGGAAGTTGC	GCTCCGCGGC	AGCCATCACC	GCCATCCCCC	AGAAAAAA	

1639UP

45	GATCGAGCGG	GTGAGGGACA	CGGTGCACAT	AACGACTGCG	GACGGTGCCCT	GCTATGTTTC	60
	CAAGTGCGCG	ATTGTGACCG	TGCCGCAAAG	CGTGCTGGAG	CTGTCTCTGA	AACCAGAGCG	120
	GGTGCCCGGG	CGCATTTAGT	TTCGCCCCCC	CCTCAACGAC	AACATCACGT	CTGCGTTTGA	180
50	GCGAGCTCAC	TACGCCCTCG	TGGGCAAGAT	CTTCTTTGAG	TTTGACAAGT	GCACCTGGGA	240
	CACGCAGCGC	CCGCGGGTTG	CTATCGCAGC	CAAAGTTCCC	GACGACTTTA	GTGCGCAGGT	300
	CCGTAAGGCC	CAAGATTTGC	AGGAGCTGCT	GCGATCCGCC	AGTGCTCAGA	CTGAGGTGAA	360
	GCTGGGACAA	GACTGCTTTG	ACTTTCCACA	AGAGTTTCAG	AACATGGTTG	CGCTGGCAGG	420
	GATACCGACA	CTTATTGCGT	TCACGCAGAC	ACCTCTTACT	GAGCACGTCT	AGCGCTTATC	480
	AAAGCAAGAG	ATTGTGGACT	ACTTCAAACC	CGCAATTGTT	GTTGCACTAC	GTGCACTGGG	540
55	GTCCAAGGAG	GAGTGCCTCT	TCGACCTCGG	AAACACGCAA	CCGCAAGACG	ATAGTCATCC	600
	AGGCCCAATC	CTAAAGAACG	TGATCTTCAA	TCCGTGGTCA	CAGGATACGT	ATTCTCGTGG	660
	CTCATACACC	GGTAGTCACG	TGGACGACGA	CCAGCTGCCC	TTGAACGTGG	CCCTCAACAA	720

1640RP

	GATCAAGCCG	AGCACGCTGA	CCTTGGCTCC	CCGACGCAAC	ATCGGGTTGA	CGGGCTCCCC	60
	CGCCGTGCGC	TCCTCGACGC	CATCGCCCAG	CTTGGCACTG	GCGGCGTCGC	GCGCCGCGGC	120
5	GAGGCGCGCC	ATGTCCATGA	AGACCGGGAT	GTACGAGCCC	TCCGTGATGG	TGTATATAGT	180
	GTTACAGCAG	AGCATCAAGC	AGTACAGCAC	CGACATCAAA	ATGAGCGCGC	CGTAGGTCTT	240
	GCTACCCTGG	CTGACAAACG	GCGTGGCAAG	TGCGCCGTAC	ATTACAATCG	ACAGCGTCAT	300
	GAGCCACTTG	CGGTAGTTTG	AAAAGTCCGC	CAAACCCATG	AGCACAAATCG	CAATGAGGCC	360
	CTCGATGGAC	GTGTACAACG	CCCGCATATA	AAGCACATAT	GCCGTGAACT	GCACGTCCCT	420
	TCCGCCCACG	TAGATGTAGC	AGTCATCGCC	GCGCGGGCGG	CAGTGC GCGG	CGGGGTGCCC	480
10	CTTGGGGTGC	CCGAGCTCGT	GTGCGATGGT	CTGTAACGAC	GCAGGCACAA	AAGAACGCAT	540
	CATCACGTAG	GTGCGCCCCG	TCGAAAAGCA	CACAAGGAGC	CATGCAGGAA	ATACCCACCG	600
	GCCCCGCCAC	CGCGCCAGCA	CTCCTCGTCG	GCGCGCTGCC	CGCCCACTAG	CGGCTGCTGC	660
	TCGTCCAGCG	TCACTGACAC	CTGCATGTCA	GCGCCCTTGC	TT		

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1640UP

	GATCAACGAG	CTGGCGCAGC	TGCAGCTGGA	CGATGCGGAG	GAAGGCCTGG	AAGAGGCCGG	60
	TGGTGCGCAG	GAGGGCGCGG	CGCTGTGGGC	GCAATTGGAC	GGTGACGACG	ACCTGAAGGA	120
	GTACGACTTG	GAGCACTACG	ACGAGGAGGA	TGCGGGCGCG	GGTGACGAGG	TGACGATGTT	180
20	CCCCGGGCTC	TGGGGCGAGG	CGCGCTTCCA	CGAGGGTGAG	GAGGGGCAGG	ACGCGTACCT	240
	GAGCTTGCCA	ACCGTAGAGG	AGGAGCAGGA	GGAGCGGGCG	GAGCTGCAGG	TGTACCCGAC	300
	AGACAACCTG	GTGCTGGCAA	CGCGGACGGA	AGACGACATT	TCGTACCTGG	ACGTGTACGT	360
	GTACGACGAC	GGCGCGGGGT	TCCACGACGA	GGCGGTGCCG	CAGGAGGCCG	GGGACGCGCA	420
	GGACCCCGAC	GTGGCGCGCG	GGCTGATACG	GGACGCGTCG	TTGTACGTGC	ACCACGACCT	480
	GATGTTGCCG	GCATTCCCGC	TGTGCGTGGA	GTGGGTGAAC	TACCGGCCCC	GGTCGAACTC	540
25	TGACGCGCCG	GCAAACTTTG	CGGCGGTCCG	CACCTTTCGAC	CCCACGATCG	AGCTGTGGAA	600
	CCTGGACTGT	GTGGACCGCG	CGTCCCCGAC	ATGATCCTCG	GCGAGCCCCG	GGACTCTGCG	660
	ACCGCGTCCA	AGAAGTCGAA	GAAGAAGAAG	AAGGGC			

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1642RP

	GATCGCGGTT	TCGGAACGGC	TTGCTTCGCA	CAAAACACAG	GGTTCGAAGT	TACATACTCT	60
	TCAAGAAATT	GACGAGGCCT	TGAAAGCGCT	GGAGCTACGC	GGGTCAGGGA	NTGATGGTAA	120
5	TGCCTCATAT	AAGTGCAACT	GCCAGGCCAC	TATGCATCCT	CTTTTTGAGC	TAGCCCCAAA	180
	TTGCCTGAAC	TGTGGCAAAA	TTATATGTTG	CCGAGAAGGT	CTTCATATGG	ATTCTTCGAG	240
	TTATTGTGGG	ACGCTGTCTG	TACCGAAGCA	GCAGCAGCGG	GATATAGAGA	AGGTGTTGCA	300
	GCGCGAACGC	GAATTGGTAA	AAGCCAAGAG	ACAAGAGACC	GGCTCGACTG	GCAAGAAGAA	360
	GGAAAAGGTC	TTTAAGATTT	CGAACGCAAA	GGGGAGAAAT	ATGTTTCAGTG	AGCAAGAGAG	420
	GCTATTTCGAC	AAACTTGACA	GGCAGCGGGA	CGTGAAATGA	AACGCAACCA	GGTACTTGGG	480
10	GCAGAGGACT	GTCTCAGGAG	GAGGACTCGA	TTCTGAAGGC	TGAGGAAGTC	GATCCGGAAC	540
	TAAGGGCGGC	CAGGCGCGCT	TGGAGAATCT	ATTGCACTTT	CAAGACACTA	GCGAAGAGAG	600
	GACTAAAATA	ATAGATACTG	CCAGTGACTA	CAGTATGTCA	AACGACGCAG	GAATTTGGGG	660
	GTCCGCATAT	GAGAAGGC					

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1642UP

	GATCTCGTAC	CCGGTACGGT	GCGCGAGCTT	GCCGCCGGCA	GCCGCGCGCT	GCCCTGCTTC	60
	TCCGCCGACA	GCCCGCCAAA	TACCGTGTTC	TACAAGCTGC	ATGGATCGCT	GCCACAGGCC	120
	GTGCGTGTGG	CGACGCTGCG	GCACTTCTCC	TCAGACGCTG	CGGCAACCCG	GGGGAAGCAC	180
20	CTGGTCTCTGT	TTTGTACCGA	CGTCGCGCTG	CGTGGCTTGG	ACCTGCCGCG	TGTCAGCACT	240
	GTCATCGAGA	TGGACCCGCC	CTTCGCGGTC	GAGGACCATC	TGCATCGTAT	CGGGCGGACC	300
	GCGCGTGCCG	GTGTGGCTGG	CGAGTCGTTG	CTCTTCCTGC	TGCCCGGCGA	GGAAGAGGGC	360
	TACATGGAAC	ACATCCGTGC	CCACCACCCT	CGTGGCTGGG	AGCTGCTTCG	CTACGATCGA	420
	GACCTACTGG	CGCCGGCCTT	CGCGGCCCTT	GTCCGCCGCT	CCGACCGTCC	GACCACCGCA	480
	ACGGACGCCG	CCTGGGACAG	CAACGCGACA	ACTTGGCACC	TCAACGTCCA	GCGCCGTGTT	540
25	GCTCGAAGAC	CCTCCGCGAA	GGATCTTGCC	ATCAAGGGCT	ACACCAGCCA	TATCCGCGCA	600
	TACGCAACCC	ACATCTCTCA	GGAAAAAGCG	CTTCTTCAAC	GTTCGCTGTC	TGCATCTTGG	660
	CCACCTGGCG	AAAGCCTTTG	GACTTCGCGA	GCGCCCCAAA	GCA		

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1643RP

	GATCGGAACA	AGGAGCAGCA	GTCCATCCAG	CTGTGCGAGC	AGCAGCAGGG	CACACTGCAG	60
	GACAGGAAGC	CGACATACCA	AGTCATGTCT	CTCCAGAGCG	ACACGACGGT	GACCAAGTTC	120
	AAGGTCGACG	ACTCCATCAG	CAAGCGTTTC	GAGTTCATGA	ACAAGCCGAA	GGCCAAGCGC	180
	GCGACCGCGC	CGCGGCAGGC	GGCGACCAGC	AGCCCTGCAA	TGGCCTCGGG	CGCCGGCAAG	240
35	CGCGTGCACA	AGCCCAAGGT	GCAGCAGGGC	CGCGGCGGCG	CCGCGCAGGC	CGATTCCGGCG	300
	AAGCAGAGTA	ATACGCCCCAG	GGGACTTCGG	TGCGCTCGGA	GAAGACCAAT	CGCTGCAGGA	360
	ATTCTCTGTCG	CAGTCCGAGA	TTAAGAGCGA	TCTGTTTCGAA	CTGGAGGAGC	AGAACGACGA	420
	GAGCGCAAGC	TCCAACAAGG	AGAACGTACC	CCCAGCTCC	TCGTCCGTGT	TCCAGCAGCA	480
	GCTTCTGCCC	ACAGATATGG	ACGACTTTT	CAACCTCGAC	CTCGACCATA	TGAAGAACAC	540
	CGATGATGAG	TGGTTCCAGG	GCCTGTTCCG	CACTCCTCGG	GACGCGACCA	CCTGCAACAC	600
40	CATGCCCATC	GAGGAC					

1643UP

	GATCGTTGCA	AAGAAGCTAT	TACGGTGTCT	ACACGTTTCGA	GAACAGCGCC	CGATGCCATA	60
45	TCCCACACCG	CCGCTGTCAA	ACGCGTCTCT	GGGCACGAGC	GCTGACGGCG	GGAGCGCCGC	120
	AGGGCTGGCG	CAGCAGGCGC	CCGCAAAATC	GTACTACCCG	CTGGTGCCCG	ACGGCGCACA	180
	GCTCACGCCG	CCACTGTCTG	CCGTGTCCAC	GGCCGGCGAT	GACGCCGGCC	TCTACCGCTA	240
	CCACAAGCAG	ATCAGCAAGT	CGTTCCAGGA	CGACCTGATC	TACTGCCCGC	GCGCGCTGCT	300
	GAGCAAAGTC	GAGCTGACGC	AGTGCTACCA	GCTGGACATG	CTGCTGCTGA	TGGAGCAGCA	360
	GCAGCAGGCC	CAGCCGAGTG	TCAAGTTCAA	CCCATATACG	TCGCAGAGCT	TCAACCCCGC	420
50	GGGCCCCGCA	TCGCCCCGCT	CCTAGGGCCG	GCGGGCCGCC	CGGGACCATT	TAGTTCGACN	480
	GAATCNCTAT	GTCAAGACTG	ACGCTTGCTC	GCATCCGGGT	TTATGTTTTA	TTCCAGTT	

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1644RP

	GATCCCTTTGC	AAATTCGTCC	ATAGGAATGT	AAACGGACCT	GCCCTCCAC	CTCTTGGTAT	60
	TGCAAACAGG	CATCTTGAGT	TCGTTTGGCC	ATTCCATCTT	TATATGCTGT	TCTTCATCGC	120
5	AAGGCACATT	TTCGTCTTCT	TCGGGCTTCT	CAAAAACAAC	CTTATGCACT	CTCTCAGTAA	180
	TATACACAGG	GTACGGGGTC	GCCGTCCCTG	AACATTAGGA	AGAACCAGCC	AAATGGGCCT	240
	GTGCCCTGGCG	ACTGGCCGGA	CTTCTGCACK	AAATCCCACC	TCAAGTATAT	GACCATCAAG	300
	TCCCTGAACC	GCGTGCTAAA	CTGCTGGTAT	GTTGTGTGCA	TATCTAGCGG	ACCGGGAGCT	360
	AGCGAATCGG	TATGCGGCAC	TTCCAATAGG	TAATCGCCCG	GCGTTTGGA	CGGATGGTAT	420
	ACCCTAGTAA	CTTTGCCTGC	AAACTCAATA	TGGGGCTTGG	GCTTTTTCCT	GTGGGCCTGG	480
10	TTTGTAATTG	GTATCAATGT	CTGCGGAGAT	GAGATGGAGC	TGTCGCTCGA	AGATATGTCC	540
	TTTAGCAGGT	TATCGTCTTC					

1645RP

	GATCTTTGGAA	GAGGAGGACT	ATTCAAGTAA	AATGGCACGG	CGGGAAGATA	AGATGGAAGA	60
	GGAGTGGATA	CGAAAGTACG	AGCGTGAGAA	GAAGAAGAGA	AAGAGAGGCG	CATAATCCCC	120
	AGTGTAATAA	ATCAATTCCG	CCGGTTCGCT	GCGCTGTAGC	ATAATAATAT	GTACGATAGT	180
	GGTCAGATAA	GGTATTTCAA	AAGTTAGGCA	ACCCATGAAA	CATCAAACCT	TTCAATGCAA	240
	TGATATGTAA	GTTGCATATA	TTACGAGCTG	TGAAATAGAG	AAACTCAAAT	GAATACTTTT	300
20	ACCACACCAT	AACAAACGCA	CAATGTTACG	AGAATGAAGA	CGATAATGCA	GCTTGAATAG	360
	TGCCACCATG	GCGCCATATG	GTACCTACTG	AACAGCAGAA	GCAAGCTAAA	CGAGCTCAGC	420
	ATGAGGGACA	CCACTAGAGA	TACCAGGATC	AACGCTGTGA	TATAATTACT	ACCTTCAAAC	480
	TCAGTCTGGT	CATTTCCAAG	AGCGCTGAAC	AATGAAAACA	TGATTCCAC	AGTGGTACCT	540
	GTGGTTATGC	AAGATACGAG	CAGGGTCGTC	AGGTAAAACA	ATGAGACCAC	CTCATCGTGC	600
	TTGTATCCAT	ATAGGACATC	AAGTTCATCG	TAACATACTA	GCGCAGCCTC	GTCATCCCAG	660
25	TTTGGAACCT	GCAGTTGGCT	ACCACTCCCG	GCAACGTGCT	TTGCAC		

1645UP

	GATCAGCGGC	GGCTGCGCGC	GCTGTTGCCG	TAGCGCTGCA	GCAAGCTCGC	GCGCGCCGCC	60
	GCGCTCTGCG	CCTGGCCCTC	CGGCTGCCGC	GCACCGCGCT	CGGGCGTCTG	CCGCCCAAGC	120
	TCCAGCCGCG	TCGGGTTCCG	ACTGATCAGC	TGATCCACCG	TGCTGCCGTC	CCGGCCGGCC	180
	CTGTCCGGCG	CCGCCGGCGC	CTCGCCCGCC	GCGCCATCGC	CGCGGTACAC	ACGGCTCTTC	240
	GGATCGTACC	GCGTCTCTCT	GCCGCGCACG	TCGTGAGGAT	ACCGCGCGCG	GTCATGCCGC	300
	GGCCGGATCG	CAGGCGCCCC	CACGCCCGCC	CGCGCCGCC	GCGCGTCCAG	TCCCAACTTG	360
	TACCGTTCCA	CTGCTGCCGC	CGCGTCTCT	CGCGCTGCCG	CGCGCTCCGC	CGCCCGGGCC	420
35	GCCACTGCCG	GCGCCACCGG	CCCCTCGAAC	CCGTACCATC	GGTCCCGCTT	GGCCTCAAAG	480
	CTCAGCGCAT	TCTCGTCCCG	GACCTGAAAC	GCGCGCTCGC	CACCATCGCC	CCGCGCCTGT	540
	TTGCGCGGCC	GGAGCAGGCA	GTCGCGCCGG	TCATGATTGG	CGCCGAGTT	TCGTGCACCG	600
	CCCGCGTCCG	CGCCCCGCC	CGCGCGCGC	TGCCCGCCAC	AAAACGGTCA	CTTATTACCG	660
	AACCTGCTGA	GCCACCGAGA	AGTCTTGAGC	GCCCTCGCCG	GGCTC		

1646RP

	GATCGAGAAC	CGCATGGACG	ACAAGCCCAA	CGTGGTGATC	CTGGGGTCCG	GCTGGGGTG	60
	GATTTTCGTT	CTGAAGCACA	TCGACGCGCG	GAAGTACAAC	GTGACGGTGG	TGTCGCCACG	120
45	GAACACTTTC	CTGTTTACGC	CGCTGCTGCC	CTCGACGCCC	GTGGGCACGG	TGGACGAGAA	180
	GTCGATCATC	GAGCCGGTGG	TGAACTTTGC	GCTCAAGAAC	AAGGGTAACG	TGCTTACTA	240
	CGAGGCGGAG	GCGACGTCGA	TCAACCCGCA	CCGCAACACG	GTGACGATCA	AGTCGGTGT	300
	GACGGTAGCA	CAGCTGTGCG	ACCCGGACAA	CCACTGGGG	CTGACGACG	AGGACTCCGC	360
	GGAGCTGAAG	TACGACTACC	TGGTGTCTGC	GGTGGGCGCG	GAGCCCAACA	CGTTCGGCAT	420
	TCCGGGCGTG	GAGGAGCAGC	GCAACTTTT	GAAGGAGATC	CCACACTCGT	TCGAGATCAG	480
50	AAAGCGCTTC	CTGTGCAACG	TCGAGAAGGC	GAACCTGTTG	CCCAAGGGCG	ACCCCGAGAG	540
	AAAGCGTCTG	CTGACCATCG	TGGTGTGTTG	CGGTGGTCTT	ACCGGTGTGG	AGACCGCGGG	600
	TGAGTCCAGG	ACTACGTGCA	CCAGGACCTG	AAGAGATTCA	TGCCCTCCAT	CGCTGAGGAG	660
	GTGCAGATCC	ACCTGGTGGA	GGCCTTGCCC	AACGTGCTGA	ACATGT		

1646UP

	GATCAAATGG	GTTAGCCCGT	CTCCAACGAG	CCCTGCAACA	TAGTGGCAGT	AGCGGTTCGTA	60
	GTCCTGGATC	GTCTCCAACC	CGCTCAAATT	AAACTTCTCG	TCCAGAATGT	AGTCTGCCAT	120
5	GCCGTTGCCC	ATCTTGTGTG	TGATGTCTGC	AATCACCTGC	TGGTACTCGG	GCTTCAGCTT	180
	GTGGAACCTG	GCTAGAATCG	TGCTGAACTC	CACCAGCACG	TCACGGTCCT	TCTCCGTCTT	240
	CGCGTTGCCG	TCGAAACTCC	ACGTATCCAG	CTTCAGTTTC	TGGTCGAACT	CCCGGAGTAG	300
	CGGCACCTTT	ACCTTGGGAC	TGATCGTCAT	ATCGTCTTCA	ACAGTATCCA	GCGCACGCAG	360
	AATCAGGTAG	AACAGCATCA	CCGCGTTGCG	CAGCTCGGGA	TGTAGCTCCA	TTATCACGGC	420
	CGCAAAAGAC	TCGAAGTCCG	CTGTAGCAGC	TGGTAGCACC	GCTTGAGCTC	TGCAGAGCCC	480
10	TGCGTGTCTG	CCGCAGGATA	AAGCGGTTCC	CTCAGAAATT	TGAGCTTCAG	AGCTGCCTTC	540
	AGCTCCAGTG	GGTGTGTGAA	TAATTGAACA	ACCTTCCCCA	TGGTCACGAT	TCGATTAAAGT	600
	AATTGCCAAT	TATGTCAAGC	GCCTGTCACT	TGGTGATGTC	GCGCTTGCTT	GTACAGG	

1647RP

	GATCCAGCTA	GATAGCGTGC	CAATTGCTGA	TAAATCCTGC	CAGAAATGCGA	TAACGCCTCT	60
	CTGAAACGCG	CAACGCCTCC	GGAGCGCCAG	GAGCTGTCTGC	GAGATGCGAG	GCGTCTGGAC	120
	TCCGATGCACA	ACTAATATTG	AATTCAGTAT	CCCAGCAGTAG	GCGGGTACAT	AACTGCTTAC	180
	GTACTCCAC	TACGACACTG	CGCCCCGCAC	GCTGCACGTG	CGATGCGGCT	TACAAAGACC	240
20	AAGTCTTTGG	CAACACCTGG	ATATGGTATC	CATCGGGGTC	TCTGAGGACG	GCGAGATTCT	300
	TGATAGACCC	CTTGTGTGTAG	CGCAACTCCC	ACTCCAGGTC	CGGGTACGTC	TCCTCGATGT	360
	CAGCGCAAAG	AGGCGCAGGG	TCACTGAGCG	ACACACCCAT	GTGGCTGTAC	CCCGTGGGCT	420
	CTGCGTTCCC	GTTGTGATAC	GAGAAGTCCG	CGTCATCCTC	GGTCCCCCAA	TTGTGCGTCA	480
	GCTCCAGAAAT	GCTCTCGCGC	TTCAACCGCT	CGTCCGCTGC	CGGATACCCC	AGGAAGTAGA	540
	GGGTGAATTT	CGCATTTGCG	TGCTCGCTCA	CCTCCAGTAG	CGACATACCT	AGCACATTCT	600
25	GGTAGAACTC	CAGCGACTTC	GTTGCGTCTT	TCACACGTAG	CATCGTGTGG	TTAAACTTGG	660
	GCCCCAGGTC	CAC TGGCTCC	GCGTCCGACA	AGTTGTACTG	TATCAACTCA	ATCCAGTATC	720
	CGTCGGG						

1647UP

	GATCCGAGCA	CGGTGCGGGT	GCAACAGAGG	AAATATATGG	CACTACAGAC	AGTGCACAGA	60
	TGCAGGAGCT	GCGCCGCCTG	GCGCGGCAGC	GCTATCTGGA	CCGGCGGGAG	AGGGAAAAGC	120
	TAGACTGGGC	AATACGGGAC	CTTGCATTGT	TAGAAGAAGA	CGTAAAGAAG	TACGGATGGG	180
	ACAAGCTGAC	GGAAACGGGAG	CGAAGAGAGA	TTGGGACCAA	GCGGCAGCTC	GTGCAAATTG	240
35	TGCGCGAGCG	CGATCGCGCG	GCGGCGGGCG	CGGAGCGTCC	ATTCCATATG	CCCGCGGAGA	300
	CCGTTGTGGA	GCTAGCTGCG	CGGCAGGAGA	AGAGCTGGGA	GGAGCAGCAG	GTGCAAAGG	360
	CGGTGCGCGC	GGAGGGGCGC	TCGGACATAA	TTGAGGTGGA	GGGCTCTGAA	CAGTACGAGT	420
	TTGTTCTGGA	CTCGCGGTCC	GTTGTGCGCT	TTACAGAGGA	AGAGACGCTG	GCTCCCGGCG	480
	AGCGTGTCCG	GAAGCAGCTC	GAACAGAAGC	TCGAGAAGGA	AATTAAGCGC	GTGGCGTCCG	540
	TTCAAGAAAC	TAGGAGGCAG	CTTCTGTGT	ATGCGTACCG	CGACGAGCTT	CTGAAGGCGG	600
40	TGCGCGACCA	CCAGT					

1648RP

	GATCCAGCTC	ATGCAGTGCG	CGATTCCAGC	CCTGCCCTGTC	GTTTAAAGTC	TTGAAGTAGT	60
45	TGGTGCTGAA	ATGCTTGTC	AATTTGTACA	GGTATCGTTT	CGAAGATTTT	GAGAATAGTC	120
	CTTCCACCAC	TTTCAATGGG	TTCTCTCTCGA	ACTTGTCTGAG	GAATGAATTC	TCCAGCTTGG	180
	AGAATGCATG	CTGTGAAGAG	TATATACGAG	ACCCAGCTTT	CGCCACGAAT	TTGATGAGCT	240
	GATTGAAGTC	GTTGCGCATG	TCGCTCTCGG	GTATGAATCG	TGGCACAGTC	AGCGTCAAAG	300
	CTCGCTGCGT	CATAGGACGG	TATGGTCCCG	GTGGGTACTC	GTGGACATCG	AAGTTATCAA	360
	GCAGATAGAA	ATCCTTGATT	TTGCCCTTGT	CTGCGAGAGA	CCGCAGGTAC	GCCACGAAAA	420
50	GGTGGTACAG	CGCGCTTCCC	CGGTTACGGT	AGATCTTGTT	CAGAAATAAGT	TCGTCGTCGT	480
	TGCTTTCATC	GTTGGCATCC	TTGTACTCTT	CTACCGCCTT	GCAAGAGGGG	AAACACACCT	540
	GGCCCGCGGT	GAATATTAA	TCCATCTGCG	TCGTCCTTCT	CACCAACAGG	TCCGTACGCC	600
	CAACGATCGT	CACCAGGATT	TCCAGAAAA	CGTAAGTCGT	GCACATGT		

1648UP

	GATCTAGCAG	GTGTTGAACA	GATAATGGAA	TGGCTCTCCT	ATATTCCAGC	TAAACGTAAT	60
	ATGCCCGTAC	CTATACTGCA	GTCAGAGGAC	AACTGGGATA	GGGATGTTGA	ATACACACCA	120
5	ACACTTCACA	GCCTTATGAT	GTACGCTGGA	TGATTGAAGG	CCGCCAAGGA	CCTGATGGAT	180
	TTGAATATGG	TCTGTTTGAC	AAGGGTTCCT	TCCAGGAAAC	ATTATCAGGC	TGGCGGAGAG	240
	GCGTCGTTGT	AGGCAGAGCT	CGCATGGGTG	GTATCCCGCT	CGGTGTTATT	GCCGTTGACA	300
	CTCGTACAAT	TGAAACTGTG	ATCCCTGCCG	ATCCGGCAAA	CCCTGCATCC	ACAGAAACTT	360
	TGATTTCAGGA	GGCAGGCTTA	GTTTGGTATC	CTAACTCAGC	ATTTAAAACT	GCGCAGGCCA	420
	TAGCTGATTT	CAACCACGGA	GAACAACATC	CACTCATGAT	ATTAGCAAAC	TGGAGAGGGT	480
10	TTTCTGGTGG	TCAAAGAGAT	ATGTTCAATG	AGGTCTTGAA	ATATGGCTCC	TTCATTGTTG	540
	ATGCTCTAGT	GGATTATAAA	CAGCCTGTAT	TCGTATACAT	ACCTCCAACA	GGTGAGTTGA	600
	GAGGTGGTTC	CTGGGTTGTG	GTGGATCCTA	CAATTAACTC	TGACCAGATG	GAGATGTATG	660
	CTGATTCCGA	CTCGCGGGCA	GGTGTGCTAG	AACCTGCTGG	TATGGTTGGT	ATAAA	

15

1649RP

	GATCAAACGC	AAAACGTGTA	CGCAGAAAAA	AGTTTCGCTG	ACAGACGACA	TGCTCGCAGG	60
	GCACCACGGG	GTGGGCAACG	GAGCGGTCCG	GTTTCCAGCG	ATGGACCTCG	GGGCGACCAC	120
	GAATCTTTTG	CTAAACAACA	CTATCAACAA	GACCAAGTTC	AGTCAGCTAA	AAAAACGCGT	180
20	AGATAGTATC	GAAGTGCATA	ACCAGCAGCT	GCGCGCAGAG	AACAATAGTT	TGAAAATCGA	240
	ATTCCAAAAG	ATGAGTTCCA	GATATAACTC	CATGGTGGAG	AACCTCGTGT	CTCTTAAAAA	300
	CTACAATAAT	TCCCTCGTTG	AGAACTTCAA	TCTGCTGGTA	TCCACGCTGG	CGCAACAGGG	360
	CCTGAAGGTT	CCCCATCCAT	TAAACCTCGG	CAACTATGCA	TCTTCACAGG	TTGCCAAAAA	420
	TTCATCTGCT	TCCGACGTTT	AACCGCATGT	ATCGCCGTTG	GGTACTGTAG	CACCTACGAA	480
	CATACCCCTT	GCGCAGGCTA	CCCCGTCGAA	AGAAGAGGCC	AATCCTCCTA	CAAGCCTGCG	540
25	CCCAGGCTTC	CATGTTCTGC	TGGTAGAAGA	ATGATTCGGT	TGTATCCAA	CTATGTTCCA	600
	AATTCTTGAG	AAAATATGGC	TGTTCCGGTG	AAGTCGTAAC	GGACGGCCTA	TCTGCTATTG	660
	AAACAGTAGA	GAAATTCCAG	TACGACCTCG	TTCTGATGGA	TATCGTGATG	CCCA	

30 1649UP

	GATCGCTGGC	GCGGGCAGCC	ACATGCGGGC	GCATTTGACG	TTCTACCACA	TGCAATCTAT	60
	GGCGGCTGTG	CGCGCGTTGC	GCCCGCAGGG	GAAGTACGGG	CTGCGCGAGC	CGCCAGCGGA	120
	GGCACCACCC	CCGGCGTTGC	CCGACGTGGA	TGTGGTGCTG	ATGCCCCGTC	TAGGGTTCTG	180
	CGCCGATACC	GGCGCGCGCC	TCGGACGCGG	GGCAGGTTAC	TACGACAAC	ATGTAAGCCG	240
35	TACGCAGCAG	CTGCACGGCA	GGAGACCGCT	GCTGGTTGGG	CTGGCGCTCA	GCCAGCAGCT	300
	GATGTTGCAC	GTCCCGCTAG	AGCCGCACGA	CCAGTGCTTG	GACGCGGTGG	CCTGCGGGCA	360
	CGGACAGTTG	AGGTGGGCGC	ANCGCGCGCC	CGGGGAGATA	GTTGATATAT	AAGTGTATCT	420
	AGCCTGTAGT	GAAGCTCCCT	TTCCGACGCA	CGAATGTCCG	CGTGCCGCTC	TGGTTGATGA	480
	TCTCGGCCCTC	CAGACGGACG	TTGTTGCCGT	GGTCCTCGAC	GCGGGTGGTG	CGGACCACAA	540
	CGAACTGGTT	CGCCAGGGTC	GGGAAACAAT	ACAAGATCTT	GATGTGCTCG	GTTACCTCCT	600
40	AATCGGTGCC	GGTCACGAAT	GTGACTGCCT	CCCGCATCAG	GTCGCTCAGC	ACCGTGGCCA	660
	GGA						

1650RP

45	GATCGCTCTG	CCGGGACTCG	ATTTTTGTGC	ACCGGCCACG	CAAGAAGGAC	CTTGCGTGCA	60
	TCATGTACAC	CTCGGGCTCG	ACAGGTGACC	CGAAGGGTGT	GTCGTTGACC	CACGCTAACA	120
	TCGTGGCGGG	CATTGGCGGT	GTTTCCGTTG	TGATCAACCG	CGCGATTGTG	AAGCCTGACG	180
	ATCGTGTCAT	CGCGTTCCTG	CCGCTTGCGC	ATATTTTTGA	GCTTGTGTTT	GAGTTGACCT	240
	GTCTCTACTG	GGGCGCCTTA	ATTGGCTACG	GCTCCGTCAA	GACGTTGAGC	GAGGCTTCGG	300
	TCCGCAACTG	TAAGGCGAC	ATGAAGGAGT	TCCGGCCGTC	CGTCATGGTC	GGTGTGCGAG	360
50	CTGTCTGGGA	GGGTGTCAGG	AAGGCTATTG	TTGCGCAGGT	CACTAAGTTG	CCTCCGTTCA	420
	AGCAAAAGAT	ATTCTGGGCG	GCCTACCACA	CCAAGCTACG	CATGAAGAAG	TGCCACATTC	480
	CAGGCGGCGA	TCTAATAGGA	AGCATGATCT	TTAAGAAGGT	GCGTGAGACC	ACTGGTGGCA	540
	ACCTTCGCTA	CATCTTGAAT	GGTGGCTCTC	CATTGTGCGC	GGATACGCAA	GTTTTTATT	600
	CCAACTTGAT	TTGCCCCGTG	TTGATTGGTT	ACGGCTTAAC	GGAGACTGTG	GCGAATGGCT	660
55	GTATAGTGCC	TCCACACCAC	TTCAAGTACG	GGGTTGTGGG	AGACAT		

1650UP

	GATCCATTTC	TCATGGAGAT	TAACGCTATA	TGCGAGGAAA	GCAATAACAA	GAAGCAAGCC	60
	AAGAAGTCTG	TTAACTTCTC	TATGCTAGGG	TTGACTGATT	TTACCAAAC	CAAAAAGCC	120
5	GATACTACAG	ATGTCTGGAG	AGCGTTTAGG	ATGTACGACG	AAGTACAAAT	GAAAAAGAGA	180
	TTTAGTTATA	AATGGGATTA	TGATAAAGTG	TCCAGGGAAT	TGGATGAAGA	GACATGGAAT	240
	AAGATTATTA	ATAGGGAAAC	TTTGAATTTA	TTTGCATTAG	TGGAAAGATA	TACGGTAAAG	300
	ATTGAAAACG	ATGCCAATAT	AACCTATTGG	AGTTCTGTCTG	TTATGCGCAA	CTCCTGTCTGC	360
	AAGCATGAGG	CTACAGGAGT	GAGGCAATGT	GCCAACTTCT	TCTGTGGTAA	ATGGGAAGAC	420
	CACCCGAAGC	AGTTTCCCAA	GTGCCGCCGT	TGCAAGCGCA	CAAAATATTG	CAGTTGTGAG	480
10	TGTCAACTAC	AATCTTGGGC	ATATCATCGG	TACTGGTGCC	ATGATGTTGG	CTCTGTCTTC	540
	ACGGGCACCT	CCTCAACGGC	AAACACCACT	GGGACACATA	CGCCAAATGC	TGTCCGGTCAG	600
	TCGGCTGGAA	CCACGACCAC	TACTACCACG	GCGGCTACGG	AGGTAGATCA	ATCCATTTTG	660
	ATGACAGCAA	GGGG					

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1651RP

	GATGGCGACG	TTTACCGAAG	AGCAAAAAGA	AAAGTACGCG	ATGGCGTTGA	AGGACAAGGG	60
	GAACGAGTGC	TTTAAGGACC	AGCGGTACGA	GGAGGCGATC	AAGTTCTACG	ACTGCGCGTT	120
	GAAGCTAAAA	GAAGACCCGG	TGTTCTACTC	GAATCGGTCTG	GCGTGCTACG	TGCCCTTGAA	180
20	CAAGCTGGAG	AAGGTTGTGG	AGGACACCAC	TGCTGCACTA	AAGCTGAAAC	CCGACTATTC	240
	TAAGTGTTTTG	CTTCGTCGTG	CAACAGCTAA	TGAATCGTTG	GGTAATTATG	CTGATGTAT	300
	GTTGGATTTA	TCTGCCGTAT	CTCTATACGG	CGGGTACAGC	TCGCAGACAA	TGAGCCCGT	360
	GCTGGAGCGG	AATATGAACA	AGCAGGCTAT	GCAAGTATTG	AAACAGAAAC	TCTCTGGTGG	420
	AGAGAAACAC	GAACCTCCTT	CCAATACTTC	CTTAGCGTCT	TTCTTCCGCA	TCTTCCCTTC	480
	GGAGACATCG	TTGGAGAACT	ACGATGAAAC	TTCCGAAGCA	GACCGCATTC	TTCTCAAGGG	540
25	ATTGTGCGCC	CTACACGCGC	GCCAGGCAGG	CTCCTATGAA	ATTGCTGATG	AAGCCTTTAC	600
	CGATGCTGTA	GAAAAGTTCA	CC				

1651UP

30	GATCGTGATT	TTGCGGGGCT	GCATCCTGCA	GGCTCCACAT	CATGCCGTGC	GCCAGGCTAT	60
	GCTGAACATC	CCCAGCGGGG	TCTACTGCAC	GTTCCGTGGG	CAGTCATCGC	CTGCGATCCA	120
	GTACGGTATC	TCGTCTACAA	ACTTCATCAC	ACACGTGAAT	GAGATCGAAA	CCCCAGACCT	180
	GGACCGCTTT	CTCGAGGTGG	TACGCACGAT	ACCAGACAAC	ACCTACTGTA	AAATCCGTCT	240
	TGTGACCTTC	GACAACGTGC	CTTTTGCTAT	CTCCCTGAAG	ACAAACTACC	ACTACTTCCC	300
	CACCAGCGAG	CTCTCCCGCA	ACTCCGACAC	CGGCCGCTGG	ATTGAGCACC	TCTGCAACGC	360
35	TACCCCGCTG	AAAAACTAGC	AATAGACTGA	TATCTCTTAT	AGAACGTATA	AACTATTTCAC	420
	ATGTAACCCG	ATCACGTGAC	GAGCGCTGCA	CGCAGCTCGT	GCAGCATGCT	CAGTGGTATG	480
	GCAGTAGGCG	CCGCAGACGC	TTCAGATGGG	CACCTCGCCG	CATGGTCCGC	CCAGAGAGCT	540
	GCTTCAGCGC	GCGCTGTCCC	AGCCTGTGTT	ACCGTGGCTG	CGGCCAGCCT	TCGAACGCTT	600
40	GTACCTCCTG	CAGTCTTCCG	CCATCTCTTA	GCTGCGCCTT	TGTGCGTCTT	CATTAGTGTC	660
	CGCACCATGA	TCAGCGACG					

1652RP

45	GATCTTCGTT	CGTGAAAACC	TTGCACGTCT	TCATGAGCTC	AAGAATTGCC	TCTGCATCTA	60
	TTCTGTCCGG	TTGGATTCTG	CCTTCCTTAT	TGTCCTGAAT	CATGCGCGCA	AAAGCGCGCG	120
	GCGTCCAGTC	ATGACGGGAT	CGGCCCTTAT	AGGACTTCCC	TGCAAGCCGC	ATGAGGCTCC	180
	GCCAGCCATT	TTCTTCAATA	ATATTGACAA	GTCCTTCGTT	TTCCAACACG	ACCTTGTTTCG	240
	CGAGACTGTG	GAACGTGTTT	ACGTCTATCT	GCTCAAGTAT	TTCTACCCTT	TCCTCAGCAG	300
	ACCATCGCAA	GTTCGAATCT	GCCTCTTGA	ATGTCCTCCAT	AAGCTTTTCA	TTGATGTTAT	360
	CCACTGCTTT	ATTTGTCAAG	GAGAGGATTA	GTATTTTCATT	AGGAGCTACA	ATCCCTTCGT	420
50	AAACCAGGTT	GTAGACTTTA	TGCAGTAGTG	TCACGGTCTT	GCCAGACCCA	GGTCCCCTGA	480
	CCACATTGAC	AGTTGTACAA	GGCTCATATG	GATGTGTTAC	TACTCGTGAT	TGGGACGTCG	540
	TCAGTGCTTT	CATTCAATGTA	TGATACATGC	TCGAGCGTCG	GCGAAGGAAA	TAAATTCGTG	600
	AATTTCCGTT	TTAAGATACT	CAAAAGAAAT	GAGATAACCG	CCCGCAAGGG	CGGAGTAGAA	660
	TTACAGCAGC	TATTGAATAT	ATTTAGTTTA	TT			

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1652UP

	GATCTCCCCA	CCATTCTCCT	CCAGCGCCTT	CTGTNAGCGT	TCCCGGCGTT	GCTCTCTCGC	60
	CTTTTGCTTC	TTCTCCTTAC	GGATTTTCGC	ATACAGCGGC	TTATTCAGTT	CGAACTGTTC	120
5	CTTCTTCCAC	TGTTTCTTCC	ATTGCGACTT	CGACATGCCT	TCGGGAACGG	GCGGCAAGGC	180
	AGCCCGTGGT	TTTGGCCGAC	TCAATGTTTC	ATCATTATTA	GTTTCAGGAG	TCATTGCCCA	240
	GTTTGAGGAC	TCTTAGCGCA	AGGTCTTGTC	ACTGAAGTAC	AGTAAAATGG	ATGCCCTTTC	300
	GCGGTGATGA	GGCAATGACC	TGGTGAAATT	TTTCGCCCAT	GGTGAGGCTG	TATAGTGGTC	360
	ACGTGACAAC	AGTTCAGCCC	ATATATGGAG	CCCCTAGGTC	ATATAAAGGG	TCAGGAGCCC	420
	GCTAAAGTCT	TTGTATTCTG	ACCTTTTATT	GGGGAGCTTT	AGGGCGTGTG	TCTCTATCCA	480
10	GAGCCGTGTG	GTGAAAAGCG	TCTCAGCTCA	GCGCGTTCTA	CTACACTGAG	ATTTAAAAAC	540
	CAACAGCGAA	GCAGCAGAGT	ATGACGTCCT	TAGCAACTAA	ACTCGAACTT	CCATGGGTTG	600
	AGAAGTACCG	GCCGAAGCTG	CTGAAAGATG	TGTGGGAAAC	GAWGAAACGG	TGGAGCGCCT	660
	GCAACAGATG	CCAGGGATGG	AAATATGCCA	CAC TTGA			

1653RP

	GATCTTTGAT	GCTATTTTCGT	ACCTTAAGGG	CTGTTCCGTG	CTGGAGATGA	TCTCCGGCTA	60
	TATAGGGGAG	ACCGTCTTCC	TGAAGGGTGT	TGCCTTATAT	ATAAAGCGGA	ATAAGTTTGG	120
	CAATGCTACC	ATGGAGGACC	TGTTTGGGGC	CATTAGTGAG	GTAGCAGGCC	TTGATCTCAT	180
20	GGCGAAGGCA	AAAGATTGGA	TTCTAAAGAT	CGGGTACCCG	GTTC TGGA CA	TCACTGTGTG	240
	TGATGGGAAG	ATTTCACTGT	CACAGAGACG	GTACCTTTTCG	AGCGGACAAG	CTGACGCCAA	300
	TGACGACCTA	ACCACCTGGT	GGATTCCCTT	GGAACTGACA	CAGGACTCAA	CTTGCACTAC	360
	AACAGAAATG	GTTTCTAAAT	CCCAAGAAAC	AGAGATCTCA	GCTACCGATT	TTGTGTTCTT	420
	TAACAACGAT	GCCCACGGCT	TCTTCCGGGT	GCATTATGAG	GATGAGACTA	TTCTGGCTAA	480
	CATCTGCAAG	AACATAGCGC	AGCTGTCCTC	ACGCAGTAAA	ATTGCGTTAA	TTTCGGATGT	540
25	TGATGCCACT	GGTACCTTCA	CGCAACTCAT	GGCTGTTCTG	TCTGCATTCT	CTGCAACGCA	600
	TTCGCAAGAC	TACTATGTTA	TGGAACCTCTG	CATTGTCCAT	TTTCCACTCG	GCCTGCTCAA	660
	TCATATATCG	CGATGCGTCG	CAGAGATCCG	CAAGAAGCTT	GCGGCGT		

1653UP

	GATCTAATAC	TGGGAGCGAC	TGGGCGTTGT	GGCGGTGTCT	ATCTGTATGC	GAACCAGCGA	60
	GGCTGTGATG	GAGACANATT	GTACTACGAT	GTCTGCGCGC	TCATTGCTGT	GAACGGCCGA	120
	GTTGTGGCCC	AAGGCTCGCA	GTTTTGCTG	AGGGATGTCG	AAGTGGTTAC	TGCAACTGTA	180
	GACTTACAAG	AAGTGAGAGA	TTACCGGATG	TCTGTGATGT	CGCGAGGGTT	GCAGGCAGTA	240
35	TGCAATAACG	TGACTTTTCA	ACGTATTCAA	GTACCTGTAG	AACTGGCCGC	GATGCAAGAT	300
	AGGTTCAATC	CTACGATTAA	CCTGACGAAG	CGGAAAGCCC	CATACTATCA	CAGCCCAGAG	360
	GAAGAGATTG	CGCTGGGCCC	AGCTTGTTGG	TTATGGGACT	ACCTACGTCG	TTGCAGAGGA	420
	ACAGGCTATT	TTCTTCCACT	ATCTGGGGGC	ATTGACTCAT	GTGCCACTGC	TGTAATTGTG	480
	CACTCTATGT	GTCCGGATGGT	TGTCAACGAA	ACATCTGAGG	GTAATCTGCA	AGTAATTGCA	540
	GATGCGAGAA	GATTGGCTCG	TGCTAGCGAT	GACTGGATTG	CAACCGATGC	ACGTGAATTT	600
40	GCAAAATATGA	TATTTACAC	TTGTTTTATG	GGAACAGCAA	ACTCCACAAA	TGAGACTCGC	660
	AGTCGGGCAA	AGAAACTTGC	GGAACACCT				

1654RP

	GATCTTATTA	ATTTTGATGG	TGCTATATTC	TAAATTCAAG	TAATGATAGC	GCGTGATGCG	60
45	GTACGTACCT	ATACATATAA	CGCACAGTTC	TCCATCGTCT	ATGCGTGTAT	GAAAATCACT	120
	CCAGCCGTGC	GACACGCCAC	GTGTAATCTA	GTGAGTTTCA	AGTTCTTCCT	CCTCATCGGC	180
	AGAAAGTTTC	CCCGCGGGCG	TGAGGTTCTT	GAGCCGCTCC	TTGAGCTGCG	CGATAAGGCT	240
	ATTCTCCCTT	TGAGCATGCA	TGCGGATACC	CTCTAGAGAC	ATATGAGCCG	AATCTGCACC	300
	ATCTAAACCA	TGTTTCGCTGT	TGCTGCCAGT	GGCAGCTGCC	AGTTTGGGAC	TGGACAGACC	360
50	TGTCTGTCCA	TCTTTGTAAG	AATCCTCGGT	CGTTGCCGAG	TTGGAATTCA	TGGTTCCCAT	420
	AGTGTGCAAG	ATTTTCTCCT	CTTCTGTTAG	TTCCAGATGG	GTACCTGTCA	GATTGATCAA	480
	GGACCTGCCG	CTTTTACGCG	GCGAGAGCTT	GGGCAGAAGA	GAGTGCCCGG	GTTGGCGTCTG	540
	CTTCAACCAAG	GTTTGTAATG	GAGGTGTGAG	ATCTCGGAGT	CCTTGGTAGT	CTCAGACA	

1654UP

	GATCCGGGGCC	GGGTCCGCSG	CAACCAACGA	TGTACGCTGT	GGATACCAGC	GACCTGGTAG	60
	GCGTTACGGT	GGGAGGAGCA	GCGGTTGGCG	GAAAACCCGG	AGCAGAGCAA	GTACTGGCTG	120
5	AAGTGGGGGC	CGTATCTGTC	GGAGCGGAGC	TGGGCGACGG	TGCGGGAGGA	CTACTCGTTT	180
	GACGGCGACG	CGTGGCGGCA	CTTCCCGTTC	GAGCAGGCGA	ATGCGCGGGT	CTTCCGGTGG	240
	GGCGAGGACG	GGATCTTCGG	CGTGAGCGAC	AACCGGCAGC	TGGTGTGCCT	GAACGTGGGG	300
	ATGTGGAACG	GGCGTGACGA	GCTGCTCAAG	GAAGCGGATG	TTGCGGCTGA	CCGGGCCGCA	360
	GGGCAACCAC	GGGAGGACT	GCAAGGAGCT	GTACTACTAC	CTGGACAACC	TTCCGAGCCA	420
	TGCGTACATG	AAGGCGCTGT	AYAAGTACCC	GNTCAAGCGG	GCGTTCCCGT	ACCAGGAGCT	480
10	TATTGCGGGC	AACGACGCGC	GCGGGTACGC	CGAGCGCGAG	CTCGAGGTGT	ACGAACCTGA	540
	CGGGCTGTAC	CGCGAGGCGG	CGACCGGCGA	C			

1655RP

15	GATCCACTTT	CCACTCTGAC	ATCGGTCAAT	CAACGCTGGG	CACTCAGGTT	CAGTTCTGAA	60
	GCAATTGCAG	TCCCCGCGAGT	TACCCCTTCAT	TTATTTAGAG	ACTTAGTGGT	GTTATAAGTC	120
	AGTCCTATCG	AACAGCTCTC	GACAGTCATC	GGAAACGAGA	AGTTACCCGC	CCTTGAGACA	180
	CAATCTGTTA	CCCGACTTTG	ATTTACATGC	GTTACCCGCT	CTGGGTACAG	TGCCGGGAAG	240
	CACATGACAA	AGGCCGAGAG	CTAGTTACGT	GAGGCTCATT	GGGGTATGCC	GGAAACTCTA	300
20	ATGACTAGAT	CATCCGAGAA	GCACCGGTAT	ATAAGACGCA	TCACGGTGGT	GCTCGAGAGA	360
	GTGTGTAAAA	TGCCAATTGC	TTAGCCACTG	ATGCCAAATA	CACTGGATAA	GAGTTACGTA	420
	CAAAACGGCC	CTTGGAGGGA	CGGGGTGTTT	CAAGGGAAAG	TGGTCTTCGT	CACTGGCGGG	480
	GCCGGGACGA	TCTGCAGGGT	GCAGGCGGAG	GCAATGGTGC	TACTTGGTGC	CAAGGCTGCG	540
	ATCATTGGGC	GCAATGTGGA	GAAGACTAAG	AAGGCGGCAG	CGGAGATCGC	GGAGTTGGGC	600
	GACTCGGCTG	ACTGCGTGCT	CGGAATTGGC	GGCGTGGACT	TCCGGGAGGT	CCCGGACATG	660
25	AAAGCGCGCG	GTGGAACAGA	CGGTTGCCGC	GTTT			

1655UP

30	GATCTCTCTG	ACCGCCCCCA	AACGCTGCTC	CGCGCACATT	GACACTGGTG	TTACCACCCA	60
	TTATGTCGGC	GGCCGTTTCA	TCCCAGATGC	CCTGGCCCGT	CGTCATGGTT	TTGATCCGTT	120
	CCCGTACTCT	GGCACCGATC	AAATACTGCG	TATTTGAGTG	CATATTGCTT	TATTCTATAG	180
	TCTGCGTACA	TAAGCCGGGG	TTTCAGAGGG	CGGGTAACGA	TGACGCGTAA	CGTTTCTTTT	240
	TGCTGATATG	TAAAAAGAAA	TGTGCAACAA	TTTTTCATGA	GATGAACGTT	ATACTGGCTT	300
	GTCTCTCTCT	TGAAGTCAGC	AATCTCTAAC	CTTTGAAGGT	GATTAATAGG	CTGTTGCGTC	360
	GTGTTGGAAC	ATTGACGGAG	CTTTGCTTGT	TGTAAGCGAT	TAATCTGTGT	TGCGAGTTTC	420
35	ACTTTCTCGA	ACTGGTAGCA	GGTCTGACGG	GTCTGCGAAG	GGCGTGGAG	ACTTGCAAAT	480
	ATAGGCGCAA	GACAACCTGC	GAGATACAGG	GGAGCTGCTG	CAGCGAACAG	GTGGAGTGCA	540
	GGCGGATCTT	GAGGACTAGC	TGCTCTGGGA	CGAGATGGCG	AAGGAAAGCC	TGCGGATAGG	600
	CGTAGCAAGC	ACGGAGCCCA	AGCGGGTGAA	GGTGTTCATC	CTGGAAGACA	GCGAGTGGAG	660
	AGACACTGGG	ACGGG					

1656RP

45	GATCTAGCGA	TCAATCGCAG	CTAACAGATG	CTCTGACATT	ATGCATGAGC	GCAATCATGA	60
	TGGACACATC	GAAGCTCAAG	CATAAAGTAG	AGGACTCGGA	CATGCAAGCG	TACGCCATCT	120
	GCAAAAGCGT	GTTGACCAAT	ATGAACGAGG	ATGCGTACTA	CAAGCGCATG	AAGGCAGCAA	180
	AGAATGACGT	AGATGGCTTC	TCACTCGATG	AGATTCTTCG	TAAGGACTAT	AAAGAGTTGG	240
	TGTTCCCGAG	CCGCGAGTGC	GATCTACGTG	TTGGCGTACC	TACTGTCTGT	CGCTCTTTCG	300
	AATGGATGCG	CGAGAAGTTC	GGCGACAATG	GGACTACGAA	GCTCTGGCAC	AGTTTCCCTC	360
	TGGAGCATAA	GTTAGATTTT	CTCGTGGTGC	TCACAATTAA	GAAGGCCAAC	GAGGGTTTGA	420
	AACGGGAGTT	GGCTATCATG	GCCAACCTCT	GCGACCGTGC	GCAGCAGGTC	GAGTTCTTGA	480
50	TCCAAAGCCT	CACCCAGAG	TTGCAGTTGA	GCAAGACCTC	TGTCTTCTCC	CCCGGCTCAC	540
	TCGTCAATTG	ACCGTGCGAG	CAGAGAATGC	TATCTGCCAG	TCGCAAGCAA	ATAGTACCTC	600
	TCCTCAAGAG	AACCGTCGCC	GAGTTATAGC	ATGCTTATGT	AACTAACGTT	CCAGTTACCA	660
	CTTCCACACA	TCTCAGCGGC	AATGTCGCGT	TTGTGGTCTC	CAACC		

1656UP

	GATCTCTTCC	TACCCTGTAT	TTCTACTTAG	CAGGAACCTA	AATATGTCGA	AATCATCGCT	60
	AGTAGGATGT	TTTTTCTACA	ACACAGACAT	TTACGCCAAC	CAGAACGCTA	AGGCATGCAG	120
5	TATCTCGCGG	AGTATCTGCC	TAGGATCGGC	GTAATGCTAA	TAGTGCTTGC	GGGAGAGGCT	180
	GGTGAGGTTG	AACTGGGAAA	ATTGGGTGGG	CATAGGTTGA	CTGTACAGT	AAATGGAGCG	240
	GCCGAGGTGA	TCGAATTGCC	CTGTGAGGTT	GATCCGCTAG	CGCGGCCGCG	TATTAGACAC	300
	TCCGAAGGTG	CATTTGAGGT	CCGGCTGAAG	GCGGTGAATG	GGACTGAGGG	CCGGGGCGCG	360
	GACTTCACTA	TGCTGGCTGC	AGAGGACGGG	TGGGGGCGAA	AAGACCTGGC	GCGTGTGAA	420
	CTGCGCTGCG	CGGCGTGCGA	CGGGCTGCTG	GTTACGGGCG	AACATGCAGG	CGCGTGAGCG	480
10	CGATGCCCTC	CGAGTTTGG	ACGGAGCTGA	TGGACTACTG	GCACTGCCAC	AAGCCTGCGG	540
	ACGAGTCTGC	GGGCGCACAG	CAGTACCTGA	CGAAATATAA	CGCGCTGCTG	CCTGCGGACG	600
	GGGAGCTGCT	GGTGGGGGAC	ACATTCTGTA	CGGTCGGCGA	GGGTCTGCTG	TCAGAGAAGC	660
	TGGCGATGAG						

1657RP

	GATCGATTTA	GATTTACCT	TCAGGCACAC	TAAGAGATGG	ACTCCTTACA	CTAAGGGTGG	60
	GCTGACGGGC	GGCGTTGAAC	GTGTTTTGCT	CGACGGACAG	ACTGTCTGTG	TAAGCGGTGA	120
	CCTAGTACCA	TCTGCAGCTC	TAGGTGAGGC	CGTTGTACCT	ACTTCAAACA	ATTACACTTC	180
20	GACTCCTCTA	TTGAACGCGG	AGCCATTGCA	CAGCTTTGTT	CCACCTTCTA	GCTCGGGTAA	240
	GAAGCGGTTT	TCCTTCTCCC	GCGAGCGGGG	AAACTCGTTT	GCTTCAGCTG	GTGACCACGA	300
	GGAAGCTGTT	ATCGACCAAC	CGCTGGAACA	AAGGTTGATG	TCTTCAAGGC	CACCAAAGGA	360
	GCTGTGCGCC	CCAAGTGCGC	TGAGAGAGCT	AGTCCGTGCG	CACAATCCAT	TCAGAGGAAG	420
	GAATATCTTA	TCTGTAAACC	AATTCAAACG	TTCGGACTTC	CACGCCTTGT	TCGCTGTGGC	480
	CCAAGAGCTG	CGTGCGGCTG	TCGAGAGAGA	GGGCGTTCTC	GAATTGATGA	AGGGCCGCCT	540
25	CTTGACGACC	ATATTCTATG	AGCCATCAAC	GCGCACATCC	TCCTCTTTTA	TCGCGGCAAT	600
	GGAGCGCCTC	GGTGGTAGAA					

1657UP

30	GATCAAGTCC	TTCCAGCCGA	GCCAGTCTCG	CACCGCATAC	CAGAAATGCA	TTCGCGCACC	60
	TAGCGGGATA	TTCTGCGCGC	TGTACTCGGT	CCACGAAAAG	GCCCAGCGGT	GTGCCAACGC	120
	AAAGGCTACC	ATCTCCAAAC	AGAGCGCCAC	ATTGTGGTAC	ACGTAGCCCA	TGTTCTGTGCC	180
	CSCGAGTCC	TGAATCAGCT	TCAGGTAGTG	GAGAAGCGTG	ATKACCATAC	CCTGCCAGTA	240
	GGATGCAAAA	ATGATCAACT	TAACACATAA	GAATTTAGGC	CATGGGTTGT	ACTTGCGCAA	300
	CTCGTTGTAC	AAGCACTTCC	AGAAGAGCGC	CAAGTTATAG	AGCGACCATG	ACGCGCTCGC	360
35	GTTGTATACA	AGCGTCAACC	ACTTACATCC	CAGATCCCAC	TCCAACACCT	GGAACGCAGA	420
	CATCCCCAAG	CAGTACACCG	GCTTGAACCA	CACGTACTGT	AGAATGCCCC	GCTTCACAGC	480
	CAATAACGCC	TTGGGGTCCG	CCATATCGAC	CATGGGCAAC	ACCCAACGTC	CCACAACGGG	540
	AATCGGGTGC	TGGATCCTTT	TCTGCTCCGG	CGCAAGGT			

1659RP

	GATCAAAAGT	TGATTAAACT	AATAAAAGAA	TTATTTTATG	TATATTGATT	GTATAGTCAT	60
	TTTCAGACAA	AAATCGTGGA	AATTTTAGCG	GCCAAACATA	AAAGTCAGAC	ATTAGAAACT	120
	GACAGATACT	TTATTTACTG	CATAATTACA	CTAAAAACAA	CTGTTCTCAA	AAACTACGGA	180
45	TTATTGACCG	CCCCCTCACT	AATAATGTAC	TCCTTCTATC	GGTTTCTTGC	GGGTAGAAGC	240
	ACGTAAAGAG	ATCAGTTTCA	CTTTGCAATT	TGGGCACTTT	TACGTTTCCA	CCTAACGATC	300
	ATTCTAGTGT	ATTTTATGAC	CAGGAAAGAA	AAGGAGCCTA	AAAACCTGAA	GGCAGCCAGA	360
	CCAGCGACTG	ATCCCAAGAC	AAAAACCAAA	TATTTGTTAT	TAGAGGTTTC	TTCAGGTGAG	420
	TATATTGGGG	TTATCATCAT	GATCAAAATC	AAATTGGAAA	GCATCCATAA	CATGACAATT	480
	CTAGTCCGCA	CATCACGGTA	GTGATCTGCT	TGCTTTTGGA	TAGGATCAAC	TTTTATTTCT	540
50	ACCATTTCAT	CCGATTTTAG	ACGACCTTGA	TTTCCTGGTA	TTTATTATCG	ATGTCCTGTG	600
	CCCATTCAGT	ACCCCTCAACT	ATTTGTTTGC	CACGGGGCCC	TGGGTAACCA	TAGCTTCAGA	660
	CTTTGGCTTG	GACCCCTGCG	AAGCGCCTTT	TGT			

1659UP

	GATCGAGTGG	TCCACCAGGT	AGTCCTGGCC	CGGCTTCACG	TTGGGCGGCG	TCGAGAAGTA	60
	GACCCGGTAC	TGCTTGCACG	CCTTCTTCAC	CTCCTCGTAG	CTGCCCGTCA	GCCCCACGAT	120
5	GTCCGGGTGG	AACTCGGCCA	GGTACTCCTT	CAGCACCGCC	GGCGGGTCCC	GCGCAGGGTC	180
	GCACGTCACG	AAGATCGGCT	GCACGTCGAT	GCCCCGTTGT	TTCAGTCCGC	GTAGCCACGC	240
	CGCCAGCTTG	TCCAGCTCCG	CAGGGCAGAT	GTCCGGGCAG	TGCGTGAAAC	CGAAGTACAC	300
	CAGCGAGAAC	CGCCCCGAGAA	GGTCTCTCTC	CGTGAACCTG	TTGCCGTTGA	AGTCCACCAG	360
	CTGGAACGGC	CCGCCACCCG	CCGGCCGCC	GTACCCCGGG	TTCCGCTCCG	CCTCCCGCTG	420
	CACCTCCAGC	CGCCGCTTCT	CGCGCGAAAA	CACGTAGAAC	AGCCCGCCGC	CGAGCACAGC	480
10	AGCACCGCCG	CCGCCCTTCCA	CGTCGTGAAC	TCGATCGCCC	CGCCCTCGAC	CGCTGCGAGT	540
	GCGTTTCCTG	CGCCCCCAGC	GGGATCCGGC	TCAACGGCCG	CCGCTTGCCC	GGCGCCTCTG	600
	GCCCCCGGGC	GCCTCCTGCG	TCGCCAGCCG	TGTTGCGGAG	AACTCCCGCA	CCCCGCCAAA	660
	CGCTGCTCTC	TGCCCTTGCAA	TTCCCGCAGC	TTGCCCTGCAA	ACACCGAGTC	CTACTGATCA	720
	TCTCTG						

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1660RP

	GATCAATTTCG	ATGCCAACCA	AGATGAAGAC	CATCTGGGTG	AGTTAGCAGT	GCACTCTGCG	60
	GATACATGGT	CTGAGACGGA	TAGGAATCTA	ATTTTGAAAT	TATTGGGCAA	GTTCAAGAAT	120
20	ATCAAAGCTA	TTTACAAATC	CGAAGATGTC	CGCCAAAGGT	TGATGGAATT	ATTGGGTAGT	180
	CGAACGCTGG	AAGTGCAGAA	ACTGGCCCTA	GATGCGTTGT	TAGCATACAA	GGATCCAGTA	240
	GCTGTGAAAT	ATAGGGACAA	TCTGAAGAAC	TTATTAGATG	ACACGTTATT	CAACGACGAA	300
	GTAACAAAGT	TATTTGCTCA	GAATGAGTCA	AGGGTTATTG	TCAACACTGA	TGAAAGATTA	360
	TTAATGCCCT	TCATTTTGCG	TATTTTATTT	GGCCGTGTC	AGACACCTAA	TACCAGTGGG	420
	ATCAAAAAGA	CAAGAAAAAC	TGCGGTCATA	ACTGTCTCTG	CAAAATTTAGG	TGAGAAGAAT	480
25	ATTACTGACT	TCCTTGGCTCT	GGGTAGTAAT	GGTATCAACT	ACCAGTACTT	CTTTGAAGAG	540
	AATGCGGTTA	TTCTTGACAG	TGAGCTTACA	GCGATAAATT	TTAGGAGAAT	GCTTGGCTTC	600
	ATAAATGTCC	TAAGTGCCCTC	GTTGAATGTT	TTAGGTTCCA	ATTTCCCGGA	GGCGGTCAAG	660
	ACAACATATTA	AACCTCTCGT	TTACGCAATT	CACATGTCAG	GTCGTACTGG	ACAGAATAAA	720

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1660UP

	GATCTTATAG	ATTTTTCATCC	CCAAGCTTAC	AAAGAGAACG	TTATCCACCT	GTTTTAGCCA	60
	GGCTTGGATG	TATTTTTTCAA	TGGTACCCAT	GTCTCTCTGG	CCCAAGTTCT	TGAACAAGTT	120
35	AGTTAGTAGC	AGACTAGCCA	TCCTCCTGCA	TTTAGGAGAG	TCGTCAATTA	CTGATACGTT	180
	TGCTAGGAAC	ACGAAGAATG	AGGATGAAAG	TTTCATTAGT	AAAGCGGGCC	CAGATTTGTT	240
	GATCAGAAGG	TTAAGCAATT	CCATAACAGA	TTGACGACCT	TCCTTGAGATG	GATACTGCAA	300
	ATTGTTGACT	AAAAATTTCA	ATTGTTTTTTC	CAGCCTGCCT	TTACTTTGAT	CATATTTCCAT	360
	GAAGAACTGG	TAATAGACAC	TCCTGGCAAC	ATCCCTGATT	TCCTTAGCAT	GATTCGTGAC	420
	CATGACTTCT	GCAACGTTAT	CAATAATATC	GTACAGCTTC	GGAGAACAAC	TATGTTTGGA	480
	AACCAAGGAT	TTCAAAAATC	CAAAAGCCAG	ACCTTGCTTA	TTGGGCTCCA	TCAAATCTGG	540
40	TTCAATCCGA	CCCAAAACAT	ATTTCGAGCG	AGAATCCTTT	AATTCAATGT	CTTTATAGCG	600
	GATAAGCGCA	GATAAAAAT	TCAGACCGAC	TTGACAAAGT	TCACCAGAAG	T	

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1664RP

	GATCCTAGGG	TGGTTCATGG	CACTGAGCGG	GACGTGTTCT	TGGACCGGTC	GAACCGCAGC	60
	AAGAGTCTGA	AGTCCCTGAA	CGCGTCTCTG	GAGCGGCTGA	AGCGCAATCG	GCAGGCGGCG	120
5	TGGATTTTCC	CAGAGGGCAC	GCGGTCTGTAC	ACAACGGAGA	TGCAGCTGCT	GCCATTCAAG	180
	AAGGGGGCGT	TCCACCTGGC	GCAACAGGCG	CAGATTCCGG	TGATTCCGGT	TGTGATGTGC	240
	AACACGAGCA	CGGTGTTCAA	CCCGCGGCTG	GGCATCTTTA	ACCGCGGCAC	GATCACGGCG	300
	AAAGTGCTGG	AGCCGATCGA	CACGGCTAAC	ATGACCAAGG	ATGACGTGGA	CAAGCTTGTC	360
	AGCGACGTGC	AGGCCAAAAT	GCATGCGGAG	TTGAGGGCGC	TTGGCTACGC	GCCTGCGATC	420
	GTGGACACGA	GCCTACCCGA	AGAGGCGCTG	CGGCCGGAGT	TTGTGGACTG	CAAGGAAGAC	480
10	ATCACGGAGG	TAACGCGCCT	CTCGAAGTAA	CCTTGGTTGG	TATCATATAA	ACGTTGCGAC	540
	GAGTTATGTA	CATATAGCGC	TGCTAAGTAG	GCATTTCAGTC	CCC		

1664UP

	GATCCGACTG	ACGGTGAATA	GGCCACCGTA	GCATGCGCCG	CTGAGCGCGC	TGGCGAACGA	60
	TAGCAGCGGT	CCTTCCGAGG	CTCTGGTGGC	CAAGACAACG	ATCCACTGGC	CCACCACGCC	120
	CAGTAGGAGG	ACTGCCCCACT	GGACTGACAT	CGTCGACACA	CCGTTGTGGA	TGCAGAGGTC	180
	AATTATCAAG	CCCGACAGGA	AGCGCGAGCA	CGTCGAGGCA	ATCGCAAATT	CTGGCAGCAC	240
	CGACGCCTGG	CCCAACAGGC	TCGACAGCGA	GCCCCATGTT	GTGAGGAACA	TCTCCATCGG	300
20	GCCCAGCGAC	AATAGCAACA	CAAGGGCCAT	GAAGTACGCC	GCTGGGTTCG	GGAAGAAAGTT	360
	GCGCAGCCGG	CGGCGGATGT	CCTGCGGCAG	CAGCGGCTCG	GTGGGGCTCT	GCATGCCCCG	420
	GAAGGTCAGT	GTTGCGGCCT	TGACCTTGAG	CATAGTGACG	ATGCTCGTCG	CAAACCACAT	480
	GCAGAAGCTG	ATCAGCGTAT	ATGCGACAGC	TAGAGTCCTG	AATACACGAG	AAAGGTCAAG	540
	GTACGGCAGG	CCATTTCCAA	AACCATGGTA	TCTTCAGCAG	CTGCGACCTA	GCACAGAC	

1666RP

	GATCCTTGCG	TACTAAGAGT	TAGACTTTAA	TTAATAATAT	TATTTGTAGA	AGATAGAAAC	60
	CATACTGACT	CACGTCGTAT	TTAACCCATC	TCACGTAACC	TTTTAATTGA	CGAACAGTCA	120
	AACCCTACTT	AGCTGTTACA	ACCAAGAGGA	TAGGTTGAGT	CGACATCGAG	GTGGCAAACA	180
30	TAACTTACAA	TAGCTACTCT	ATCGTTATAT	TACCCTGTTT	AATTTTGTGA	TCATAATTAAC	240
	ATTTAATTAT	TATTTCAATA	ATTCTCATT	TTGTTTCAGC	TATTTTCATT	TGTATTATTT	300
	ATTAATTAA	ACATATTGGG	CTTTCGTGGA	TATAATTATT	GTTAATCCTA	CTCATATATC	360
	TAGTCGTTGA	ACGTTCTTAT	AACTTTATAA	AAAGGATTGT	TATAAGCTTC	GCTGCAGATT	420
	GTCTTTTATT	ATTATAAAAT	AATATTAGGA	GTTCTTTGCA	ATTAACCCAA	TTTACTCAAT	480
	ATATTTTAAAT	ATTGATAATT	AAATTTTACA	ATTTAATGGG	ACTATTAATT	AATCCCTAGC	540
35	GTAACTTTTA	TTCGTTATCA	AATACCATT	CAATATGTAT	ATTTTTGTTC	ATTATGCCAA	600
	ACTTACGTTA	TTGTTCTACT	TGTAGGTATT	ACAATTATAG	CACAGTTATA	CCATTATATT	660
	TATTTAATAT	ATTATCCCTA	TATTATGTTT	TATTAACATA	TAAACTGTGA	CAT	

1666UP

	GATCCTTATA	AAATGGGCAA	TAGACGTGTT	ATAATATAAT	ATACAAAATT	ATAAATAAAT	60
	ATTTAATAAA	ATATAAAAT	AATAATTAAA	GTATTATAAT	AATTAATAAA	ATTATTTATT	120
	AATAAGTATG	GATTTTTTAA	TGAAATTTGT	TAAAAATGAA	TAAGAATTGC	TAGTAATCTA	180
	TTAATAAGAA	AGTAATGGTG	AATACTCTAA	CTGTTTCGCA	CTAATCACTC	ATCACGCGTT	240
45	GAAACATATA	ATTAAATAAA	GAATATTAA	TAATTTATTA	ATTATTAATT	ATTATTAATA	300
	TTATTTAATA	AATATAATAA	ATATTTTAAT	TTAAATTATG	AATTAATGCG	AAGTTGAAAT	360
	ACAGTTACTG	TAGGGGAACC	TGCAGTGGGC	TTATAAATAT	CTTTAATATT	CCATTTTTTAT	420
	AAAATAAATA	TATTTTTTTAA	TATATTTTAT	AATAACTATA	ATTAAATAGT	TAAAATTTAA	480
	ATTATAATTT	AATAATTTAA	TAACCTATTA	ATTAGAGAGT	TAGGGTACAT	CCCCCTAAT	540
	GCTATGCATT	ATGGTTGGTA	CCACTCTAAT	TAATAAACTA	TAATAAATAA	ATACTAATAT	600
50	TTTATATCAA	TTAAATTATA	ATTATTTTTT	ATTAATATTT	TAATATTATT	TAATGAAATA	660
	TATAAATAAA	GTATTAT					

1667RP

	GATCCATCGT	GGTGTGCTTC	ATTACCTGTA	ATTCCATTGA	TATCCTGGCT	ATGCAGTGCT	60
	GGAAACGCTC	CTCCAGCGCC	TCTATTTTGT	TATTCAGCTC	CAAGTACTCC	GCGAGCTTAA	120
5	AGGTCAACGA	GAGCGACCTT	GGATTGCACC	TGACGGCGAT	CTCAAGGACC	TTCTCGTGCT	180
	CGTTCTCGTC	CACAAACATG	GCGTAGTTGT	ACCATATCTC	CGGCGCAAAG	CACATGTGCT	240
	GCACAGCCTG	GCGGTGCACG	TATTCCACGC	GCTGGCGCAG	CACGACTTCG	GGCAGGTCGA	300
	GCTTGTTGTG	CAGCTCCCAC	TGGATCCACT	TCGTCCAGAT	CTGCAGCTGG	TACTCATCGT	360
	ACTGACCGGG	CGCAGGCAGG	TTCTGCTGTG	TCGCCTGGTT	TAGCTTCGTG	GGCAGCGAGC	420
	GCCGCAAGCC	CTTCGTCAGG	TTCGACCACT	CCTGGTACAG	CGAGCGCGCA	TTCATGTAGC	480
10	TCGCCGAGAG	CTCTCCGATG	AACTTCCGCG	CCGTCAACTG	GTTGACCTCC	TGCTCCCACT	540
	GCGTGATTTT	CTCCCAGTAC	CGCTCCAGCG	ACTCCACTGG	CAGGCACAGC	AAGGCGCTTG	600
	TACAGCTTGC	GCAGAACTCT	GACCCGGCTC	TGCTCCTCCC	ACTTGCTCAC	CGGCTTCCAC	660
	TGCTCCAGAA	ACTGCAGGTA	GTCTTGCCAG	AACTGCATCG	ACCGCGG		

1667UP

	GATCTAAGGG	ATGGGTGACT	GCTGCCGGTG	CTCACAGCAG	TGGCACGTAG	CTAGTAATGG	60
	TGCGAAATCG	ATCAAAGAGG	GTGCGTCTGG	CGGTACAGGC	AGAAAGCACG	CCCCCGGATA	120
	CAAGTTCCAG	TTCTACAAGC	ACCTGCAGTT	CCAGGGTACG	AGGTACCAGG	TGGTGACTTC	180
20	GCGGCCGTAT	CTGATAGAGC	GGTACGGGGA	GCGCAAGGCG	GCGACGATCA	GGTCGTTTGT	240
	CAAGTGCATC	CATCCGAAAA	TCAACGACGA	TGTGACACGG	ATCAGCGACG	AGCGGGTGAC	300
	GCACGGGGTG	TCGAAGTGGG	AGAAGTCGAA	GCTGTTCTTG	CTGCTGGTGA	CGCTGTCCGA	360
	GCGGGGCGGG	CCGGAGTACT	GGCTGGACAA	GACGAACGGG	TGCCAGAGCC	GCGCGGGCGG	420
	AGACGGCGCG	CGGAAGAGCG	ACGAGGTGGA	GGAGGGCGGG	AGCCGGCGGG	GCCAGAGGCT	480
	CGTCTGCACA	CTGGTGGAGC	AGATCATGCG	CGAGAACATC	ACGGAGGACT	ACGACGAGAG	540
	CGTGCACGAC	GAGAACTACG	TGTTCTCGTC	GATATGGGCG	AACTTCATGG	AGGGGTTGAT	600
25	AAACCACTAC	CTAGAGAAGG	TCATCATACC	CAAGTCCGAG	CTGAAGGTGT	GCCAGCAGCT	660
	GTACCAAGCC	GATGATGAAG	ATCATCTCAC	TCTATAACGA	ATACAACGAG	CTCATGGACA	720
	AGA						

1669RP

	GATCAACAGC	ACCTCCACCT	GCGACAGGTC	GAAGTCATCG	TAAAAAGGCA	GCGACGCGAT	60
	ACCTTGGTGG	GCGGGATGCA	CACCGGCATC	CAGCATGACC	GTCTTGCCCT	TATACTGCAA	120
	TATATGGCAT	GAGCGTCCAA	CCTCATTGCT	GCCCCAAGC	CCGAAGAATC	GGAACGAATT	180
	CGTATCTAAC	TTCTCTCCG	TCATCCGCAA	TTTGTATTAT	TCTGCCTGCT	GCGAGGTGCT	240
35	GTGCTCTCTA	CCCAATGCCT	GCGACACTGG	CTACTGAGAC	AATTCCACGT	AGCTGTGCT	300
	GCAACTTTT	TGCAGCTATG	GAAATACCGT	GGTTCGGTAG	ATTTGATTCT	GTGGAGATGA	360
	ACGATCAAAC	GGGAACACTG	GTTATCGGGT	ATGCGTGTGG	TTAGTACCCA	ATCACCCGCA	420
	GAGACAAAGT	CCACTATTAA	TTGTAGTACT	TACAGGAACA	CCGATCGCAA	GAACCTTAA	480
	CGGCTCCGTT	TACCAACGAT	CAACACTTTT	CTCCTCGAAC	GTTATGCTGT	GCGGCGGTGG	540
40	CGATTGCGAA	TGATTGTTGA	ATTGAACCAG	AGAGCGGAAA	ATTTTCGTTT	TCACGTGACC	600
	GTATCTTACA	TAAGCTACTG	AACTATATGA	AATACCGACG	TTGCTCGAGG	ACCGCTAGCG	660
	CAGTGTCTCA	AGCAGTGATC	ATGAGATTGA	GTTGTTCTGA	TGTGTACAT	GAGAGTACTG	720
	GG						

1669UP

	GATCAACAAG	TGCAACAGCA	AGGTGCAGTT	GCGCCATGTG	CCCTCGGGGA	TCGTGATTGA	60
	GTGCCAGGCA	ACCCGCAGCC	GCGAACAGAA	CCGCAAGCTG	GCCCCGCGAG	AGCTAGCCGC	120
	CGCGCTGGCG	CAGCCCCCGG	GTAGCGCCAG	CGAACGCGAG	CTGGCGTTGC	GCACGTGGGC	180
	GCGGCAGGGT	AAGCACGCGC	AGGCGCGCAA	GAGCCGCGAG	AAACACGAGC	GCGCCCCGCG	240
50	CGAACGCGAG	GAGCTCGCGC	GCGCCCCGCA	CGCGGAGGAC	GCCGAACTTC	TGCGTCAGCT	300
	GCTCGCGAAG	CCGCCCGCCA	CCTCCTAGTG	CCCCGCGGGG	CCGCGGGGGG	ACGCAGGGGC	360
	GTCTTTTTCG	GCAATTCCAA	ATAGACACCC	TAGTCGCCCT	TGCTGCCCGC	GAGCGCAGAG	420
	CAGGCAGCTA	GCACACCACC	GTCCACGCGC	AGCGCTTTTG	CTGGCGAGTC	GTGCCGCGAGT	480
	CCGCTGGCTC	TGGTGTGCAC	ATGCCGCTCC	GGCGTGGCAC	CGCAGTGCAG	AGCTACCTAC	540
	GTACGTTTGC	AGGCTTCGCA	GTACGCCTGA	TACTGGCTCT	GGTGAAACTT	CCCGACAAGA	600
55	GTAAATCTC	ACCAAAGAAC	AAAAAGATAT	GTTAGTGAGG	ATATCTCACA	TTCTGTTACT	660

EP 0 866 129 A2

GGAAGTACAC AAAGT

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1670RP

	GATCCGGCAA	GATCGTCGTT	CAGTTGACCG	GCAGATTGAA	CAAGTGCGGT	GTCATCTCTC	60
	CAAGATTCAA	CGTCAAGATC	AACGACGTCG	AGAAGTGGAC	TGCCAACCTA	TTGCCAGCCA	120
5	GACAGTTCCG	CTACGTCATC	TTGACCACCT	CCGCCGGCAT	TATGGACCAC	GAGGAGGCC	180
	ACAGAAAGCA	CGTTGCTGGT	AAGATTTTGG	GTPTTGCTA	CTAAGCGGCT	GCTATATAGC	240
	GTATCTAGCT	CTAATGTACG	ATACTCAGTG	TCTATTACGA	CGGCCCGGAG	CTCCACGCGC	300
	CACATACGAG	GCCAGCCGGC	GACGGCAAGC	GGGAATTCAG	ATGCGTTAAT	TAGCAGTAGA	360
	TTAGTAGTAT	ATATGTACAA	ACAGCATACA	CATGAACGGC	GTCGCCGATC	ATAATCTTCT	420
	ACCTCTTCTA	CCACCTTCT	TTCTGGTAGA	GTCCGATGGG	ATAGGAGTGA	CGTCCTCGAT	480
10	ACGGCCGATT	CTCAAGCCGG	ATCTGGCCAA	AGCTCTCAA	GCAGCCTGAC	CACCTGGACC	540
	TGGGGTCTTG	GTCTTGGTAC	CACCGGTAGC	TCTGATCTTG	ACGTGCACAG	CAGTGATGCC	600
	GACCTCCTTA	CACCTGGCAG	CGACGTCTCG	AGCAGCCAAC	ATGGCAGCGT	ATGGAGAGGA	660
	CTCGTCTCTG	TCGGCCTTGA	ACTTCATACC	ACCGGTA			

1670UP

	GATCTATTTG	TGCCGTCCGC	CATTAAGCAA	GCGGCAAGCA	TCGATCCAAA	TCATGAGAGT	60
	ACCCTCGGGC	TTTCACTTTC	CAAGCCTTTA	TCAACAAATC	TGGTACACGA	TACATCCATC	120
	GCGACAGCAC	ATATACCAGA	ACGGGAAAGC	CGACAAGATG	GCACTAGACT	CTGGTAGGTA	180
20	ATCTGAGTTC	GACCATATCC	ACTTCGTTAA	TGGTGATAGT	TGATAAAAAG	AAACGATACT	240
	GAAAATTTTA	ATGGTTACCA	ATCTCATCTC	ATCGCCATAC	TGAAAGAATA	TTGTAGGTCT	300
	CGCAGTGGAA	CAAGGATCAA	GCCCAGGCTA	AGACAATAAT	GGTTGCAGCG	GAGGCAGTAC	360
	AGGAACTACC	CCCAGATGAA	GAAGAACTGG	CCTTGGCTAA	GCTAGTGTTC	GGCGACACAG	420
	CAGACTTCCA	TGAAGCGCTG	CGAAATGCAG	ACCTTAATTA	TGTTTCTTCA	GATGAAGACG	480
	TATATGGCCA	GGAGTCGTCC	AGTGATGACG	AAGAAGGGAC	TGAAATTGGT	CACCTGAATG	540
25	ATGACCAATT	GTTTTTTTGTG	GACGAAGGTG	CAGATACCGA	GGGAAGAGCA	GATGGAGAAC	600
	CGGAGGCCAT	GGAGGTGGAC	CAGGTTAGCG	AGGAAAGCGA	CTCCGGAGAG	GAAAGCGGTA	660
	GCAGCGCTGC	ATGGTCAGAT	TCGGATGACG	AACACTTAAA	CGTTACAATA	GGG	

1671RP

	GATCGCTTTC	AAACCATCCT	GTAACACGC	TGAACCACAC	TTTACAAGAC	AACGGCATAT	60
	CGACAATCAC	AAGACTTCCT	CGAGACATGC	CCGCCACCAA	TCTTCATCGT	GTACTGACGG	120
	ACTATAATCC	AAGTGCCCAT	TTGAATTCGC	AGCATGATGC	CACGCTTTC	AACCTGAGCT	180
	CGAAAACCTGG	AGATGTACAT	CGGCCTTCCA	ATTCTCTTTC	GAGTTTAAAT	GGAGCACAAA	240
	AAAGGGCTAG	CATCCCAAT	ATCTTAGGCT	CTGCTCCACT	TAGTAATCAA	TCAAGAACTC	300
35	CAGACAACCG	TTTAACACAT	GGTACATCGA	TCCATGAGAA	CCCGCGGTTA	GAATTAAACG	360
	GTGATCAGTC	TTTACTCTTT	GGCGGTAATA	CAGGGCAGGC	ATCGGGTAA	TTGGCGGGTG	420
	TTTCACCGGC	CGAAAACCTCC	CGAAGGAGCA	ATTGCGATGA	TCAGAGCCAA	TATAGATTAC	480
	ATTCCAACGC	TTTCCATTCC	ACTGCCCCCTC	CAAACGAACC	TTCTAAGAAC	ACTAGTCCAG	540
	GTACAACGTG	TGCACCTGCG	AGCGTTGTTG	GTACAAACAC	AAGGAACACA	CAACGTGGAC	600
	CCACGGGAGA	TGTCTCCCAA	GAATCAGTCG	AACAGCCGCA	ATCAGCTTCG	CGCGCATCCG	660
40	ATGAATCTAG	CGCAAGAATT	ATGTCGCCTA	GTCATCATAC	GGAGCCAGTA	GTGTCTGTTT	720
	CGACAATCTC	TTCTAACACA	CGC				

1671UP

	GATCAGGGAT	GCGGAGGACA	TTCCGCGACG	TTATCGGCGA	GCACGACCTA	CGCGTCTGGA	60
	ACTATGTCAA	GTACGGCAAG	AAAGCTATTA	AGGCCTTCGG	CTTCTCGCCA	GACGCATATA	120
	TTCAACAGAT	CATCCAGCTA	GCCATCTACA	AGTATGTGGG	CAGACAATTG	CCAACCTACG	180
	AGGCTGGGTC	GACCAGAAAG	TTCTTCAAGG	GTAGGACCGA	AGCGGGCCGC	GGCGTTTCTC	240
	CGGCCTCCGC	CAAGTTTGTG	AAGACTTGGC	AGTCGCCGGA	AGCATCTCCA	AGTGAGAAGA	300
	TTGCTGCTCT	ACGTGAGTCT	GCTAAGAACC	ATTGCTCGCT	GCTAAAGATG	GCGGCGGACG	360
50	GCCAGGGTGT	TGACCGCCAC	TTCTTCCGTA	TGAAGAACAT	GTTGCGTGAT	GGCGAGGAGC	420
	ATCCTGCACT	CTTCCGCGAC	CCGCTGTTCC	AGCACTCCTG	CACGTGGTAT	GTGTCTACCA	480
	GTCAGCTATC	TTCCGAGTAC	TTCCGAGGAT	ACGGCTGGTC	GCAGGTGAAC	GAAAATGGCT	540
	TTGGTCTGGC	GTACATGATC	AACAATGACT	GGTTACACAT	CAACATTGTT	ACMAAGCCTA	600
	AGAAGTCGGG	CTATAGTGTG	CACGAGCTTT	CACTACTACT	TGACCGAAGC	AGCAAACGAG	660

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1672RP

	GATCGTGTAT	TTGTCAGGCC	CATCCAAGCC	CTCCCCGCA	CCCAAACCA	CTATGATGGG	60
	CAAGAAGTGC	TCCAACGTCG	GATGGGCAGC	CTGCAACAGT	TCTCGTCCCT	CCGCGCTCGA	120
5	GAAGAGACGA	AGTAGTCTGC	CGAATTTACA	GGCGTTGGGC	GGCGTGGTTA	GCAGGACGTT	180
	GGACAGTGCC	CAGTGAAAGG	CAGATGAGCG	CGAGTGGCTT	TTTGCATGG	CAGATCCGCA	240
	GAAGAGATCT	CTCAGGTTGT	GCACAGCCAT	GCCAGACGTT	ATTATCAACC	CGCCGAGGTC	300
	GCGGTACCTG	GACAGGAGGC	GCCCCGAGCG	ATACTGGTCC	CGCAGGTCTG	TTCCCCCGCG	360
	CAGTGATATT	TGGACCAGCG	GTACCGGGAC	ATCCCAATCG	TCATCCACGC	ACTTCGAAGC	420
	GGAGAACGCA	ACTTTTAGGG	GGACCCAAAC	GCCATGGTCT	ATGCCGCGTT	CTGTGAGCAC	480
10	AGCGCATAGC	GGGCTGCGTA	TGTGGTTGAT	GGTGTCCGCG	ATGTCCGTAA	CTAAAGCCAT	540
	GCTTGATTGT	CTATGGAAC	CCTCCTCGTA	CATCCGGGTC	GAGAACCCAT	AAAAATCGTA	600
	TATCAATTCTG	TTCTCCAACG	GGT				

1672UP

	GATCCAGAT	TAGATATTAC	TTAAACGTTT	CACAGCTTTT	TGATGGCCTA	GTTCTGCTGC	60
	ACGTCTATAA	TGGTCCATCG	CCCTGTGCAAT	GTCCGGATGA	CAGCCGACCG	CGTGCTCCGT	120
	ATAGAAGCCC	AAGGCATACT	CCGCTTTCCG	TAGCCGGCCT	TCGGAAGCAA	TGGATGCTTT	180
	ATACGCCCAT	TTGTAAGATT	CTGAAGCGTT	GGGTTCCAGC	ACGCCCTTGA	CACCAGTTAG	240
20	GTACCAACCA	CTCAAAGCGA	GCATAGCCAT	GGCATTTCCT	TTTGGTGTCTG	CGTTTGCAGC	300
	CTTCAAGTAC	CACACGATGG	ATTTCCTCAGG	GCTATACGGC	AAGTGTAAAT	CAGCGTACTC	360
	GTAGCAGTGT	CCCAGCTTCC	ACTGAGCAAG	CGGATAATTA	AATTTAATGG	CACATCTGAT	420
	GTAAAGGTCT	AGAGCCTTTA	GGGTATCTTG	TGGAACGTGC	TGCAACTTGA	CAGCCTGTCTG	480
	CAGCTGTGGA	TGCAAACAAT	CAAATTCATA	GATCTTTGCG	AGTTCTGTATA	ACGCCTGGGG	540
	AGAGACGGTC	TTGTCGTGTG	CAGCAGCCCC	CTCGAACCAT	CGTATAGCAG	AAATGACATC	600
25	CTGTTCAACA	ATAATTTTAC	CTGTGTCTATC	ATCCACCAGG	CCATTTCAGTT	GGGAACATAC	660
	CCAACCTTATA	CATGCTACTG	CTCTGTCCGG	AAGA			

1673RP

30	GATCCCAGCT	CTTACGCTCG	CTCAATTGAA	AACCTTTTCT	ACACTAGCTT	TCTTATCAAG	60
	GAAGGACGGC	TAGTCCCTAGA	AGATGACGAT	GAGGGCTTCC	CGGCCATCCG	ACCCAAGGAA	120
	CCCCTCCCGC	AGGATCCCGC	CGAAAAGGAA	CTGGAACGGC	AGCGACGGAA	TGACGCGCGC	180
	CAGAAGCATA	TCATCTTCCA	AATGGACATG	GCCACGTGGA	GGAAGCTTAT	AGACAAGTTC	240
	CACATCACAG	AGTCATTTTT	ACCGTGATCA	TGTATAAATA	GCGCGCATCT	ACGTATCACC	300
	CGCTGGCCGG	GCGCTGACCC	AACCAGGCAC	TGCTAGCAGC	TCATCTATCG	GCCACTTCGC	360
35	AATGGTCAGC	GCGGCAACGT	CTGTCTGTAC	GCCGTGTCCC	TCGTAGAGCT	CGATGCCCGC	420
	CCAGCCGATC	ATCACCGCAT	TGTCTGTACA	TAGATCTGGA	GCTGGATAGT	GAAAGGAGTC	480
	GAACGGTCTG	AATAGTTTCA	TCTCGAGTCT	GGCACGCAGG	CGCCGGTTGG	CGCATACGCC	540
	GCCGGAACAC	ACAAACTGTG	CCACATCAGC	AACCTTATCA	GCATTTGAGC	CGCAGCACCA	600
	GGTTAATCTT	GGTAATCAAA	TGGTCGAAAT	ATGGCCTCCT	GAATCTGAAT	TGCTGCTACC	660
	CGGCGTTCCG	CCTC					

1673UP

	GATCGCTCTA	CCGACGTACT	GCATGCCTGT	CTTGGTCTTA	AGTTAAAAAC	CACAGCACCC	60
45	AATCGTTTAC	ACCGCAATCT	TAGACCAGGA	GCTAGTGCTT	GCGAGCCCCT	GTCGTTCAAA	120
	TGGCAGGACT	GTTGTTTGGT	TGTGAACCTC	GCGGACTGAG	GAAAGGGGGC	GGAAGATCTA	180
	TTTTGACCTT	ATTCGCAACC	GTTTAGATAT	TGAAAGCAGG	GCAACACTAG	TAAAACTCGA	240
	AATTAGGACA	TTCTGTGAACA	GATGTGAGCA	GAGGATTCCG	GATGCGCTTC	GAAATGATGA	300
	GGGCGCATGC	TGCATACCTT	GGCCGTGCGG	CGTAGTGTAG	ACCGTGCAGC	GCATGTGCA	360
	AAACAACGGC	GCCGTGGCGT	CGGCATGCAG	CTAGCACAGC	ACCTGCAGCA	GCGCAGGCGT	420
	GCATCCAAGA	GTTACGCCAC	ATGTCCGGCG	CGTTGCTCCG	TATGTACAAG	TTATGTCATT	480
50	ATTTCTACAG	ATATCATGTT	GAATATTAGC	CCGCGATCAT	CTACTCAATG	GTATCGTTTG	540
	GTCTATCTCG	CTTACGTCAA	GATGCAGGCT	CCGCCCGGGG	ACTACGCGCC	AGGGTGCGCA	600
	GAGCAGTTTG	GTATAGGAGA	AGCATGATAC	TGCTTTGGAT	GCTGGTCCAG	ATGAACCTGG	660
	GGCCACACAC	GCTGAAGGCG	CCACCCAGTC	CCTCGTAGCG	AAGTACGACT	AACAAGCTGC	720
	GGAAGA						

1674RP

	GATCTCATTTG	AGGTACACAG	ACACAGCTGG	CAGCGACGCC	CACGCCTGGA	TGGACGAGTT	60
	GGCGAAGCAA	TCATTCCGGT	TGTTTGCCAG	CCCTGTCGTG	TGTTTGCTTT	TCCTCGTGGA	120
5	GCTCTGGAAC	ATAGCAGAAC	TACCAGGGGA	ATAGCCACGT	GTAGATCGTC	GGACCTAAGA	180
	TATAGTATGA	AAGTGCAAGT	GTGCCACAAA	GAAGAAGTCT	TTGTGGTATG	TTGTCCGTTC	240
	CGTAGAGAAA	GCTTCCGACC	TTATTAATAG	AGAGTGTACC	GTCGTAAACA	GAAGAGGGGT	300
	ATGTCACCCCT	GTGCAGCATG	TAGATGGACT	TGGGTATCTA	GTCAGCCGTT	GTGCTTGAAG	360
	GTGGACCAAA	CTAATCCTTA	GTGCATAGTA	TTTATGTGGG	GCGGCCTTTG	AACCAGGCTT	420
	TTGGGATGCT	CGAAGGCGGA	ATAATACTCC	ACGTGACAA	AATATACGTC	AACATTTAAC	480
10	GGCTAAATTA	TCCCTTGCGA	GGAGAACATC	CCGTAAATTA	CAATTATCAT	TCTATATTAT	540
	AAACATATTA	TAAAACGTCC	ATCTTGCTAA	TATAAAAAACA	ATCTAGGTCG	GCTTACCAAC	600
	CATATTACAT	CAGTAGGCAG	CGCGATCTGC	ATCCGTCATG	GCGTGGAGTA	TCCAGTT	

15 1674UP

	GATCATCATC	AACTATATCG	AGAAGGAGTG	TGACCGCGGC	GTTGCTATGG	GTAAATACCC	60
	GTCTACCCTT	GACCGGGAAG	CGGTCCGAAA	GCTGGTGGCA	AAAGATTTGG	AGAACTTCCG	120
	CGTAACCAAC	AGCCTCACGC	TGAACAGTCT	CTCCCTATAC	TTTCGCAACC	TAACACGGGA	180
	GCAGCGGGAA	ATATGCATAT	ACAACAACCT	CACCGACTGG	AGCTTGCTAA	TCCTTCCGGA	240
20	AGAGGAGAAA	ACCAAGTACT	GCAAAAAGAAA	GCAGGGTTCT	TCGTGAGAT	AACAGTAATT	300
	GTAACATAT	AATCTGGAGC	TTCTCCCAGC	GGTAGAAGGT	CCCAATTTGT	AATGTACTAC	360
	TACCTGAGCA	CTTGTGTCCG	CCTCATCGCT	CCTTAGAAAC	TCGTGTTCAA	GAGCTCGGAT	420
	GGCATCTGAC	ACAAAGGTTG	CAGACGCAGG	AGAGTATATC	TCCAAAGCCT	TGGGTTAACT	480
	TTCTAACCTA	ATATTTTGCA	AATAAAGCCG	AGTCGCAGTG	TATCACTGCT	CCAGTCAGTA	540
	GATTCTGACT	TCGTAAATA	TGTGTTCTAT	GGGTGGAACA	TTTTAAGTCA	TAGTTTTGCT	600
25	TTTTCCCCTG	ATATACTTCC	AAATACATAT	ATCACTGAAG	TTCCATCGGA	AGCACCTCCA	660
	CAGTACGGCC	TAAGAAGAGC	AGAATAATTG	CTCCA			

1675RP

30	GATCCGTGCA	ATAAACCGCT	TGAATGCACT	GTGGAAGTAG	TTGCGGGTCT	CGATATCAAA	60
	GTGCACAAAG	AATATCTGCA	GGTTGTTACG	CAAAATGTCA	AGCACATATC	CACGCACTGG	120
	ACGCGAGCCC	TTATGCGAGT	AAGTTAGCAC	TTCAAATGCA	CCGAGCTTGT	ACTTGTGCGAT	180
	TCGCAGAAGG	CTTTCCAACG	TCGACAGCAT	GATCAGCTTG	TCTTCGTGGA	ACGGCTCCTC	240
	CTCTATCCCG	AGCTCCTGGC	CAATTTTGAG	AAGCGGTAGA	AGGAGAGCAG	GGTGCCCTTG	300
	CATGTTCCCG	AAGATAAACA	GATCGAAGAC	CTTCGGCCGA	ACGGTCCGAA	AGAGCCGGTC	360
35	CAGCACGTAT	AGTTGCACTC	GTTTCGCGCA	GGTGCCCTCA	AGAAGATGCT	GAACCACCTG	420
	CTGCTCCAC	AACTGCAGCC	ACATCTCCAG	TTTATCCTCT	GTATAGTGTC	GCACATATAT	480
	ATTGGCCAGC	AAACTCGTCA	CACCTCTGCC	AACCGCCGTC	GCAAGAGAGT	CCGACCACAT	540
	GTATCCGAGA	GCCGTCGCAA	TGAACCTCCG	CCGGACCTCT	AGAACAATT	CCAGGTCAAT	600
	CCGCTCCGAT	AGCACGTCCA	CCATGAAGTA	CACGAACCTC	TTGAAGGAC	TCAG	

1675UP

	GGATCCGCTT	CCACACCGAA	AACGCAGAGG	ACCAGGACCG	TGTCTCGAAT	GTGCTTGGCG	60
	ACGCCATCAC	GCACGTCAAC	ACGCTCTTTG	GCGACAACGG	CATTACGCC	TACGTTTATA	120
45	AGAACATCGT	GTTCGTCCAG	CAGTCCGGCC	TGTCCGTGCA	GGCCCTCAGG	TTCCGTGCTA	180
	ACCATAACAA	CTCGGTGCGAC	GACACCCCTG	GCTCCACCCC	CGCGCACTCC	CCGGCTGTCT	240
	CGCCCGTCAT	GACCCCGGTC	AATTCTCTCG	TGGCCATGTC	TCCAAGCACC	GCCGCACTA	300
	AAACCCCTC	GGCCGCGACC	GCAACAGCCA	GCTACTTTAG	CAATGGCCGT	TCCACCAGTC	360
	GCGTCGAGTT	TGTCTGTGTC	ACTGGGACTT	CATCGCCGTT	CCTGGAGCCG	CTGTTCCAGT	420
	CTATCAATGA	ACTGGCCAAA	AAGGGCGACC	TGCCCTACGG	ATACACTGTC	GCCTACGGCG	480
	ACGCTATTAC	CACATACGCT	AAAGAGCAGC	TCGAAGGTTT	CAACGAATTA	TTTGGCATTC	540
50	TAGACAAACT	GAACCTTCATT	GGCTGCTGAG	CGCCCTGTT	ACATAGGTTA	TTAATCAATT	600
	AAATCCTTTC	TCTGGAACCT	TATAGAGCCC	TGCACCTTGC	GCTCCGGACG	CATATCCTTG	660
	CTGACTAGTT	GTCAGCGGTA	GCCTTTAATA	AATTACGTAA	TATGTGGTAT	TATCA	

55

1676RP

	GATCCCGACA	CCAGCATGCG	CTCGTCGAAC	GGGTCGAAGT	CTGTGTCCAG	CACCTGTGCC	60
	GTGTGCCCCG	GGAACAGAGG	AATTGTGGTCT	GGCGCCTTGC	CCACCTCCTC	CACCGGCACT	120
5	ACCGCGAACG	CCCCTCCGCC	CGACGAATTC	CACGTAACCG	AAATGAACTT	GCCGTTAGTC	180
	TTGATGAGAT	TGGAATCCCA	AGCATTGATT	GTCACCTTGA	GGTTCTCGTA	GAAGAGTTCC	240
	TTCTTTGTTG	ATTGTCCGAA	GACGTGTCTA	TACTTGGAAG	CCCGCACAAA	CTTCCCACTG	300
	CAGTGCCGTT	AGTTTGCCGT	CCGCACAAAG	TCCAGTCCTG	GAGAGTATGA	CATACCTCAT	360
	CCTTGCAATT	CTTTGGGGTT	TAGCAGCTCT	ATATGCGTGT	ACACCGTAAA	CATCCGTAAC	420
	TAAATATGTA	ACGTGGAAC	GAAGGGTACT	GGAATCTAAA	GGGGAAAGAA	GTACCCGTTG	480
10	ATGGTGATGG	TACTGTCAAG	ATGGCTAAAG	CGAACCTCTG	GCCTGGTTGG	AACTCAGAAA	540
	GGTCACCAGA	CTCTTCTTAT	TCTTGTTT				

1676UP

15	GATCGCCGCG	CTCGTGCCCTC	GCCTGTATTA	CTACGCCACG	AAGCAATTGT	ATAACCCACA	60
	TATTGTAAACG	TTTGTACTAT	CCTCCATGGC	CTCGCCACC	CGACACGCCG	CCTTTCCTGC	120
	ATTCGGGTGC	CGGTGGCCGC	CGCGTTTCAA	CCTCGGCCCA	TGGCTCGCGC	ATTAGCTGCC	180
	AGTAGCGATG	CAACCCGAAT	GGCGAAGATG	GAGCCGGCAT	TGGTGGGTAC	GAAAAAGCTT	240
	TTTACGCGTA	CTGTTTGCTG	GTCCTAACGCA	TCCACGCCAC	GACGCTAACC	AGTATGAATA	300
20	CCGACCTCTT	TGCGCAGCTG	GTACTTGTGC	CGATCCTCCG	GTCCCCCATA	GCGTTTGTGT	360
	TGCTTCTATC	ACGGTATGCA	ATGTTATGAT	GCGTGTGTCC	GCGAACATGT	WCTAACAGGC	420
	GACAGCGTGC	TCGATACGCC	GTGCCCGCGG	CTGGCAGCCG	CACTGACGGT	GTACACAGTA	480
	GTGTGTAATG	CGTGCCCTAAG	CGCCAACCGG	CGCGCCAAGC	TGGCAGGCCG	TGGACGCCAC	540
	TGGAGCAGAT	GCCGGACGCG	ACTTGCGT				

1677RP

	GATCTGCAAT	TAGGGCATAT	AAACTGTGGG	TACTGTGTCA	TCAGTAGTCG	GCGTATGCAC	60
	TGGTAGTGCC	AACTATGCGA	ACAAGGGGAT	ATGAAGATGG	CCTGGCAGGG	CTTAATTTTA	120
	CATAGGCAGA	TTGAGCAATC	TTCTCTCTCA	AGGCCTGCCG	TTAGCTTTTG	TAGGTTCCGT	180
30	AGGCGGGCTA	GTGCCCTCTT	GTTGAACGCG	TTGGCCCTTC	GCTTCCACGA	TTTGTTCAC	240
	TCGACTCTCA	TTTTGACGCA	TCTATATATC	TCCCTCTGTG	CGCCACGGAA	ATCCATTCCC	300
	AGCTGCAATA	TGTCGCCGTC	TTTCAAGGGG	TAGTCTTTTC	ACATAACCGA	TGCCTGTGCA	360
	AGCCGCATCT	GATTAAGGAA	CGTGCCGGAC	GAGGACTTGA	CGTCGCGCAC	ATACCAATTG	420
	CCCTGCTCAT	CCACCTTAAA	CACCCCGTGT	GTGCGCGACA	CAACCTTGCT	CTTGAATACC	480
	ACGGGGTGGA	AATGATCCGG	GAGCGAGCCG	ATCGCCTCGC	GAACCCGTTT	TGTGTAAACG	540
35	CCGATAACCA	ACTGCGAGCT	GGGGCCTGCG	GTCCGCACGA	TGGGATCAAA	AAAGAGCCCC	600
	GGATTATTCTG	TGGTCGAGTG	GTCAATGAAC	GGCGTTAACC	GGAGCGAGAA	GAA	

1677UP

40	GATCGTGGCC	TTAAGCCCCCT	CGCCGCCTGC	GCCTGCGCAG	CCCTCAATGC	ACTCCGTCCG	60
	CGTCGGCTAC	ATCCCAGAGC	ACTTCAGCGC	GCCGCTGCTG	TTTGCGCAGA	CGCTCGGCTT	120
	CTTTGCGCAG	CGCGGCGTCA	CCGCCAAGCT	CGTGCCCTTC	CCTAGCGGCT	CTGGCCACCT	180
	GATCCAGGCG	CTCGACGCCG	GCGAGCTCGA	CCTCGCGCTC	GGCCTCACCG	AGGCGTTCTG	240
	GCGCGGCATC	GCAGACACGC	CAGCCGGCGC	CGCGCCGCGC	TACCAGATTG	CCGGCACCTA	300
45	CGTGCGCTCG	CCACTCAACT	GGGCCGTCTC	CGTCGGCGCC	GCGTCGCCCC	TGGAGCACGT	360
	GGACCAGCTG	GACGGCGGCC	GCGTCGGCCT	GTCACGCGTC	GGCAGCGGCT	CGTACGTCAT	420
	GAGCTATGTG	CTCGCCCTGC	AGCGCGGCTT	CCGCCGGCCC	TTTGCCGCGC	ATCCGGTGTG	480
	CCACACCTTT	GCCGGCCTGC	GCGCCGCCGT	CAACGAACGG	CGCCGCGGAC	GCTTTCTGT	540
	GGGAGCACTT	TACCTCCAAG	CGCTACCACG	ACGCGGGCGA	GATCCGCTG	CTGGGCAACA	600
	TCCCCACCCC	CTGGCCCTCG	TGGGT				

1678RP

	GATCCGCTGT	CGGCATCATC	GGAGACATCG	CCTCCATGTT	CCCCGATGGT	AGGATAAAGC	60
	AATTGTACGC	CCAGACTTGG	GTCACAGAGT	TTATCAAGAA	AACAAGAAGT	AACCCCAACT	120
5	TTAGTCAGGC	AACTAAGGAT	ACTGCTAGAT	GGGCTAGAGA	ACAACAAAAG	CATCAACTAA	180
	CCCTATAGCC	TTACACTCCA	GAATAATTTA	TCTTATTACT	CATTTTCTTC	TGCGTTATCT	240
	CGCTCTCCTC	CTGTTATTCT	ATAATACTTC	CCCTGCAATTG	TCTTCATTAT	TGTGTCTGCC	300
	TCGCGACAGA	CCGCTTCGTT	GTCTCTTCCT	TTGTTTCGACC	CTGCACTGAC	CTGGCCATGC	360
	TGCTCTTTCT	AGTGGTTTGG	TACAGGTTGC	GGGTCTTTTT	ACACAACCTT	TCTACTACGT	420
	CTTCTATCTA	ATCCCATCTA	CTTTTCTACT	TTCCTCTCCT	ACTTTATCCG	TCGGACCCGC	480
10	TGCTCGTCTT	ACGTGGCAGC	TTGTAGCATC	TATATAATTG	TATATATCGT	GGTGGCAACT	540
	ATCTACGGCT	GCTATACATC	TGCTGCCCGG	TCTGATCGGC	CGAGCCGTTT	ACCAATGCAG	600
	TAAACCACA	TAAACTTTTA	AGAGTTACAA	GCTCAAAAAC	GTT		

1678UP

	GATCCGGGTT	CGAGTCCCGG	GAGGGGCTGC	AGCGCACCAG	CGCTTCTTTT	TGGCGCTGGT	60
	AGTCGAGGAT	TGTTGACTGC	TAAACCCATA	CAACCACATA	TTGCACTGGT	GGCTTGCCCG	120
	CCTAGGCCGC	CCTGCGGCTC	CCGCGTAGCC	CGCCGGCGGG	ACCCACGCAA	CGAGACCGTG	180
	CGGGCCCCGG	ACGGCGATCA	CCAGCGGCAG	CCGGTGCAGC	GTAGGCGGGA	CAGCTGAAAA	240
20	GTTACTACAA	TTTGAGGTCT	CGCATACTGA	CACAGAGGGT	CTTACACAGC	ACCAGACGAA	300
	TCAGCAATGG	CTAAGCAATC	TCTAGGTATG	TGACAGAACG	ATGGTGGCTC	CGAAACATTG	360
	GGAATGAGCG	TCTCTGGCGC	TGCGATCCGT	GCTAACCTGG	GCATACGGCC	CAGCGCGCAG	420
	GCGGACCTAG	CATAATCCAG	TGCGTGGAAC	AAGTTGGTGG	CCCGGCACAG	TACTAACATG	480
	TCTGCAGACG	TTTCTTCCGA	CAGAAGAAAG	GCCAGAAAGG	CGTACTTCAA	CGCGCCATCT	540
	TCCGAGCGCC	GCGTGATCAT	GTCTGCTCCT	CTATCCAAGG	AGTTGAGAGA	GCAGTACAAC	600
25	ATCAAGTCTC	TACCAATCAG	AAAGGACAAC	GAGATTATGG	TTGTGCGTGG	CTCCAAGAAG	660
	GGCCAAGAGG	GCAAGGTTCT	TCTGTCTACA	GATTGAAGTA	CGCTGTCCGC	GTCGACAAGG	720
	G						

1680RP

	GATCCGTCTG	ACGGTGGTGC	AGTTCTGGAC	AAACGCCGTG	CTCTTTGACG	AGATCGTGCA	60
	GCCACTGGGC	GAGATCATCG	ACCTCTACAC	CCAGTTCAGC	GGCGTCCACG	AGATAGACCG	120
	CGCTGTGGCG	AAGACATTTG	AGGAGGCGAG	GGAGGTATTT	TTGTGCGCCG	CGATGATTAA	180
	CGAGAACAGC	ATACTGATTG	GCCACGGCCT	GGAAAACGAC	CTGAACGTAT	TACGGATTAT	240
35	ACATGATAAA	ATTATTGATA	CAGCTATATT	ATACCCGAAT	GGTAAGTTCA	AGTCTCTCCT	300
	CCGGAATCTA	GCCTTTCAGG	AGCTCAGTAG	ACGGATCCAG	ACGGGCGAGC	ACGACACGTC	360
	AGAGGACGCC	ATTGCAGCAA	TGGACGTCGT	CAAGCATAAG	CTGGGCATCC	CGCTCGACCG	420
	CAAGACGTGG	TAGCCCTACG	GCTGCTCCTC	CAGCCGCGTG	AGCCTGTCTT	CAAGCTGGTC	480
	CTGCCTCTCA	ATTAGCGTGT	GTATAAGCTG	CTTAAGGTTT	TGTAACCTAA	TCGCGATCAT	540
	CCTATCTTCT	GGAAGCTCGA	ACTTGACGTT	CCTGCTGCGG	GTCACGATCT	GGCTCTTGCC	600
40	CACCTTGATC	CTCGATGCCT	CCGGAATTTT	GCC			

1680UP

	GATCGCGGCG	CGCGGTGGCC	GGCATTTCCG	GAAGCGGCCA	CGGAGCAGAG	GTGGCGCATT	60
45	CGAATCGCAT	ACGTCTTCGC	CACGCCGGAA	AAAAAATTTT	CGGCTATATA	AGGAGAGGCG	120
	GCCGTCTTGC	TGCAGGCAGT	TTCACTTTCT	CTAAAACCAA	AGAACATCGA	TTTCTTTAGT	180
	CACTCGCTTC	CTTACACCGA	AATGCAATTC	TCCACCGTCG	CTTCCATCGC	AGCCGCTGCC	240
	GCCGTGCGCT	CCGCTCACGC	CAACGTGACC	ACGGCCACCG	CCACCAGAAA	CCAGACCACC	300
	TTGGTCACCA	TCACCCACTG	TGAGGACAAG	ACCGCATGCA	CTGCGCACGT	CTCTCCAGCT	360
	TTGGTCTCCA	CCGCCACCGT	CACCATCGAC	AACGTTGTGA	CCTTGAGCGA	GACCTGGTGC	420
50	CCACTATCCA	CCACTGAGGC	TCCTAAGCCA	CCAGTTTCCA	CCGCCAAGCC	ACCTGCTTCC	480
	TCCAACGCGA	CTGTTCTCTC	AACTGAGACC	CAGTCGTCTC	CTCCTTCACT	GGTGCCCGTG	540
	CCAAGGCCCT	ACCAGCTGCT	GGTGCTTTGT	TCGCGGGCGC	TGCTGCTTTG	TTGTTGTAAG	600
	TTTAGTTCCG	CCGCGTGAGC	CCTCGTTTCG	TTTAGAGATA	TATAGGAAGT	TATGTGACTG	660
	ATTCTAAGCT	TTTACACCAG	CATGATTTGG	TTCTGCGGCG	CACCGA		

1681RP

	GATCATTCTA	AACAGATTAA	CCTTCCTCCA	AATTACTTTA	TTTCCTTAAT	CTCCGATAAA	60
	TGGTTACATT	GCGACAATAA	GGTGCCCGTG	GTGCTTACAG	ATATACATCT	ACCGAGAAAA	120
5	TTTCCGCCAC	ACACTCGTAT	AGAAGAAAAG	AATTTGATTG	AAACTTCTGA	GCTAGATCCG	180
	ACGTTCAAGT	GACTCTTCCC	ATTTAAGGTT	TTCAACAAAT	TCCAAACTCA	TGTGTTTAAT	240
	GCCTTGATCC	ATACCGATGA	AAATGTATTT	ATTGGAGCTT	GTAAGGGCTC	GGGTAAAACT	300
	GCAATGGCAG	AATTAGCTTT	ATTGAGTCAC	TGGAGAGATG	GTAAGGGACG	TGCCGTCTAT	360
	ATATGTCCAT	CTCAGGAGAA	AATTGATTTT	CTGGTGAAGG	ATTGGCGAAA	CAGATTTTTA	420
	AATGTGGCAG	GTGGAAGGTT	TATTAATAAA	CTCACATTGG	AATTAACTAA	CAATCTTCGA	480
10	ACGCTAGCCC	AGTCGCATTT	AATCTTAGCG	ACCCAGAGCA	GTTTGACCTG	CTTCTCGTC	540
	GCTGGAAG	AGAAAAAAC	ATCCAGACAT	TAGAGCTGTT	GATTCTAGAT	GATCTTCATA	600
	TGATCAGTAG	TGACTTGCCT	GGCGCAAGGT	ATGAAAATAT	AATATCCAGA	ATGCTGTTCA	660
	TTCCGGGTCA	ACTTGAAAAC	GGCCTTGCCT	ATAGTC			

1681UP

	GATCAGGAAT	GATCCCTCAA	TTGTCAGGAA	TTATGGTTCC	ATATTGGTTG	AATTTGCCAA	60
	GATTACTCCT	GATGGTATGG	TANTGTTCTT	CCCCTCATAT	TTATATATGG	AATCCATTAT	120
	TTCAACTTGG	CAGACAATGG	GGATTCTAGA	CGAGGTTTGG	AAATACAAGC	TCATCCTCGT	180
20	GGAAACACCA	GAGCACACAG	AAACTTCTCT	AGCTTTAGAG	ACTTACCGAA	AGGCCTGCTC	240
	GAATGGGCGC	GGCGCAATAT	TACTTTCTGT	GGCCCGTGGG	AAGATTTCTG	AGGGAATTGA	300
	TTTTTGACCAC	CATTACGGTA	GGACTGTATT	GATGATTGGA	ATTCTTTTCC	AGTACACTGA	360
	ATCGCGTATT	CTAAAGGCGA	GGTTAGAGTT	CCTAAGAGAA	AACTATCAGA	TACGGGAAAA	420
	TGACTTTTTA	TCCTTTGATG	CAATGAGACA	CGCCGCTCAA	TGTTTGGGAA	GAGTCTTGAG	480
	GGGTAAGGAT	GATTATGGCG	TGATGGTGCT	CGCCGATCGG	CGATCTCAAG	AAAGAAAAAC	540
25	CAACTTCCAA	AATGGATCGC	ACAAGGGCTC	TCTGATGCTG	ACCTGAACCT	TTCTACTGAT	600
	ATGGCGATAG	CTAATACAAA	ACAATTCTTA	AGGACGATGG	CACAAGCAAC	TGATCCGAA	

1682RP

	GATCGTAAAA	TTTGCTATAC	AATGGTTTGG	GTAGGTCCTT	TAAAAGGTCG	TCAATCTCAT	60
	AGTCGCTCAC	ATCAAGGGGA	ATGTTTAAAA	AACGCACTCT	CTGATGTGTA	GGCGGAGGAG	120
	GCCTTGCGTC	TCGCCGGTCC	CTGAAACGTG	AGCGGCGCGA	GGGGCCGTAC	TCTCGCGCCC	180
	GATACGTGCT	TTCCCCCAGA	CCCATGCGTG	AAGCTAGTCC	ATTACGTAAG	TCTCGACGGC	240
	GATATTGCTA	TAATAACAAT	GTAATCGTTA	ATACTCACGC	TCAAGTAACC	TTGCGGTGGG	300
35	TCATGTATCA	CTTACGGTAG	TAGTGCGGTG	TGTCTTTTGT	CCGTTAGTAT	CCGATGAAAT	360
	TTGGTATCGA	GGAGAAAAAG	ATGTTTCATC	TTTCTCACCA	GTACCCTGGT	TCAAGTGTTT	420
	GTCACACAGC	ATTGTCCCCT	CCAAACTATC	CTGTTTGAAG	GGCAAAGGCT	GTGTGTCAAG	480
	AACGAAGTTT	TCACCATTTT	TCCGGAAGGC	TCGGGACAGC	GATCGAAAGA	AATAGGATAT	540
	ATACGTACAC	CTTCTTTTAA	ATATCATTTA	AAATATCCTG	GAATTTTCGAT	ATGTGGCCAT	600
	ACTGGCTCTT	CAGCTTTCCT	ATCCATGAGA	TAGAAGGAGC	AAACTGTGCG	AAGGTGCCTT	660
40	CCACAGTTAC	TTAAGTTTCC	GTAAGCAACA	AGGAGTCTGT	ATGCGGC		

1682UP

	GATCCAGTGT	GTACGGCCAG	AGTCGCGCTG	GGGCACCAGC	AGTACCTGCT	CCGTCTCGTT	60
	GAAGTTTCGA	ACATTCCCCT	CCGCATCAGC	ACCGCGCCTG	AAGTATCTTG	TACCCGCCCT	120
	GAATCTGCTC	CGGCGCGTGA	TCAGACCCAC	ACTAACTGGC	GTACTCTGCA	ACACAGTGTC	180
	TACCACTTTG	ACGTAGCCGT	AGATTAGCGG	CAGAACGAAC	TCGTTTCGCCA	GAGCGTTTTC	240
	CTCCGCCAGG	TTTCGCAGCG	GCTCTGTGGC	ATAGTAGTTC	CAGAAGAACC	GCGTGTCTGC	300
	AGTGCGCCAC	GAGGCTGGCC	CCAACCCCTC	GTTGCGCTGC	ACAGAGTGCG	TCAAGTCATA	360
50	CGTGATCGAA	TAGTACAGCG	TTGCCTTCGC	GAGGTGGTGC	CGCAGTAGCG	CAAGATACATG	420
	GTTGTCCCTCT	GCAGATGGCC	GGATACTGGT	GTTGACCAGC	ACCAAAGAGT	GCGCCGTCAC	480
	TTTGAAAAGA	GAATGGGCAC	CCAGGTTTCC	CACCACCTCC	ACGCGGTCCG	CCGTTAGCAC	540
	CACGCGACTA	TTGCGCAAAT	GTAATATCCC	GATCAGGCCCT	GCGATCTTGC	GAGTTTCTCC	600
	ATCTTTAGGG	AAATTGCTGG	GGTCTACGAG	TGTCACGCCC	GAATCGTGAT	GCGAGATAGA	660
	CAACACCGCT	TCACTCTGGG	AAGTATTAGA	TGGCTTGAAA			

1683RP

	GATCTATATC	ACCAATCATC	ATGGTTTTGA	AACATTCCGT	GCTTAAAAAG	GGACACAGCA	60
	AACTACAAGC	AGGCAGCACG	AAGCACTCTG	CAGACTAAGG	GCAGGCCTCA	TCATAAGATG	120
5	CTTAGGGCTG	AGCTAGTAAA	TGCCATTCCG	TGCCAAGGTG	CTCAGTGTGT	CGCTGTGGTT	180
	GATGGCGTTC	GACAACTTGT	GGTGGTGCGA	AATAATAGGG	ACTTCTTGGT	GTACTCCAGT	240
	ATGGACGAGA	GAGGCCTGCG	TCTAGTTTCT	ACATATACAG	AATTGCTTGG	CCCGAATTAT	300
	GGTGTAGAAG	AGCTGCTGTA	CTCCGAACGG	CTGCGGACAA	TATTCTGTCG	CACGACCAAG	360
	TGCTTACTGC	TACTTCATTG	GAGCAACTTA	CAACATTACG	ACAAGATAGT	TGACAAACGA	420
	GGCATTGACC	ATGCCCTGGC	GTTTGAACAT	CCATGTGGGA	AGGCTGAGAC	GTGGATGACG	480
10	GTGCTTGTTT	ACTCGGTCAC	AGGGTCGAGC	AAGATAAAGA	TGCTGACATG	GGTGGGGCGG	540
	CAGTTCCAAG	CGGTGCATGA	GGTCGCACTA	GGCACGCGAT	CGGAAGTCAT	CCAGCTCAGT	600
	AAGTGGCGGC	CCGCATGCTG	TGTGGTTGCT	TACCTCCGAC	GACTGTATAC	CA	

1683UP

	GATCTCGTCA	AATTCCTGCTC	TAGCATTATC	AACCTTGTGA	CCACAACCTTA	GAATTCCCCC	60
	ATCATGCATT	ATGTTTATAG	ATGTACAGTT	CTAAAAAAT	CGGTAATATA	ATGAGACCTA	120
	TCCTCTTTTC	TCATCCTTAT	AGTCACCCAA	AGTTTAAACA	TGTGACATGC	TGCCAGATTT	180
	ACAGTCATCT	GCGGCTATGA	TTTCTTGCGA	AGACCTGCCA	CAATTATAAT	GTGTTAATAT	240
20	ATTGCTTCCT	CTGAGGTTGA	AGAGCGAGAA	AAGTTCACCT	CTCCCTAATG	TTAAATTCTT	300
	CTGGCAAACG	TAGCAGCGGT	TATCTTTCATC	TACCACCAAA	AATTCAGATA	TGATCTGGGA	360
	TAAGCGATAG	GTGCTTCCGA	TGAGGTTGAC	TTTCAAAGA	TTGTTCTGTA	TACGCGATTG	420
	GTTTTTCTTC	ATGGACGCAC	TTTTAATCCT	TCTACTTAGG	AATTCGTTAA	GCGTGTATTAT	480
	CGGAATATTG	GGCGGCAGTT	TCTCAAACAA	TGTTATCGCA	TCTAGCTTCG	AACCATTCTC	540
	TAGCAGAAAC	AGATGAACGT	TTCTCCATCC	GCTAAATTCT	ACCTTCGCAA	GCAGCTTTTC	600
25	AAACAAGTTC	ATGAGAGCTG	CTGTGCCTGC	ATTTTTGTTT	GTGGCATAGA	GCTCATTACA	660
	ATATAGAGAA	GCTTGTTTAT	AATTCCCTAG	ATCATCAACT	AGGATCCCTA	ACGCTGTT	

1684RP

	GATCTGTACA	CTTCAATATC	GAACGAAGTG	TCACCGGCAT	ATTCTGCAGA	GATTTGAAAA	60
	AGCCACCAAA	GCAATATGAC	ATCAGGGTAG	AGCTTCGAGC	GAGTAATCTC	CGGTGATTCTG	120
	TCGATCTCCT	TTAACCAAGC	AGCAAACCGT	GTCTCATGTT	GCTTTTCCCA	GCTAATAATC	180
	TCATGCACCA	CAGCCATAGA	TTCAGCATAA	TGAAGGTATG	TTGCGCGCGC	CTCATTACAC	240
	CATTTGATAT	ATATTTTCCC	CAGGCCATCG	ATGAACTTCC	CTTTCGTCTG	CAGCTTCCCA	300
35	AAAATAGGTG	TCAAAGCAGC	TTCTTGTGTC	AAGTCAATCA	GCGGATAAAA	GATGTCAAAG	360
	GCAAGAGAGG	CGAAGTTTTC	GTCCGTGGGC	AGCAACGCCG	GCGAGAATTG	TGCGCCGCTAG	420
	ATTTCTACGG	CAGCATGGGC	CAGGTTGAGA	CTTTTCTCTT	CGAGCACAAT	AAGGTCAAAT	480
	ATGTAGCTCT	GGCGCTTTAC	TTCTCTAGGA	TTAATCTCTG	AAAGCTCCTC	GTCCGTCAGT	540
	TTCCAGTACT	CGGTCCAAAG	TCCCAACGGG	CGGCTGA			

1684UP

	GATCCATGAC	GAGCAGCTGG	ACCTCGTCTG	CGCTCTGGGC	CTGGCGCCAG	AGAACAAGGA	60
	AACGCTGCAG	AACCTCCCGC	TCGCGCGCGT	CAGCGTCACG	TTCAAGGACG	TGGTGACGGA	120
45	CTACTGCGAG	GCGCACGGCC	TGCTGTCTGA	AAAGACGGGC	GACGTGCGCA	CCCTCCGCGT	180
	CTACCAGCAT	GCACGTACTG	TCCCGGTCTT	CACCGTCACA	CACGTACACC	GCCGCCGGCG	240
	TGTAGCTCTG	TGCGAGGACG	TGCTTTGGGT	TCAGGAAGGG	ATAGGCTTCA	AACCTACGTA	300
	CTTATACGAA	CTAGAAACTC	TTCTAAAGAG	CGCTTAGTCT	TCTCATATAT	ACAGGACCTA	360
	GTACTCTTGG	CGCACTCAGT	GGCCCTCGTC	GCTTTTTCGG	CTCTCGGCCG	CGGCCTCCGT	420
	CTCGCGCACG	GCCTGCTCCT	CGCTCTCCAG	CTGCTCCGCG	TAGTGCTCGG	GGTGCTGCCG	480
50	GAAGCATCCT	GCATCACCTG	GAATTCTCCA	CGCAGTCAAT	CCCCTTAGGC	TCGGCCTCTG	540
	AGTACACGAA	GCACGCGAAC	GCAGCCTTGA	ACTCCTCGCC	GACCGGCCCG	TGCGCCATGC	600
	CGCCAGGCA	TGGGCAGTCC	CAGTTGATCT	CGCCCGTGTC	GGGATTGTAT	GCTCCTGCTG	660
	CCCTGCGCAG	CCTCACCCGC	GCTAGCTTTG	TCCTCCGCGG	CGCTCGG		

1685RP

	GATCAACTTC	GCCTAATCCC	TTAATCATTTG	TCACGTGCTAA	CTTGAACTTA	GTCTGTGTGT	60
	ATGCCCTATAG	TGAACGTTTA	ATGTGATGGT	TTTATAGTAA	TCGATGGAAC	TTTATCCGCG	120
5	AAGCCTCAAG	CTGATCATCA	CGTGAGTAAC	CGTCGATATG	CAGAACAGAG	GATACCATAA	180
	ATTGCTATTA	GTAATCAATT	AATAGACTTA	CATATAGCTC	AAAGCTGATC	ATTGATGCGT	240
	CTCAAACCTCT	TTTCATCGTC	TGAACCTTTC	GGATTTCAC	TTCTGTATC	ATTATACCAT	300
	GTATAATCCT	CTAGTACGCT	AGTAGTCTAG	TATCTCGGAT	AACCCCCCTA	TATTACATAT	360
	AATATGAGTA	AAATACAGAA	TGACGTTAGC	GGATAATCTA	AGGCTAAGGT	TGCCTACACT	420
	AAGTTAACGG	GGGGCTTCTT	ATCTTGACAG	TTGTCTCTCT	AATCAATAGA	ATTCGTTTTC	480
10	TTTTTCCACT	ATTTGGTCCC	TGGCAAACCTG	CGAGCCACCC	CGCGTATCCT	TAGCCTCTGA	540
	GGTGTCTCTCT	TCGACATCAC	CTTCGTCTCT	CGGGATCTCT	CGGGACGTGG	TTCAACTGTA	600
	CGCTCGGTGC	ATATTTTAGTG	TGCTCAAGGT	TGCTGAAAAT	AGATGCGAGC	ACCTTGTTCA	660
	GATATT						

15

1686RP

	GATCCTCTCC	GAGGTCAAGA	GTTGTGTCAT	GAATTAACCTT	CATTTTAGGA	ACAAACTTGT	60
	CTAGGGTTCC	CGCTACTAAT	TCCTGCTCGA	CTTTGAAATC	CCAAAATTTG	ACAGTCTTGT	120
	CTGCGGACGC	AGTCAC TAGC	CTCTTCCCAT	CACTAGTTAG	GTCTAAAGAC	CAGATTGCAG	180
20	CGGTGTGTGC	CTCTTCAATA	TTTTCTAGCA	TAGTAGAAGA	TGCGAGATCA	AATAGCTGAA	240
	GTTGGCCCGC	TCTTGTAACC	AGAATAACCA	AGGCGCCACC	TGGTAAAAAC	TTACAGCATA	300
	AAGCATAGCC	ACAGTCAAGA	TTGCGGATAC	AAGTTTTAGT	CTTGATGTTT	CAGACCTTTA	360
	GGTTTCCATT	TGAAGCAGTT	GCTAGTAGCT	TATCATCGCT	ACTGATGTCT	GCAGCACGTA	420
	GATCAGTCCCT	ATGGCCCGGC	GATTCGATAC	TATGCAATTT	GATCGCAGTA	GGCTGGAGCG	480
	GTTCTTCTTT	TTTGTATGGG	ATTGAGTAGT	ACTCTATAGT	GTTGTTTGCA	GTCTGTATCA	540
25	CCAGTTCCAA	TTTAGATGGG	GTACAGACCG	TCCATGAAGA	TGCTTTTAGC	TTAAATAGGG	600
	ACCTTACGAG	TTGGAAAAGG	ATGCAAAAGT	AAGTTCGCAT	AC		

30

1687RP

	GATCAGGACA	GTAGCAGCTT	GACTGAGTAT	CAGCAGGAAA	AGCCTAGCTA	ATTGGCGCGA	60
	GTACAATTAC	AAGTACCTGT	CTGACTACTT	CTTTTGTGG	GATGCCATAT	TTTTTAGGAT	120
	GGCCTGCAAC	GGCCCGGTGG	GGGCGCCATC	CAAATTTATG	GAGTTGAAGA	GCTGTTCAAT	180
	GCCCTTTATC	CCATCTGCAC	CGTCTTTATC	GCCGAACATG	GCATGCAACT	CTTCAAGCAT	240
	GATATCTTCT	TCCTCGTGCT	CTGATCCGGC	GTTGTCTGTC	TTTGCGCAGT	CTTCGTAGGC	300
	GCCATTTCTG	TAATGTTGAA	GCTGTTCTTT	GTTTCATCTT	AGACCCTCCG	TCAGGAAATA	360
35	TTCAAAGAAA	TCGTCTTCAC	TAATATCTAC	GCCTTCACTC	TCGAAAAATG	TCCGAGCCTC	420
	TTCAATCCCA	GCTGAAGACC	CCTGACCAGA	AACATGCTCA	TTGCTACCTT	CATCGTCATC	480
	TTTAATATCT	GTCAGGAAAG	TCTCCAGCGA	CAGGGCCAAG	GCATCCATAG	ACGCCTCTTT	540
	GTCCGCAGTC	GGTACCTCCG	TAGTTAATTC	AGTCGTAGAG	AACTCCACCG	GGCGCTCTAG	600
	CTGTTTTGTA	TGTACCAGAG	CGCTTACTAG	GTCACCCTCT	AACCTTCTCT	TGGGTTTACG	660
40	TGTCGTTAAC	TGGCC					

1687UP

	GATCCGTTCC	AGTTTGGCCA	GCGGAAGCTG	GCGGACGAGG	CGGACATCTG	GGCTCATAAC	60
45	GCGTGGGATA	ACGTAGACTG	GGGTGACGAA	CAGATCCGGC	TCGCAAAGGA	GAAGATAGAA	120
	GAGCAGAAAG	AATACCCGGT	GCAGGAGTTT	GACAAAAAGC	TGTATCATAG	CAACCCCGCA	180
	AGGTACTGGG	ATATATTCTA	TAAAAATAAC	AAAGAAAAC	TCTTCAAAGA	CAGGAAGTGG	240
	TTGCAGATTG	AGTTTCCCTC	TCTATACGAA	GCTACCAAGA	AAGATGCTGG	TTCACTGACT	300
	ATCTTCGAGA	TTGGGTGTGG	TGCGGGCAAT	ACCATGTTCC	CGATCTTATC	TGCAAACGAA	360
	AACGAACACT	TACGCGTTGT	GGGTGCGGAC	TTCTCCCCGA	AGGCCGTGGA	ATTGGTAAAG	420
50	ACGTCGCAAA	ACTTTAACC	CGCGAATGCC	CACGCGACGG	TATGGGACTT	AGCCAACCTT	480
	GATGGTCTTT	TGCCCCGATG	TGTCGAGCCG	CATTCCGTCG	ACATCGCAGT	AATGATTTTT	540
	GTTTTTAGTG	CCTTGGCGCC	CTCACAGTGG	GCCCAGGCTA	TGGATAATTT	GCACAAAGTT	600
	CTAAACCAG	GCGGTAAGAT	CCTCTTTAGA	GACTATGGCA	GGTATGACTT	GGCTC	

55

1688RP

	GATCTTGTG	AGAACA	ACTCA	ACATCGGCGT	AATTGCAGAG	CCCCCGGTGA	CCATACCGAT	60
	TTTCTTG	TAC	GCATT	CGTCA	CATAGCTGAA	CCGTCCCTACA	GGACCTTTGA	120
5	TTGGCCTGGC	TGTAGCCCAG	CAAACCATTT	GGATACCTTA	CCGTGCACAT	AAGATTTGAC		180
	AATGATATCG	AAATGGCCCT	CGGCAAATTT	GTTGGAGATA	GGCGTGTAGT	AACGCACTTC		240
	TTCTACACCA	TCCAGCATCA	CCTTCGCAGC	TAAATGAAAG	CCAGTAGGTA	TATCAAGAGT		300
	TTCCACGCTT	GAACGGAGCT	TGAATCTGTA	TATCGCAGCA	TTTTTGCTTA	GAACGATCCG		360
	TTCTTCCAAT	TCTAATGGCG	TCCACTCATT	TGGAAGAATT	GAAATCCTGC	TTCTGTATGC		420
	TAGTAGCAGG	CGTGCACCTA	CAAACATTCG	CAAAGCTAGA	ATGCCTAGAA	GGTACCATGC		480
10	GTTCCCCGCT	GACCAGGCGA	TAACAAGAAC	GCCCAATGTA	AAGATGCCGC	TGGGGATGAA		540
	GATCCCATGA	ATGGGATCAT	CCAATATCTC	CATACCTCTG	CGTTCGGTCA	TACTAATATT		600
	TTGAAAGCTC	GTCGTAGCTA	TCGTCTAGTA	AGGATGAGAA	CGGTTAATAT	ATGCTTCCTC		660
	CTAGTTCTAT	AAGCACGGAC	TCCTTTGCAA	CTGGTGAAGT	ATCGTCTAAC	GGTCAT		

1688UP

	GATCAGGCCG	GACGGGTACT	TGCAGGAAGG	CCTCACGAAA	CCCAAGGGGG	GCGAGGAGGG	60
	CTTCTCGACG	TTTTTCAACG	AGACGGGGCTC	GGGCAAGTTC	GTGCCGCGCG	CGGTGTACGT	120
	GGACTTGGAG	CCGAACGTGA	TGCAGCAGGT	GCGCACGGGC	GCGTACCGCG	AGTTGTTCCA	180
20	CCCGGAGCAG	TTGATCAGCG	GAAAGGAGGA	CGCGGCGAAC	AACTACGCGC	GTGGGCACTA	240
	CACGGTGGGG	CGCGAGCTCT	TGGACGATAT	CCTAGACCGC	ATCCGCAAGA	TCTCGGACCA	300
	GTGCGACGGG	CTCCAGGGCT	TCCTCTTCAC	GCACTCGCTT	GGCGGTGGTA	CGGGCTCCGG	360
	CTTGGGGTCT	CTGCTTTTGG	AGCAGCTTTC	TATCGACTAC	GGCAAGAAAT	CGAAGTTGGA	420
	GTTTGCCGTG	TATCCGCGCG	CACAGGTGTC	CACCTCGGTC	GTGGAGCCAT	ACAACACCGT	480
	GTTGACCACC	CACACCACAT	TGGAGCATGC	CGACTGTACG	TTTATGGTTCG	ACAACGAGGC	540
	CATCTACGAG	ATGTGCAAGA	AGAACTTGGA	CATCTCGAGA	CCTAGCTTTG	CGAACTTGAA	600
25	CAACTTGATC	GCCCACGTCG	TCTCCTCGGT	GACCGCGTCA	TTGCGTTTCG	ACGGCTCCTT	660
	GAACGTGGAC	TTGAAC					

1689RP

	GATCGTGCAC	AAGTTTGACG	AGCTAAAGCT	AAAGGAGGTG	TTGTTGAGAG	GTATCTACGG	60
	TTATGGTTTC	GTTGACCCAT	CTGCCATCCA	GCAGCGTGCG	ATCTTGCCCTA	TCATTGAGGG	120
	CCACGACGTT	TTGGCGCAGG	CCCAGTCCGG	TACCGGTAAG	ACTGGTACCT	TCTCGATTGC	180
	TGCGTTGCAG	AGAATCGACG	AGAGCATCAA	GGCCCCACAG	GCGTTGATCC	TAGCTCCTAC	240
	CAGAGAGTTG	GCGCTACAGA	TCCAGAAGGT	TGTGATGGCG	CTTGCGCTGC	ACATGGACGT	300
35	TAAGGTCCAC	GCTTGTATCG	GTGGTACGGA	CCCTCGTGAG	GACGCCGAGG	CCTTGAGAGC	360
	CGGTGCGCAG	ATTGTGCTCG	GTACCCCCGG	CCGTGTGTTT	GACATGATTG	AGAGACGTTA	420
	CTTCAAGACT	GACCAATCA	AGATGTTTCT	CCTGGACGAA	GCCGACGAGA	TGTTGTCCCTC	480
	CGGCTTCCAG	GAGCAAATTT	ACAAGATTTT	CACCATGTTG	CCACCAACCA	CCCAGGTCTG	540
	GCTATTGTCT	GCCACCATGC	CAAAGGAGGT	GTTGGACGTG	ACCGACAAGT	TCATGAACAA	600
	GCCCGTCCAG	AATCTTGGTC	AAGAAAGGAT	GCCTTGACCT	TGGGAGGGTA	TCCAGCAGTA	660
40	CTATATTAAC	GTCGAGAGCG	AAGAGTACAA	GTACGACTGT			

1689UP

	GATCGCGCTG	AACCTCAGCG	AGGCACGGCT	GGTGATCAAG	GAGGCGCTGC	AGCACCGGCG	60
45	GCGGGTGTTC	GGGCAGTGCG	GGGACGGGCT	GGAGGAGGAC	GAGGCGGACG	GGGGAACACA	120
	ATATGACGCA	GGAGAAGGAG	CTGGCGATGC	TGGACAAGCT	GCTGGAGAAG	ACGACGGGGG	180
	GACAGAACCA	GGCGCTGAAG	CAGACGATGG	TGTACCTGAC	GAACCTTCGCG	CGGTTCCGGG	240
	ACCAGGAGAC	GGTGACGGCG	GTGACGCAGC	TGCTGGCGTC	GACGGGACTG	CACCCGTTTCG	300
	AGATTGCGCA	GCTGGGGTCG	CTGGCGTGCG	AGGACGCGGA	CGAAGCCAAAG	ACGCTGGTGC	360
	CGAGCCTGGG	GAACAAGATC	TCGGACGAGG	ACCTGGAGCG	GATCCTGAAG	GAGCTGTCTGA	420
50	ACCTGGAGAC	GCTGTACTAG	ATAGCTATAC	AGACAGGAAG	AACCTTGCCGC	CGCCGCGGCG	480
	CCACCAAGTG	TCGAGACAGG	AGTGCATAGT	GTGCTCGATG	TCGACGGCCT	CGCGGCCGAA	540
	GTTGCAGACG	CAGCGCTGCG	CGAGACGCGC	GACGTGCGCG	GACGGGACAG	TGCCGTAGGG	600
	CACGTGGAAG	TTACCGATCT	CCTCGAAGTG	GTGCACCTCG	TCCGCGCGCA	GGAACAC	

1690RP

	GATCTGAAAC	TAATGTCATC	CGCGGAAGAA	CATACTAAGA	GCTCATCGTT	ACATCGAGAT	60
5	GAGACAAAGT	ACCTGATGTA	TAAGAGTTTT	ATTGACATAT	GCGCTCGGAG	GCAAACGGCA	120
	GGCTACCGCC	TGCCCCGTGT	TCCGTCTACA	CATGACAACA	TAATTGTGGC	AATGTCAGGC	180
	GGCGTGGACT	CTTCAGTATG	TGCTGCTTTA	TACGCTCACT	TCCCAAAAGT	CCGTGGGCTC	240
	TACATGCAGA	ACTGGTTCGA	GACGTCGGGC	TCAGGGCCTG	TAGAGGGTAA	GGCCGAACCT	300
	TGTTACGAGC	AAGATTGGAA	GGATATTGAG	AAAGTGGGCG	CGTACCCTTA	TATTCGCCGT	360
	GAGAGAGTCA	ATTTTCGAACG	GGACTACTGG	CTGGATGTTT	TCGAGCCTAT	GTTACAACGG	420
10	TATCAACAGG	GTTATACTCC	GAACCCAGAT	ATTGGCTGCA	ACAGGTTTGT	AAAGTTTGGA	480
	GCGTTGCGGG	AGCACCTGGA	CAAGGAGTAT	GGACGCGGCA	ACTACTGGCT	GGTAACAGGC	540
	CACTATGCGC	GAATCCTATC	CCCCCAGACT	CGCAGAGAGA	CCCACCTGCT	GCGGAGCCAT	600
	TATGCGCCAA	AGGACCAAAG	TTACTACTTA	TCCCAAGTCC	GGCGGGAGGC	CCTCGCGGAC	660
	CTCTTTAATG	CCCATGGGAT	TTCTAACAAA	ACCGGAAGTC	CGACAATGGG	CCGCAGAA	

1690UP

	GATCAGAAAC	ATCACCATAT	GGTGTCTGAA	GACCTTACGG	CGACGGTCGA	TACACGCTAC	60
	CATCTCCAAG	CCGATGATGC	CGGCTATTAT	GGACACCGCC	GACGCCGTGA	TTGCCAGGAT	120
	TCGCAGCTTC	AGCAGCTGGC	TCGAGGTGAA	CGTCGAGAAC	ATCCCCGGCA	GTCCGAGCAC	180
20	GAGGTTCAAC	GTGGTTGTGT	TGTAGGACCC	GAATACACAT	GTGTAGTTGC	TGTCCATGCA	240
	CTGTATCTGA	GACGCGCCCT	CCATCTTGCA	CGTGCCTGCG	CTACACGTCT	AGCTCCCGCT	300
	CGCACCTATA	CTTTGTATCT	GTTTCGCCCT	TGCTGCGCGC	TAGCCCCCTC	GCGCTTGCCT	360
	CTTATCCCTT	CTCGAAGTCG	TCTCCCCTAA	GTTGGATCCC	AGCGACCTCC	TAGTCGAAAA	420
	CTGCTGTCTA	CGTTCGCCAG	GCACTAGTTG	CCTCCCCTG	CAGGTTATCG	ATAAGTCCTA	480
	AAATACCACC	AAGCAGGCGT	TGTACTGCTT	CTATACGCCA	ACCCTCGCTT	TTCGTTGGGC	540
25	TGACACACTC	AAGTGACTGC	AAGAAGACTA	CCCTACTCAC	AGATACCGTC	GTCCGTTGTA	600
	CGCACGCTAA	AAGACAAGTT	AAATCTACGA	CACATATAGT	GCCTCGCAAG	CTCACCGCAT	660
	CCGGAAGGAA	CAAGCTATTA	GAAACTGAGA	CACCTC			

1691RP

	GATCTTCTTT	GTATTCCTCG	TCTTACCTGC	CCCAGACTCC	CCTGTTACTA	ACACCGACTG	60
	GTCTTGCCTC	TGTGTCAACA	AGTTGCGGTA	TGCTTGCTCC	GCTACCGCAA	AGATATGCGG	120
	CTCGTTGTCT	TCCTTGGGTG	ACCCATGGTA	CAAGTTCACA	TAGTCCTGCG	TGTACACCTT	180
	GATGTTGCTG	TACGGATTCA	ACGCGACGAG	GAATAGCCCA	GAATAAGTAT	ATATCATATC	240
	GTCCTTGTAT	CGGTTCTCCA	AGTTGTACAA	CACAGACGCC	TCGTTCAAGT	GGGTCAACTC	300
35	GGCAATATCG	TCTATCTTGT	CAAACGTTGA	CGGATTCAAC	GCCGCGGTCT	CCACCTCCAG	360
	CACTTCTCGT	TCCTTGCCAT	TCACTCTCAC	AAGACAGACC	TTCTCATCCT	TGTTCTGTTT	420
	GTTTTTAATT	GTCTTTGTGG	AAACCAACTG	TCCTTTTACA	AACACCTCCT	CAGCATCTGG	480
	AACCCAAATC	ATTTGACATT	GTTCACTCAT	CGGGACAGAT	GCTCTTGAAC	TTATCTAATA	540
	TGCAATAACC	AAATTCAACT	TTACTTTAAT	CACCTGCTTG	TTACACACGA	AGCAATGTTG	600
	GATCTCATAT	TCACACGACC	TACTTTTTTCG	AAACACTTAT	TTGTTTATGT	CGGGCTCGAG	660
40	CATACACGTC	GGTCACGTGA	CAAGCGCATG	TAC			

1691UP

	GATCATTATG	CAACCGAATC	TGGTATCTCA	GAAGATTACC	GTAGGACTGT	GCCTGTCCGA	60
45	TCGATTACGT	TAGTGGGGTA	GAGAATGAAG	TAAGAAGCAG	CTCTGCGATT	ATTGTGCGTT	120
	TGCGCCTCAT	GTGAGGTAAA	GCCCTATCCC	GCAGGGTGGC	GGCTTTCTGC	AAGAAAATCT	180
	GGGCATCAGC	CCCCCGAAAC	GAAATGCGAT	AGTCACCTGT	GCCATGGCGA	CGAGTCATTT	240
	CCCCATTCTG	ACAGAAATGA	ACGGGCAGAA	TCGCGTAATG	GATTTTCTGT	GGCGTTCGTG	300
	CCAAAAGGTG	ATCTCCACCT	GCGTGCTGCC	CTGCGGGCGT	GGTTGAGCAG	AGCACCTGGA	360
	AAAAGAACAG	CACAGAAGGC	CAATGCAGTT	GGCCAATTGA	GGCAATAGCC	GAGCAGGAAC	420
50	AGTCGAAAGT	GGGTGTTCTG	GCGCTGTTGG	ATCTGAAAAA	TGCAGGAAGT	TACAAAAAAC	480
	AGTGGGGCAA	TACATAGAAA	CCGGCGACCC	GGCGATCGCC	TAATCATCTG	CCATGGAGAC	540
	GCGGGTCCGG	CGCTCGAACC	AGCGGTGCAA	ACCTTGAGGG	CATGGTGATA	CGGGCCCCGT	600
	GGCGGGGCAC	TCAAACAGGC	ACGTGTTAAT	CCTGACAAAA	CGCAGCGGGG	TAATTCCTTT	660
	CCGCAAGCCG	GACGGGTATA	TGAATCGTAC	GATACCAGTT	GTCGA		

1692RP

	GATCTAAATA	TATATAATTT	AATTTATAAA	GATTAATATA	AACTTTTTTA	TTATAATATT	60
	TAAGTATTAA	ATTATTTAAA	CTATTATTAT	CATTATTTAA	TAAATTAATT	ATTTGATTAT	120
5	TAATACTTAT	TATATAATTA	TTATATAAAT	TACTTAATTC	ATCATTATTA	ATATTTATAT	180
	AATTATAAAA	ATAATATTTA	ATATGAATAC	TATTTAGTCT	ATGTTCAAAT	TTTAAATTAG	240
	TTATTAAAAAT	ATTATTAGAT	ATTATTATTT	TCTTTAATAA	ATTATTAAAT	AGATTATCAA	300
	TAATTAATAT	ATTATTTATT	AATTGTTTAT	TAAAATAATA	TATTTTATTA	TTATAAAGAT	360
	TTAATTTATT	TAAATATTGT	AAATTATTAT	TTTTATTATA	ATATCTATTT	TTATAAATAT	420
	TATGTTGATT	TATATTATTT	AATCTTTTTA	TAAGAATTAT	TATTAATAAT	AATTTTAACT	480
10	TTAATTTCTT	ATTATTAATT	TTTATATTAT	TTAATAAATT	ATATTCATTT	TATTTATTTA	540
	TTTATTTAAT	TAAATTAATT	ATTTAATTAA	TATTTTATCA	TTATTTAATT	AATTAATAAA	600
	ATATTATAAA	GAATGTAGTT	AAAAATACTT	ATAAAA			

1692UP

15	GATCTTGATA	CTAGAGCTTA	TTTTACTTCA	GCTACTATAA	TTATTC TTAT	TCCTACTAGT	60
	ATTAAAGTAT	TTAGTTGATT	ACTAACTATT	TATGGTGGTT	CATTAAAGATT	ACTAACACCA	120
	ATATTATATC	TATTATCATT	TTTATTTTTA	TTTACTGTAG	GTGGTTTAAAC	TGGTGTAGTA	180
	TTAGCTAATC	TATCATTAGA	TGTAGCATT	CATGATACTT	ATTATGTAGT	ACTACATTTT	240
	CATTATGTAT	TAAGTTTAGG	TGCTGTATTC	TCTATGTTTG	CTGGTTATTA	TTATTGAAGT	300
20	CCTCTTGTTT	TAGGTTTAAA	TTATAATGAA	AAATTATCAC	AAATTCAATT	CTGATTAATT	360
	TTCTTAGGTC	TTAATATTAT	TTTCTTCCCT	ATGCATTTCT	TAGGTATTAA	TGGTATACCA	420
	AGAAGAATTC	CTGATTATCC	TGATCTATTC	CTAGGTTGAA	ATTTAGTATC	TTCAATTTGGT	480
	TCTATAATAA	CTATTATATC	ATTAATGTTA	TTCTTTTATA	TTATTTATGA	TCAATTAATA	540
	AATGGTTTAA	CTAATAAAGT	TAATAATAAA	TCTATTAAAT	ATATAAAACT	ACCTGATTTT	600
	ATTGAATCAA	ATAATATTTT	CTTAATGAAT	ACTACTAAAT	CATCATCTAT	TGAGTTTATA	660
25	TTAAATTCAC	CACCTCTTAT	TCATTCATTT	AATACTCCTC	TAATTCAATC	TTAAAAATAT	

1694RP

	GATCCGTTCC	TTGAGAAGCA	CCTAAAGCCT	GAAGTCTCTGG	CAGAAGCGAT	CAAGGGAACC	60
5	TCTTGGGAGG	GTAAAGTTAG	TATTAACCTG	GTAGACGGAT	TCGACCACTC	GTATTACTTC	120
	GTCAGCACGT	TCGTGCCGGA	ACACGCAAAAG	TACCATGCAG	AAAAGTTGGG	TCTAGTTTGA	180
	GATTTGACGT	TGCGCCTGTT	AATTGGTATA	TACTTACATA	TTTAGTCATA	TGACGGCTTC	240
	AAGTACTCTG	ATTCTGCATT	ATAAGTGCAG	CCGAATGCCA	GCCTCCGGCA	GTAATGGCAA	300
	CGCAAACGTA	ATTTGCCGGT	AGTTCAACCT	TGGCCGGTTG	CAGCACGCGT	ATGCTCCGAG	360
	CAGACTCAAA	CGTCGCTATT	TGGCGGGTAT	CTACAGCCTC	GTCGGGATCT	CCCTGCCCAA	420
10	GACAGCCACA	GATATCACTC	TCCAGCCCCC	AGGAGTAGAG	TTCACCTTTG	TCGGTTAGAG	480
	CTAGGTTGTG	GTAGTCTCCC	GCAGATACAG	CAATAAACTT	CTGGCCTTGT	TCCAAATTCA	540
	TCTTCATGAA	TGAGTCCCTG	ACGATATCAC	CATTATTAC	CTTCAGGGTG	TATGTGCTAT	600
	TCTCGGTACA	TAAAACCAGT	GTCATGCAAG	ATGCCTCAAT	CTTCGTTAAC	CGTCCATCAA	660
	ATGGCAAAAT	CAA					

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1694UP

	GATCAGCCCC	CGACCGAAGA	ACACTCGCTT	CCCTCTGGCG	AGCGCCGAAA	TTCTTGGACC	60
	GAGTATCAAC	AAATCCAGTT	AGATAACGAT	CACATGATTG	CAACACTGCG	GGAATTCAAT	120
	AGTTACCAGA	CTGTTTCCCA	ACTCCCAGAG	CCCCAAAATA	TCATCGATTTC	GCGTAGGTGT	180
20	GCGAACTTCC	TGCAAAATCT	CTTCACTAAG	CTCGGTGCTA	ACCATTTGTGG	GCTTATACCT	240
	GTCAGTACAG	GCAGCAACCC	GGTGGTTCTC	GCGCAGTTCA	AGGGCAATGC	AGCCGCGCCC	300
	AAACGCATAC	TATGGTATGG	CCACTACGAT	GTGATATCCG	CGGACCACCC	GTGCGAGTGG	360
	GACAACGACC	CCTTCACGCT	CACTTGCGAA	AATGGGTATC	TTAAGGGAAG	AGGCGTGTCT	420
	GATAACAAAG	GCCCCGTGCT	TGCCGCCATC	TTCAGTGTAG	CCGAGCTTTT	CCAGAAAGGA	480
	TACCTGAACA	ACGACATCAT	CTTTCTAGTC	GAGGGCGAGG	AAGAAAATGG	CTCTCGCGGC	540
25	TTCAGGGAAG	TTTTCGCTTG	CTCCGAAGGG	CTTCTCAATC	AGCGGTGGGA	CTGGATCCTG	600
	TTTTCGCAAT	CCTACTGGCT	GGATCAGAAG	GTGCCCTGCC	TCAACTATGG	CCTCCGAGGC	660
	GTCATAAACG	CCGAAA					

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1695RP

	GATCTGCCCC	CAAAAGATTT	CGGTGCCGGC	TACCCCAAAA	GATTTTCGGT	GCCGGCTACC	60
	CCATCACGAG	ATGGCACTGG	CTCATTTGGC	AGCTCCTGGG	CATTTGCCTA	TGACAGAGGA	120
	ATGAGTCAGC	TTTACTCCGC	CACACCATAC	TCCCGGGCTG	TCAACAAGCT	TCTGTTTGCC	180
	ATCGGTCAGC	TGGCCAGTTC	TTACACTGCG	GCCCCACCTG	CATCGGCCGT	CATCGCAGCC	240
	GTTTTGTAC	AGTTCTCCCT	CCGCAGGTAT	CGTCTCCGCA	CCGGTAACGG	ACGCGACTAC	300
35	GCAGCGGCTG	CCGCACTCAC	GTGCGGGCGG	GTCTTCTCTC	CCACCGTGAT	AGTCACTTTT	360
	CAGTAGTGTG	TGCTGCCTTG	AATTGGCAGG	GCAATCGTTC	AAGCTGCTCT	GGCGCGGACG	420
	ACGACCCCAT	CTCCGCAACG	GCGTTGGCGG	AGAAAGGGTG	TTTCGGACCA	GACATCGGCC	480
	ATCTGCCGCA	GTCAGCAGCT	GCCTTGGTAC	GGAGCTACCT	GTCTATATTA	TCCCCTTAAT	540
	AAACATTGGA	TATGCCTGTT	ATTGTATGCC	AACGGTTCTC	CGGGTACAAC	GGGGTAGTCC	600
	CGCCCCCTCC	TGAGCTATCC	TGGCCGATGT	GAAGTGCCCT	TGGTTAAGTG	GTCTGCTTTT	660
40	CCGGGCCACT	TGTAAACACT	ATGGCGGATC	ATACAGCCAG	GACTCAAATA	C	

1695UP

	GATCTGAAAA	GCAGGAAGTC	GCAGTGGGAG	GCGCCTGCGG	GCACGTCGTG	GCCAGCGAAG	60
45	GGTGCGCCGG	ACGCGCCACC	GGCGTACGAC	ACGGCCGTCG	CACGCGCCGC	CGCGCACGGC	120
	GCGCAGGCCG	TTGCGCCCCA	GCCCGACTAC	GGCACACAGG	CCGGATACGC	GCCCCAGGGG	180
	TACGGCGCGC	GGGCGGGGTA	CACGCCCCAG	CCCGGCTACG	CGCGACAGCC	CGGCTACGGC	240
	ACACAGCCCG	GCTACGGTGC	ACAGCCCGGC	TACGGCGCAC	AGCCCCGCTA	CGGCGCACAG	300
	CCCGGCTATG	CGCCGCAACC	CGGTTACGGA	TACGCGCCGC	AGCCGGGCTA	TGGTGCCGCG	360
	CCCGGGCCGT	ACGCGCAGCA	GCCCGCGCAC	GGTTACCCGG	CCGGCGCAGC	CGCCGCGCCG	420
50	CAGAACGGCG	GCCGCAACAA	CATGATGATG	GGCGGCCTGA	TGGGTGCCGG	CGTGGGGTTG	480
	ATGGCCGGGT	CACCTAATGAC	CACAGCCATG	TATAACCAAG	ACAAGGACGT	GGCCGATGCT	540
	GCCTACGACC	GCGGCTATGA	AGACGCTTCA	TCGACGGCGA	CTTCTAGGCC	GCACCCCGTC	600
	ACGTGCCAGA	CCCGTAGAGA	GCTAGGACAA	CTTACGTAAC	GCGTCGACGT	ACGC	

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1696RP

	GATCTTGTTTC	TCCATTGACA	TCGAGGCGTT	TGAGAGCAAC	ACATCTGTCG	TCACAGAGGT	60
	GGGAATCTCG	GTCTACGATC	CCCGCGAGAA	CGAGGACACG	CTCGTGCCCC	ACTTCCGCAC	120
5	GTACCACCTC	TGTCTTGAGG	AGTCTCTCGG	GTTGATAAAC	AAGCGGTTTG	TTCCGAATCA	180
	CAAATGCGAG	TTTCTCCATG	GTGAAACCAT	GGTAATGCCG	CTCTCCGAGT	GCGTTGAGTT	240
	CATTACGGG	CTTATCGAGT	ACTACCTGTA	CCCACCCACG	GGCGTGGACG	ACAAGTACTC	300
	GCGGGCAATT	GTGGGTCATG	GTGTCTCTGG	TGATCTGCAA	TGGCTTAGGA	GTCTGCTCAT	360
	CGACCTGCC	ACGATCGCTG	GCCCAGGCAA	CTCCCATCCG	CGCGACCATG	TTTCTGTCTT	420
	AGATACCGCG	CATTTATACC	AGTACTTCTA	TGGTCAGAAG	GGTTCATCCC	TAGGTAAGAG	480
10	CTTAAGATTG	CACGGTGTCC	CACATAGCTA	TCTGCACAAT	GCAGGCAACG	ATGCATATTA	540
	CACATTACAA	CTGCTCATGA	AGATGGGCGA	TGTGCAGCAA	CGCATCCGGC	ACCAATGGGA	600
	CGATCTATAT	GCTGTCTTCC	ACACGTTGAA	GCAATGGGAA	GAGTATGAGA	ACTCCACGCC	660
	CTCCACTCAG	CACGCAGAAT	CCGTCCATAA	CAGCACCCGC	GCTACCGGGA	A	

1696UP

	GATCCGTCAG	AAACCCATCG	CCTCGCTCGC	TCGTCTGCTA	ACGCCCAGAA	CGCCACCTGT	60
	GGTCTTTTCA	CTGCCGCTGG	TTCTTTATTC	CGCCAGGGGG	CCTCGTGGGC	CCGCCAGCGC	120
	TCGCCAGCGC	GGTTGTCTGC	ACCCGCAGCA	ACAGGACGAG	AACTCTCCGC	TTTCGGCCTC	180
20	GTGAGATTTT	GGATTTCAGT	ACGTGATTCA	CGTAGAGGTT	ACCCGGAAAG	AGCGGCTTGG	240
	ATGCCAGTAA	TCACCGCCGT	TATCCCCGGC	CTTCTTAAGC	ATTCACTCTG	AGCCGCTTCT	300
	CCCCGCTTCC	TTGTTCTCCT	GGAAATTTCAA	AGGGCGGGCG	GTATATAGGC	GGCGAGAAAA	360
	ACACGGTGGC	GAACGTTGTT	GCCGCCAAGC	GTTATCGTGA	AGAACAAGCA	TAATGGTTTC	420
	CCCTTCGGTT	ATTAAACAGG	TGCAGGCGCT	AATCCAGCAG	AACCGCGTGT	TCATTGCATC	480
	CAAGACGTAC	TGTCCGTATT	GCCAGGCGGC	AAAGCGTACG	TTGCTGGAGG	AGAAGCGCGT	540
25	CCCGCAAGC	GCAGTAAAC	TGTTGGAGCT	TGACACCATG	GGCGAGGAGG	GCGCGGTGAT	600
	CCAAGCGGCG	TTGCAGGAGC	TGAGCGGGCA	GCGCACCGTG	CCCAACATCT	ACATCAACGG	660
	GCGCCATGTG	GGTGGCAACA	A				

1698RP

	GATCTGGTGC	TTTTCAACGC	GCCGCCCCAG	ACAATTTCCG	GAAGCATACA	TATCGCCATT	60
	ACATAAACAG	ATTTTATGAC	TAGTACAGTT	AGGTATGTGG	GAGATCACCG	GAATAACTCC	120
5	TATATCTTAT	TTCTGTATTG	TCAGGTACTG	ATCGCTGTGG	ATGAACGGGC	AACCCTGTGA	180
	CTTGGGGATT	AACACTGTAT	GAAGCCGGAC	GGGGGGGTAG	CACATTGGTA	CTAGGCTGGC	240
	TGAATTCATA	ATTGGAATAA	GGTGTGCTTT	GCCCCGATGG	CTGGTATGTC	CGGTGCTGGG	300
	TTGAAGGCAT	AAAATTGCTC	GAGCTGTAGC	ATGTTGCCTT	CTCTAGCATC	ATGTTGTATG	360
	TAACCTCCGC	ATTGGCCAGA	ACCTCGCGCA	ATGATGCAAG	ATCTTCCTTC	TTCTGCGCAT	420
	ATTTACCGAT	GAGTTTCGTG	ACATGTGGTC	TAAGCGGTGT	GACGGTAGAG	TAAAGTTCTG	480
10	ATATCTCGTC	TTCTGTGTGTC	ACATCCACAT	TCTGGGAGAC	CCTTAGTTTC	TGGAGCAAGT	540
	TCTCGACATT	GCCGGCTTGC	GCAAAGACAG	CATGCTCCTG	AGCAGCCTCC	TTAGCTACCT	600
	CCTCTGCAGT	TGGCTCAGGG	CATACGCCGA	CATAATTAC	TGGGAAAAAT	ACCAACCTTG	660
	CCGCGCA						

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1698UP

	GATCAGCAAG	CTGGCCGCCG	CAGGTGTGCA	TCTGGGGCAG	TCTACGTCGT	TGTGGCGCTC	60
	CTCCACTCAA	CCATACATCT	ACGGCTCTTA	CAAGGGCATC	CACATCATTG	ATCTAAACCA	120
	GACGCTGTTT	CACCTGAAGA	GAGCTGCGAA	GGTCGTTGAG	GGTGTTCGGG	AGAATGGTGG	180
20	CCTGATCTTG	TTTTTGGGTA	CCAGAGAAGG	GCAGAAACCA	CCTTTACGGC	GGGCTGCAGA	240
	GAGGGTGCGT	GGCTGTTATG	TCGCCTCGAA	ATGGATACCG	GGGACCTTGA	CAAACCCAAT	300
	TGAAATATCC	ACTGTCTGGG	GCAGGCATGA	AGTTGACTTC	GAGGGCAATC	CAACTGGCAG	360
	GGAATTGACA	GAAGAAGAGA	ACATCCGCAT	CATAAAGCCG	GACTTAATTA	TTGTTTTGAA	420
	CCCAACAGAA	AACATGAACG	CGTTGAGAGA	GGCTATGCAG	GCTAGAGTGC	CACCTATTGG	480
	GATCATTGAC	ACCGACTCAG	AGCCTTCAAT	GGTCACATAC	CCGGTCCCTG	GTAACSAACG	540
25	ATTCGCTACG	TTCTGTAAAGT	TTACTTGTAAC	AC			

1699RP

	GATCTGCGTG	TATATTTGGA	TGTATATGGA	CTTCACACTT	TCGGAAGCAA	TGGAACTCGA	60
30	AAGCTGGTTG	ACCACTCTGC	TGTATTCTCG	TAGTCTTTCT	GAAACGACGG	TAAGAAAATT	120
	AACCTTGAGC	GGCGATAGGG	AAGATGCAAC	TTTAAATTTT	TCTACTTGGT	TACTCAAATA	180
	CTGATATAAT	AATGCAGCCT	CAAATATGCT	GTGGAAAACA	CCACTTTCGC	CGTTCGGAAC	240
	ATTGGGTGGG	ATTTCGATAA	CCTGATTGGA	GATCGGGAAC	AAACTCGACG	TAGTAGCCAG	300
	TAACGTGTAG	GAAATATACT	TTAAAACGTC	GGCCTCGGGC	ACCATGTTGC	TGTAGTATGG	360
	GTTAGACAGA	TATGCCAATG	GAGTATCGTG	CTGCTGCGGC	CGCTTGGGGA	CCGGGCCGCC	420
35	GTAGGCAGAG	GTTACCGCCG	ACCGGCGCTC	TGAAAGCCGC	TCCACATTCT	CGAACGACTC	480
	TGCATAGACA	CTAACCGCCC	TCGACGGCGT	CATCAGCGAG	TTGTGCCGTT	GCAGCGTGGC	540
	GTTCCGTAAGA	TATCCAGACG	CGGTGCGCCT	GTGTGCGAAG	GGCGTGCTCT	CCTGCGGCAC	600
	GCTGTTTCAGC	ACCGTCAGGT	ACTTCAGCAC	CTGCTCCTTG	CTACCGAAAC	TCTCCAGCAC	660
	TTTC						

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1699UP

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	CCGCGCGACG	CTTTCGAAAA	CCGCCCGTCC	CTCCGCGGTC	GCAGCCCCTC	CCCCGCTGTC	120
	GTGCGTCCGG	TGCTCGGCCT	CCCGCGACCG	CAGCGTCGCC	ACCACCCGCT	CTATATTAC	180
45	GCCCGCGGGC	TTCAGCGTGT	CGCGCTTGAT	GCCAGGGCTG	GTGGGTTTCT	CTCCCACCAC	240
	CTCCAGGCTC	TTGATAAACG	TCGTCTTAAT	CACCTTAAAG	CTCGCAGTAT	GGCCCTTGCG	300
	CCCACATAGT	AGCGTCAGCG	TATGGTTTCC	CGAATCGTAC	GCGTATATCT	TGCCCTGTGT	360
	TACACCGTCC	AGGACGTTGG	TCACCCGCAC	CTTGAATCCA	AGGATATGTT	CCAAGTTGAT	420
	GCTCATTCTG	CTCACTTCCA	AGCCCCACAC	GCTATCCTGG	CCACCTTAGA	ATGCCACGCC	480
	TGCTCCCCGT	CCACTGGCTG	ACTCCCAATC	GTTCAAGTTG	CGGTGTGGGT	ATTTTTTTGA	540
50	AGTGGCGCTC	TAACGATGAA	GTAGGATTTT	CTATGTATTA	CTATGTCGCA	CAAAGGTTAG	600
	TTCCAATAGT	GCTTGCAACT	ATCAGGTGCT	GTGGAATTCC	AA		

1700RP

	3ATCAGCAAC	CGCAGCGGAT	GAGGGAGTCC	GCTCACGCAC	GGTCTTGTTT	TCAGCGCTTG	60
	3CTTGCTTTT	CTCCTTTATG	CGTTGTACTA	CTTCTGTGAT	GTGCTCGGCA	TCCAGGCCCC	120
5	FTTTCCTTAG	CCTGCTTCGT	AACCTGCGCA	GGCGGCGGTT	GCTACGAACA	CGCAACTTGG	180
	CTTCTGGATC	AGCAAGCTGC	GCTCGGTGTT	TGCGCAGCCG	TTGGCATGCT	CGCGGATCCT	240
	CGCGTTCAAT	ATACCAGAAT	GCATCATGCT	TCGCTGGCTC	TATATTGACC	TGGTGGCCAT	300
	ATATGAAAAG	GCGGTCCTTG	AAGTTTTGTA	AAACTCGTC	TGCCTGAGAT	GGCGTAGCGA	360
	ACCCAAGGAA	GCATTTATTG	CGGCATTTAC	GAGGCCTGGA	AACACTAACT	ACCCCGTACT	420
	TCATCATCTAC	CAGTGGGAAG	GGCACGTCTG	CGGAAGGAAG	CGGCTCTGGC	AACGTTTTCT	480
10	CCGCCGATAG	AGCATATGGG	TTATCCTTGT	TGATGGACTT	CAACAGTTGT	CGAGCATATT	540
	CTATCCTGGA	GGCATTTGAC	GCTGGCAAAT	TTGACAGGTA	GACACTGGAT	GGCGGGGTTA	600
	3TATCGAATC	GACAGCAGTA	TAGC				

1700UP

15	GATCACTGGG	CCTGGAGGGG	CGCGCCTTTT	TGCGGCTGTT	GTAGAACAGC	ATGCCGCGGC	60
	GGACCTTGTC	ATAGAAGTGT	TTAGACTGTA	GGGTTCCCAT	CGAATGGGAG	CGGCGGTAGC	120
	TGTGACTTTT	CATGATAATG	GGGGTGCAAA	GCTTGAGGTG	GTCGTCTGTAC	GGGGAGGAAA	180
	TGAGGTTGCG	GCCGAGACGG	AGGTCGTCCG	CGCGCGCGAG	CGACGAGCCG	CCGGATGGCC	240
	ACTTCCAGGA	CTTGCGCGAC	GACGGCGCGT	GGCGCGAGGA	GTAGGAGCGG	ATGGGGAGT	300
20	CGCCGCCAAG	CTGCGAGCCG	CGGAGCCACG	ACGTGAGCCG	CTTCAANAAA	CGGCGACGGC	360
	GGTTGGCGGG	CTGGAGCTGG	CCGGCGACAA	ACGCAGAGCC	GCTGTCTGGC	AGACCGGTGG	420
	GCGCGCCTGC	GCTGCTGGTA	AGCCCAGTGG	CGGACTCAGG	CAAGCCGGAC	ATGCCCGGGA	480
	AGTAGCGCGC	GCTGTTGGCG	CTGAGCTTCG	GAAACATCTT	GGAGAAGAAG	CCCGGCTCCG	540
	TGGAGCGCAA	CACGCGGTCC	GCCTTGGAGA	TGTGCTCCTG	CGTGGAGTGC	GCCAACTGCT	600
	CCA						

Ann x to the des ription

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Novartis AG
- (B) STREET: Schwarzwaldallee 215
- (C) CITY: Basel
- (E) COUNTRY: Switzerland
- (F) ZIP: 4058
- (G) TELEPHONE: +41 61 324 11 11
- (H) TELEFAX: +41 61 322 75 32

(ii) TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHEYA GOSSYPHII
AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 1152

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: EP 978 110 20.3
- (B) FILING DATE: 24-DEC-1997

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: CH 0016/97
- (B) FILING DATE: 31-DEC-1996

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTACTAGA TATTTTATAT CCAAGAAGCA ATAGATCAAA ATGGCTGCGG TAAAGAGAAT 60

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGGAGCTCC ACCGCGGTGG CGGCCGCTCT AGAACTAGTG CGCCAACGTT GCGAGATATA 60

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: AgLEU2

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..1116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

25	ATG GCT GCG GTA AAG AGA ATT GTG GTG CTT CCG GGC GAC CAC ATC GGC Met Ala Ala Val Lys Arg Ile Val Val Leu Pro Gly Asp His Ile Gly 1 5 10 15	48
	CGC GAG GTC GTG GAG GAG GCG GTG AAG GTG CTT GGC GCC GTG GAG CAG Arg Glu Val Val Glu Glu Ala Val Lys Val Leu Gly Ala Val Glu Gln 20 25 30	96
30	AGC CTG TCG GAC GTG CAC TTT GAC TTC CAG TAC CAC CTG GTC GGC GGC Ser Leu Ser Asp Val His Phe Asp Phe Gln Tyr His Leu Val Gly Gly 35 40 45	144
35	GCG GCC ATC GAC GCC ACG GGG TCG GCG CTG CCG GAC GAG GCG CTG GGC Ala Ala Ile Asp Ala Thr Gly Ser Ala Leu Pro Asp Glu Ala Leu Gly 50 55 60	192
40	GCG GCG AAG GAG GCG GAC GCG GTA CTG CTG GGG GCA GTT GGC GGA CCG Ala Ala Lys Glu Ala Asp Ala Val Leu Leu Gly Ala Val Gly Gly Pro 65 70 75 80	240
	AAG TGG CAG GGC GGC GCG GTC AGG CCG GAG CAG GGC CTG CTG AAA CTG Lys Trp Gln Gly Gly Ala Val Arg Pro Glu Gln Gly Leu Leu Lys Leu 85 90 95	288
45	AGA CAG GAG TTG GGC GTG TAC GCG AAC CTG CGT CCC TGC AAC TTT GCG Arg Gln Glu Leu Gly Val Tyr Ala Asn Leu Arg Pro Cys Asn Phe Ala 100 105 110	336
	GCG GAC TCG CTG CTC GAG CTG TCG CCG CTG GCG CCC GAG ATT GCC CCG Ala Asp Ser Leu Leu Glu Leu Ser Pro Leu Arg Pro Glu Ile Ala Arg 115 120 125	384
50	GAT ACC GAT ATT ATG GTG GTG CCG GAG CTG CTG GGC GGG AGC TAC TTC Asp Thr Asp Ile Met Val Val Arg Glu Leu Leu Gly Gly Ser Tyr Phe 130 135 140	432
55	GGC GAG CCG CAC GAG GAC GAG GGC GAC GGA GTC GCG TGG GAC ACC GAC Gly Glu Arg His Glu Asp Glu Gly Asp Gly Val Ala Trp Asp Thr Asp	480

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	145		150		155		160	
	AAG TAC ACC GTG AAG GAG GTG CAG CGC ATC GCG CGC ATG GCG GGG TTC							528
5	Lys Tyr Thr Val Lys Glu Val Gln Arg Ile Ala Arg Met Ala Gly Phe	165		170		175		
	CTG GCT CTG CAG CAC GAC CCG CCG CTA CCT GTG TGG TCG CTG GAC AAG							576
	Leu Ala Leu Gln His Asp Pro Pro Leu Pro Val Trp Ser Leu Asp Lys	180		185		190		
10	GCG AAC GTC CTG GCC AGC TCC CCG CTG TGG CCG AAG ACC GTG GAG GAA							624
	Ala Asn Val Leu Ala Ser Ser Arg Leu Trp Arg Lys Thr Val Glu Glu	195		200		205		
	ACC TTC CAG AGT GAG TTC CCA AAC GTG CAA TTG CAA CAC CAG TTG ATA							672
15	Thr Phe Gln Ser Glu Phe Pro Asn Val Gln Leu Gln His Gln Leu Ile	210		215		220		
	GAT TCA GCT GCA ATG ATT TTG GTC AAG AAC CCG CCG GCG TTC AAC GGG							720
	Asp Ser Ala Ala Met Ile Leu Val Lys Asn Pro Arg Ala Phe Asn Gly	225		230		235	240	
20	GTC GTG GTG ACG AGC AAC ATG TTC GGG GAC ATT ATC TCT GAC GAA GCG							768
	Val Val Val Thr Ser Asn Met Phe Gly Asp Ile Ile Ser Asp Glu Ala	245		250		255		
	TOG GTG ATC CCA GGG TCC CTA GGG TTG CTG CCA TOG GCC TOG CTC GCG							816
25	Ser Val Ile Pro Gly Ser Leu Gly Leu Leu Pro Ser Ala Ser Leu Ala	260		265		270		
	TCT TTG CCG GAT AGC AAG AGC GCC TTT GGC CTC TAC GAG CCC TGC CAC							864
	Ser Leu Pro Asp Ser Lys Ser Ala Phe Gly Leu Tyr Glu Pro Cys His	275		280		285		
30	GGC TCT GCG CCC GAT CTG CCC GCC GGG AAG GCG AAC CCG ATC GGA TGC							912
	Gly Ser Ala Pro Asp Leu Pro Ala Gly Lys Ala Asn Pro Ile Gly Cys	290		295		300		
	ATC CTC TCT GCT GCC ATG ATG CTG AAG TTG TCG TTG AAC ATG GTT GCT							960
35	Ile Leu Ser Ala Ala Met Met Leu Lys Leu Ser Leu Asn Met Val Ala	305		310		315	320	
	GCC GGC GAG GCG GTC GAG CAG GCA GTG CAG GAG GTG TTG GAC TCG GGA							1008
	Ala Gly Glu Ala Val Glu Gln Ala Val Gln Glu Val Leu Asp Ser Gly	325		330		335		
40	GTC AGA ACG GGC GAC CTG CTC GGC TCG AGC TCC ACT TCG GAG GTT GGC							1056
	Val Arg Thr Gly Asp Leu Leu Gly Ser Ser Ser Thr Ser Glu Val Gly	340		345		350		
	GAC GCC ATT GCG CTT GCA GTT AAG GAA GCC TTG CCG AGG CAA TCC GCA							1104
45	Asp Ala Ile Ala Leu Ala Val Lys Glu Ala Leu Arg Arg Gln Ser Ala	355		360		365		
	GCT GGT CTG AGC TAGCCTCGAG GACCCCTTCTC TTTAGACTAT TCTACTCTTA							1156
	Ala Gly Leu Ser	370						
50	TGCACGTAAA AAATTCTAGG AAATATGTAT TAACTAGGAG TAAATAAACC GGCTAGTGGC							1216
	ATTTCATATAG CCGTCTGTCTT ACATCTACAT CACACATTTT GAGTGTATAT CTGCAACGT							1276
	TGGCG							1281
55								

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Ala Ala Val Lys Arg Ile Val Val Leu Pro Gly Asp His Ile Gly
 1           5           10           15
Arg Glu Val Val Glu Glu Ala Val Lys Val Leu Gly Ala Val Glu Gln
          20           25           30
Ser Leu Ser Asp Val His Phe Asp Phe Gln Tyr His Leu Val Gly Gly
          35           40           45
Ala Ala Ile Asp Ala Thr Gly Ser Ala Leu Pro Asp Glu Ala Leu Gly
          50           55           60
Ala Ala Lys Glu Ala Asp Ala Val Leu Leu Gly Ala Val Gly Gly Pro
          65           70           75           80
Lys Trp Gln Gly Gly Ala Val Arg Pro Glu Gln Gly Leu Leu Lys Leu
          85           90           95
Arg Gln Glu Leu Gly Val Tyr Ala Asn Leu Arg Pro Cys Asn Phe Ala
          100          105          110
Ala Asp Ser Leu Leu Glu Leu Ser Pro Leu Arg Pro Glu Ile Ala Arg
          115          120          125
Asp Thr Asp Ile Met Val Val Arg Glu Leu Leu Gly Gly Ser Tyr Phe
          130          135          140
Gly Glu Arg His Glu Asp Glu Gly Asp Gly Val Ala Trp Asp Thr Asp
          145          150          155          160
Lys Tyr Thr Val Lys Glu Val Gln Arg Ile Ala Arg Met Ala Gly Phe
          165          170          175
Leu Ala Leu Gln His Asp Pro Pro Leu Pro Val Trp Ser Leu Asp Lys
          180          185          190
Ala Asn Val Leu Ala Ser Ser Arg Leu Trp Arg Lys Thr Val Glu Glu
          195          200          205
Thr Phe Gln Ser Glu Phe Pro Asn Val Gln Leu Gln His Gln Leu Ile
          210          215          220
Asp Ser Ala Ala Met Ile Leu Val Lys Asn Pro Arg Ala Phe Asn Gly
          225          230          235          240
Val Val Val Thr Ser Asn Met Phe Gly Asp Ile Ile Ser Asp Glu Ala
          245          250          255
Ser Val Ile Pro Gly Ser Leu Gly Leu Leu Pro Ser Ala Ser Leu Ala
          260          265          270
Ser Leu Pro Asp Ser Lys Ser Ala Phe Gly Leu Tyr Glu Pro Cys His
          275          280          285

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Gly Ser Ala Pro Asp Leu Pro Ala Gly Lys Ala Asn Pro Ile Gly Cys
 290 295 300

Ile Leu Ser Ala Ala Met Met Leu Lys Leu Ser Leu Asn Met Val Ala
 305 310 315 320

Ala Gly Glu Ala Val Glu Gln Ala Val Gln Glu Val Leu Asp Ser Gly
 325 330 335

Val Arg Thr Gly Asp Leu Leu Gly Ser Ser Ser Thr Ser Glu Val Gly
 340 345 350

Asp Ala Ile Ala Leu Ala Val Lys Glu Ala Leu Arg Arg Gln Ser Ala
 355 360 365

Ala Gly Leu Ser
 370

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CATGATTACG CCAAGCGGCG

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCAAGCACAT TTCACCTGCG

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1489

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	GATCGTAACA TTGCCAATA GCTTGTTTAG CTGTCATCG TTCTGATGG CTAGCTGTAG	60
	ATGTCCTGGG ATGATTCTGG TCTCTTGTT GTCTCTGGCG GCGTTACGG CCAACTCTAG	120
10	GATTTGGCG GCCAAGTATT CTAGCACAGC GGTAGGTAC ACAGGCGCGC CGACCCGAT	180
	TCTCTGTGG TAGTTGCCCT TTCTGAGCAA TCTGTGGACT CTACCGACAG GGAAAGTCAA	240
	ACCGGCTTA GCGATCTCG ACTGGAAGC CTGGGCGCA GAACAGCTT TACCTCCTTT	300
15	ACCAGACATT ATTGTGTG TGTTGTGTG TGTTGTGTTA GTGTGAAGT CGTGTGCTAT	360
	GAGAAAACAC TACGCTGAAA CTGCTAAATA ATCCAGACAG GTCCCCCAC CGCAAAGGAT	420
	CCACGTATA CTCTCTCTA CATATTTATA CTGTCTCTT TGCTTCTAA TCCTCGATCG	480
20	TACCGTCTG ACGCTTCAAC AGACGCTTCA CCTAGAGCT CGACCTGTGC GGCCTGGTTT	540
	TTTCGCATGA CATGTCCGTG CTGGTTTTTT CGCGCTGAAA AGGAAAGCG GTGGCTCCCA	600
	GCACCAGAGC CGTACTAGCT CTTTCGGTG CTGTCTATG TGCAAGGAA ATTTTCATAC	660
25	TGTAGAGTGT GCCATCAGCT TCACAGAGTA CAAACGGTAG GCGAGTGGAT ACGCGTCTG	720
	TAGCCGGACG TGAATGGCAG AACTTTTTGG CAGTCGGTA ATCTTAGATT GAAAGTATTT	780
	AAGTGAACG TATAAAACA AAGTTCGGC TGAAGAGGAC CTCTTTTGGC GTCTGCTACT	840
30	TCCCAGTTAT CTGTTGGATA CTAAGCATAT CGAACTCTAA TTGCAATTCT AAAGATGGCA	900
	CCAAAGGCTG AGAAGAAACC TGCTTCCAAG GCGCCAGCG CAAAGAAGAC CACTGCTTCT	960
	ACCGAGCTT CTAAGAAGCG GACGAAGACT AGAAAGGAGA CCTACTCTC TTACATTTAC	1020
35	AAGGTTCTTA AGCAGACTCA CCCAGATACT GGTATCTCG AGAAGTCTAT GTCCATTTG	1080
	AACTGTTTTG TGAACGATAT CTTTGAGAGA ATCGGTCTG AGGCATCCAA GCTTGGGCG	1140
	TACAACAAGA AGTCTACGAT CTCTGCTAGA GAAATCCAGA CTGCTGTCAG ATTGATCTG	1200
40	CCCGGTGAGC TAGCCAAGCA CGCGTGTCT GAGGTACCA GAGCTGTTAC CAAGTACTCG	1260
	TCTTCTACCC AAGCCTGAAT GGAATCATT CTTAGAATGA AAGAACTCC TTCAAGAAGG	1320
	TTCTGCTCAG CTAGTGCTTG TGGACCCGC CTCTTATCC AGAGCAGCTG CGGCAGAGCG	1380
45	GTATGTGGTA CGTTCGTTT CATCATTTTG TATTATTAGT ACATGTAGAA ATAGGGTTTT	1440
	CTGGTTTCAT AATTCGGTAT AAATCCAAC GTAATGTATA TTAGATAAGT TTAAACTAG	1500
	TAATCGGAGA GCTTCTTTTC AACCAGTCT ACCTTGCTT GCGAGTCTG CTGTTTGCT	1560
50	GTCTAGTTC CGAGCTCAT TTGGTGTGG ATTCTAACG ATCCAATTC GTGCTGTAT	1620
	TGCTGCAACT GCGGATGAG GCTCATGACC TCGTCCCAAG GCGCTCAAT CGTGTGCA	1680
	AAGCTGTGCA TAGTGCTTTT CAAGTACTC TCCCTAATC GTTCTCAAT CTTGGTGACA	1740
55	TAGTCTGAGA CACTTGGTGA GCTAGTACCT AGCTATGATT CAAAAGTTTA GTATATTGTT	1800

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	TTATATATGC AGCTGGAGAT GTGAACATAC CGGCACCATG CAAATGTCCA CTAATGTGTG	1860
5	CAGCTTCGAC ATTTTGATTT CTACCTTCAG AGTATTGGAA TATGTTCTTG TATGTAAOGT	1920
	CTACTAATTT TCTGGTTTAT ATCGCTGATC TTAAGGGAGA TAATTTGGTT CACCCATCAC	1980
	ACAGAAGTTT TAAGTACAAA ACTTGTCOCOC AGATATAGCA AGTCATCAAT TCAGGTATAA	2040
10	TTGGTGTGCA TGCTAATTTG AAGGGCTGTT ATATAGTTGA AGTTGTTCTT TTGGCATTTA	2100
	GCCAAATTTG GATTCCTATC AGTAGTATTG AACATCAAGT CTCCAAAGCT GAAGTCTGAA	2160
	GCAAAACATC TCAATAGCTA TAGAACTCTA GCAAAACAACA GACCAGAGCT TATATCATGA	2220
15	CACATTATAA GCTCAGCTAT TACTCTGAGT GATAGAGTGA CCTCAATTA GTTGGTTTAT	2280
	TTTATATATA AAAATATAAA ACTATAGCTA TTTCAAATGA CTACTAACTA ATACGAGAGA	2340
	AGAAAACAAA TTAAACACGA TGGTCTACAG ATAGCTTTGAA AGAGACACTA AGAGAAATTT	2400
20	CAGGAAACAG TTCAGAAAAT AGCCATTTCAG CTCTACAGCT CTCTTTTATTA TCAAGAGTAC	2460
	AGTTTCTTTC ACTAATATCG CTTAATTAAT TATATTTCTT GCCATTAAAT GCGACGGTGA	2520
	CGGGATAACA ATTTTITGGCA ATTCTTCATA TTTTGATTTA AAAAAAAAC AATTTACCAG	2580
25	AATTAGACGA AATAGTGGCT TACTACAAAC AGGTTTCAGC ACTGGATAAA TCTCATAGTT	2640
	TAAATATTG AGTTACAGAA ATTGGCTTAC AGAAAGCACT AGCGATTAGG CCATTITGCCA	2700
	TTGATTTAAA CATGAACATA CGAACCTCCA TGAATTACAA TAACCACAAA TTAAACGGGA	2760
30	CAATTAAATTT TATGTAGCAG GCTCTGCCAT GGGAAATAGCT TTACGTGAAC AGGATATTTA	2820
	ACGTATATCC TTGTTATGAT AAAGACTTTG ATAGGTGCTT ATACTTGCAA GTTCATATTT	2880
	TACAGTTAAA TATCTAAATT TAATATATTA CGCAGTTTAC GCAATGTAGC ACGTGACATA	2940
35	AATATGAAAT TFACTATGTG CTGCTTTTAT TTAAAATAAG TTTATAAAGT TAGTAAAAAT	3000
	ATCAGAGTAT ATATATTTAA TAAATAATA TCCTAAAATA TACTAATACA ATTTATCAAT	3060
	TAAGCTTTAT ACACTTTATA AATAGTTATA ATTATAGATG TGTATACGAT TTCCGAAACA	3120
40	TAAAAATATT TCACTGCTTT CGTGAAAAAT AATTTTTTTT TTATAAAACA ATCCCTAATA	3180
	TAGTATTACC TOCAATTATG AGTCTATCGT AATATATGAA GTACTACCAA AATTTACCAC	3240
	TGATTTTICA AAAAAAAAC ACCATTTTTC AAAAATATTT TATTAACTGA ATTTTITATA	3300
45	ATTAAATTTT TTATATCTAT ATAGAATATC TATTATACGC AAGAAAAACC AAAAAGTACC	3360
	CTATAAGTAG GTACCGCTTG TCCACATTAT AATAAAAAAA GTGAAGTACT CATCAATACT	3420
	TTTATTTAGG ATACCTGCAG TCTAATATCC CTTACAGTAA GTTACTTAGT GCACAATATT	3480
50	CACAGTGAGT TAGTAACCCG GTTCAGATCA AGGCATACCG AGCTTTCTCT TCTGGCTTCA	3540
	TATGCTTAAA GAAAATATCA GGGACGGTGC AGTTAGCTAA AGCTCTCTTA GCATAAGTAT	3600
	TCATAAATTT CAAACCTAAG ATATAACTGG AATTGACCCA GCCAAATCCT TCAGTAGCAA	3660
55	CACCTTTAAA GTCGCACTT TGGTTACCAT ATTGCGCATC AACTCTATGA GGATCTGTGC	3720

CTCTGGTAAC GTCTGTTTTC TCTACTACGA TACCATTGTA GTGACAAAT GCCTTGGTCA 3780
 TTAAAAATAA CCACCTATAG GCGAACCTTC TTGCAACTCC TGTAATCCG TAATTATCTA 3840
 5 ACCCGGTCCA AGCAAGCATT TGATGAGGGG CCCAACCATA AGGGTAATCC CATTGCCTGC 3900
 TTGGTCTATT CATTGTTATC TCACCCGAG ACTCCTCAGT ACAGGCAACC AGGCTCCTA 3960
 GCATTTCAG CTTGGCAAT GCTTCTCGA CCATAGCGTT GGCTTGTTCC TGGGTTGCCA 4020
 10 AGCCTGCCCA CATGGCCAA AATGTTGTTG CAGAATCGTA AGATGTTCTC TTCCAATAT 4080
 GGACATGTGA GTCATAGAAA AAGCCTGTTT CCTCGTCCA CAAATATTTC GTGATTCTTT 4140
 GCTTACGAAT GTCTGCAAGT GCTCCCAAT GAGAAGAAGT GGTGGTTTCA CCAGCATAAT 4200
 15 CAGTAATACT ATCATCGAAG TACTTGGAAA CCACATATGC AATATCTTTT TCGTACTTGT 4260
 ATAGTAACGA ATTCAAATCA ATCTGCGTA AGTAAGCACA GACGTCTCT AGACGGTAAG 4320
 AGGTGTCATG TCCACTCTCA CGTACAGCAC GATCATGCAA AAAGAACTCA TCTAGTTCGG 4380
 20 GCTCGTGTAC TTCCGCGCA TCGTACATGC ACCTGAACCTC CGGAATCGTT ACATTGTGCT 4440
 TTTCGCAAA TTTCGGCAA ATTGCGTCAA AGTGGTCAGG CTCGGTTTCT GGTGGGAAAC 4500
 CGATACCATC TGGATGATAA CATGAAAGAC CCGTGGTTTT GTGTACCGC GGTCTGCCA 4560
 25 TCCATACACT CTTGTATTCC TTAATGGCTG CGATGAATGC TCTTTTCAAG AAATCCACAG 4620
 CGGTAGGATT TTGGTCACCA CCGAATTTT CGAAGACCTT CAAAGCCATG TCGGTTAGGA 4680
 ACCGGGGTTG TGACCGACAG AGGTAGTAGC TCCTATTGGC GTTCAATATT TTACCGTAAT 4740
 30 GCTCTATCTC AAAGATGAAA TGCTCAACCA TCCCACGTG TATGTCCACT TTGTTACAGT 4800
 CTAGAAGACC CAAAGCCATT AGGTATGAGT CCCAGCCGTA AAGTTCATTA AAACGACCGC 4860
 CCGGAACAAC GTAGGGAAAA CCAACCAATG TACTCTCACC GGTAATTGGG TCCTGTGAC 4920
 35 TCTCCATCGC CAAAGCAAGC AACCCCGGC TTTCGTTCAA TGATTGCACG TGCTCCGGCG 4980
 TGATC 4985

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTTTAGTCTG ACCATCTCAT CTG

23

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCGCAGACCG ATACCAGGAT C

- (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTAGGGATA ACAGGGTAAT

- (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGCATGCAA GCTTAGATCT

- (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTITTTTAGAA TATACGGTCA ACGAACTATA ATTAACTAAA CATGGGTAAG GAAAAGACTC 60

A 61

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGTATATAAA AATATTATAT GGAAGCAATA ATTATTACTC TTAGAAAAAC TCATCGAGCA 60

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGAGATCTG GTGTATTTC CAATAAT 27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGAGATCTG ATGAGGCGGT CTTTGTGTG 29

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1001RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

GTGATTGCTC CGAGATTGAA AAGTCCCTAA CAATCAAAAA CAACGGGAAG GCGTACGAGG      60
AATGGCTGGA CCTGGGTAAT GGGTGCTTAT GTTGCACTCT GAAGGACGTA GGGGTGAAGG      120
CCATCGAGGC GATGGTTTCG CCGTGGCCAG GTAAAATCGA CTACATCATA CTGAGACAA      180
CGGGGATAGC GGACCCAGTG CCGATCGTGA AGATGTTCTG GCAGGATGAG GGCTCAATA      240
GCTGCATCTA CATTGATGGG ATTGTGACGG TGCTGGACGC AGAGCATGTG ATGACATTGC      300
TGACCGAGGT GGCCCTCCCG CGCCAATTGC GCGGCGACCA GGTGCTGATG GAAAACCAGA      360
TGACCCNNGG GATCTTCAG GTTGCCATGG GGGNGCGGG GNGTTGATTA AATCNACCC      420
TGNAGGCTGN NTAAAAATCT TGGNNGGAA AANGGTGANT ATAAGCGCC TTTTTOGGCN      480
AATNCGGGAN TTTNGTANN AAAGNINT      508

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 490 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1001UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

TGATCCGACC AAGAGCAGGG CTTTGGTGG GTGAATCTCG AACTCCTGCC CCTGTGTCAG      60
CTCACCCCGG CCGAAGTCTT TCCAAAGAAG AGCTTGTTAGA AAGTGTCTTT CGAACCCTC      120
GAGCTCAGCC TTGTGCGCA GCGGCCGCA GGTCAAGGTG ACCGTGGACA GCGCGGATC      180
ATGTTAAGCC ACGTGGGCAT CCGGAATGTC AGAGGCACCA AAAGCATGGA GATTCAAGTA      240
CCTTGTTTAT CTCCAGATCG CCGAACTTGG TCCGATAGA TGGGCGGAC TGCATTAAATG      300
CTACGCATT TTTCTCCAA CCACAGCGAT TCGTCATCAA NGCCTCCAG CCNGTCGGAT      360
TTATCAAAAC AACCNNGTCC GCCATGGCNA GTTGNAGATG GCANGGCACT TTNTTCCAC      420
AGACTGGNGG CCGGCAATGG GGGGGGCACC CGGACATTA NAATTNTGTC AGACCNAAAC      480
CNCAATTGNN      490

```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1002I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATCTCCGCA AATTCTCCCA AAATGGTAAG TCGTTATCCA CCTTAAATGC TTGCTGGGGT 60
 AGCTTGTGCC CCAATAAATA ACGTGACCCA TCATTGAGAT CCAATACCTG GGGGAGCAGT 120
 TCGCTCCAAT CCGGTACTTT CTTTAAAAAC GGAAATAGTT CATGATGGAG AGAGTACAAG 180
 TTTATGTCTT CACCAAAAAC CTCACGAAGA CCTATATCTC CTTGCATGAA ACAAGTGTGG 240
 AACACTCGTA GTGGTTCCAG CATGGCAGCT GTCACCGAGG CATCCTTCAT GCGACCAAGC 300
 GACCTTTTGA TAATTTCGTT CAGCCATTGT TGTCTCTTTT TCTTTGCAA AGTACCACTG 360
 GCATTCTTTT CCAGGGGGCA TCTCCGAAC TGGGTTGGTC AACAGAATGT ACTGTINTGGG 420
 GNGGGGTTTG GTGTTGGACG ACNTTTINGTG AAGATGGGGC ACAGTTINTGC CGTTTTTTGAG 480
 GNCAGGCAGA TTTGAAACAA ATTNNCGNNA ANTTCTGTTT CCNACGCAC GGGGCCCGAN 540
 TTCAGGCAAC CTNGACATTN TGAAGTACC N 571

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1002I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATCTTCGAG TGGGCGAGGG ATAGTAGCGA CCGTGGCAGA CATTCATCTT GATCAATTGA 60
 AGCGCCTGCT CCATGTCTTT GATGAACTGG GGAATAAATT GCCTATAGAG TTGGTGTACA 120
 AGGGTAACGA CTTCTCTCGA TTGCCTATCA AAAGACTGAA AAGGTACGTT CGGCAGCACA 180
 CAAAACAGCG AGTTCGGCTG GTGGACTGTT CCGGTGTACT ACGCAGTACA CATATACCTA 240
 AGATAAAGAG GTTCATGAAT AAGTGGTTAG CCACTATATT CAATTCATTT GGAGGAAATA 300

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ATACTACTAG ACGTGGATTG TTGGTGCCAC TGGGTTCCAA TOGATAGCTA CTTCAAACTT 360
 CCGGCTACA CTAAAAACGG GCGCTCTTGT CCTTCAAGGA TAGAACGCTT CCGGAGTACC 420
 5 TCCCTGTTTC ATGCACAAAA GCGAACTACT CTTGCCACCA CCGCCGGAGG AGACAAACTT 480
 TGGGGCAATC CTTTGAGATT TOGACACCAN TGNAAAAGNT N 521

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 518 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1002RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GATCTACTAA GGAATTATGG GAATCGTGTG TTTTCTTCTT AGAAATGAAT TTGTTTGCAG 60
 25 TOGAAGACGA GGTGGAAGAC GAGCGCGACT GTTTACTCTT GGGGAAGTTA GTCAAACAAT 120
 CGCTAGATTG TATCCGCATG GTATCACCTG AGTTTCTATC TATAGGAATG CTACTATYAC 180
 GGAAGTTGCG ATGCTGATGG GCATGGTTGT CATGAAAAAT AGGATGTTGG CTCCGGTTAG 240
 30 ATGACTGACC GAATACCTCT TCTATGATTA ATTCTWCAA GCGGTATTG ATTAATGTGC 300
 ATCTGTGGC GTATGATGAA ATGACTGCGC CGTCATTGCC GGTACGCCCT TGGAGTGTTT 360
 GGANITGACA AGAANNOGCT CTTAGGTGCC NGGATTCCCN GGGTTGGAAA GATGATNGCG 420
 35 AATNCCAATT TNGGTCCAAT AGGGAATCTG GNATTATTTG TTATTGCAAT NAGGATNCCC 480
 GGGAGGGGGT TNCNCTACGA AGAAGGATTA GGTNNNC 518

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 441 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1002UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GATCCACGKG AGTCGCAGCG CCAAAGGCGG CTGGGCGTCA CGATGCAGGT TATGCTGTGC 60
 CGTGACAGA GTGCGCCCCG CTGGATGAAG CCCATAAGAC TATTGAGCCA CTATATAATA 120
 55 CCAGCTGGTT ACATGATACT ATATGGTCAT AGCATCAATT GTAGTAGCCA GGGCAGTGAG 180

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GCTATAGCAG CTGGAAAGGC GACTCTGAAA AGGGATTATAT GCCAAGAGCT TCAGAAGTGG 240
 ACTCAGGCCA CGCATCCAAC GGATTCCTCC TCAATTOCTC TATATTGAGC CAGAGCTCCA 300
 5 TCTTGACCGA GGTCCTCAT TCATATTCAT ACGAGTTACT TGAACATCCA ACAGGTGCCA 360
 TATTTAGKTT GGGGGGGTAA GTACAATANC GVTGNNGGCC GTGGAACCCC GGTCGGTTCC 420
 CNGGGTTTTG GAATTTTNG G 441

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 513 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1003RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

25 GATCGCTCAT GACCAAAACA ACGAAATCCA CTACATTTG CTGCGACTG CTCACCCAGC 60
 GAAGTTTGCG GACGCTGTGA ACGAAGCTCT CTCTCTTAC GATGACTACA ACTTCGATGA 120
 CGTCTTCCA GACCGTCTAA GACGCTTAGG TGACCTTGAG AAGAGAATTA AGTACGTGGA 180
 30 CAACACCGAC GTTGATGTTA TCAAATCTAT CATTGAGGAG GAACTGATTA ACATGGGCAT 240
 TTACAATCCA TAGATGATCT GAACTCTAGA TGATTTATAG ACTATCTAGT TAGCCTTCTA 300
 GTCCTATATA CCTAATTOCA ATAGGCAGGG GGGCCTATGT CAAGTTTAAA TCCATTTTGC 360
 35 CTTCTACTGC CGCAACGIGG TTTTITGCAA AGCCAATTTT GCGTGGGGG CCAACTTCAC 420
 CTCANTACCC AGNICTGNGA GTCATCANCA TTCCCGCTIN TAGGCCCCAG TGANTAGAAG 480
 TGGTCTAGGT CGTTTCAAGA GGAACATNAA TNT 513

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 504 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1003UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

55 GATCTTTAGA CAATTATGAC ATCCAAGTTT GGTCGGTTCA GACTGGTCAG TTGCTTGACA 60

CACTCTCTGG TCACGAAGGC CCAGTCTCTT GCTTGCTTT CAGCCGGGAA AATAGCATA 120
 TAGCCTCTGC CTCTTGGGAC AAAACTATAA GAGTGTGGC GATATTTGG CGGCCCCAGC 180
 5 AAGTCGAGCC TATAGAAGCA TACTCTGATG TGCTGGATAT TTCCATGAGA CCGATGGTA 240
 AGCAGGTGCG TGTCTCCACG CTGAATGGTC AGCTGTCATT CTTCGACGTT TGAAACCTCA 300
 CGGCAGGTG GCAACAATTG CTGCAAGAG GGACATCATA TCAGGACGCC ATTTAGAGGA 360
 10 CCGTTTACT CAAAGAACTT CGGCAACGGC CCAAATATTC ACAACAATCC ACTACAGTTC 420
 GCGGCTTTC AATGNTGGAG NIGGGANAA ATCTNTTGGT NTAGAATCCN ATAAGGGTAT 480
 AANCGTCATG TTCCANAAAT NATC 504

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1004RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GATCTTAAAG AGGCTCAGTA TGCAGAGGCA GTTTCAGAA GAAGACAGGC TGGGCTTGA 60
 AATCCCTCAG CTCCCGCCGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGGCCA 120
 GCAAACGCG CTGCGGCGGC CGCGTGCAT CCTCGGTGCC CCTTATGAAC CGAGCAGGGC 180
 35 GTCGTCCACT GGTGCAGGCC AAAAGCGOGA CTACGACTAC TCGTGTTC AAGAGAGCAG 240
 GCTCCTCACT GAGAGCAAGA TAGACCAGTA CTTGAAGAGC GAGGCGCAA CGCACAAACG 300
 CGTATTCCAC CGCGACCGC CCCCACGAG ACAGCTACCC GCCCCGACTT TGCAGCCCCG 360
 40 TCTGCTTGG ACAAGCTTCG GACGAGAGG GAGAGCCCCN CCCCCCTCNC AGAGNGCCN 420
 TTINGAGCC CCNIGGNTG TTCATCATCC CCCCANTCCT CCAGGAGAGT TTINGAAAG 480
 GCGCCCCNA NACNCCNTAG GATTGTTGA GGATGGAGTN GGGCCCTTTT 530

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1004UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATCACCGAG CCTAATGAGT GGTGCTAGGG TAGCGGTAT TACCGGTACT AATAGGTATG 60
 5 TTAATATGCC ATCAGTGTCT GAGCTCACGA CTGACATATA TTAGCAATCT TGGCCTGAAT 120
 ATCGCATACA GGTGATTGA GCAGTTTACT GATGACAGCA AGTTGGTTAT CGTGGTAACA 180
 TCGCGTACCC TGCCAAGAGT AAGGGAGGTG GTAGACCTAA TCAAAACATA CGCCGAGAAA 240
 10 TGTGGYAAGT CTGGAGCAGT AGATTTOGAC TACCTGCTGG TGGATTTCAC CGACATGGTT 300
 AGTGTGCTGG GCGCGGCATA CGAATTAGAA AAACGATATG ACGCTATACA TTACTTCTAC 360
 GCTAACGCTG GCAGGGTGTG TATTCCCCGA ATTGATTGGT TGGGTGCACC NGGTGTTTAC 420
 15 GGGATCCNCG GGTGTGTGAT ATCCNCGTTA GNCNCGGTGG ANNAATCAGG ATGGTINGGT 480
 AGTTTCAAGC ANTC 494

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1005RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATCTCCCC AGGAACCGCG ACGGGTACGC AGTCGTGCTT CTTCOCAGCG TGGTGTGCAC 60
 35 GAATTCCATC AGCATGTGGA ACTTCAGCGC GAACATCTCC TCACGCAGGA TCCGGTCTT
 CCTCCTCCTC TCGGGCCACC GAGAGCTCCG CCAGCTGCTG GCACCCGGTC AGGAAGCACT 180
 CCGCGCGGTT CCCCTCGGC CCCACCTCCC TGAAGCAGCC CACCAGGAGC CGCCACACCA 240
 40 TATCATCCCC GAGCCCTTCG TTGAGGTTGA AGTTGTCTGC CCTAATGCAC CGCACAAGCA 300
 CCTTCGGGAT ATCCCAACCC AAATCTOCCA CGAGTGCAGG GTGCTCCCGG AGCTGCTCCC 360
 ACAGCGCCTC CAGGAAGCTC GCCAGCGGCC CCGCGTTACC GCTGCAAGC GCCTGCTCCG 420
 45 CGCACAATC GATCCCCGCT GCGAGCGAGA TCTGTCCCC GCCTGCTCCG CGAATAGCAC 480
 GCCCAGACTC TCACCTTCCG TATTGCGTGG CGTTTCATAG AATCACTCT 529

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1005UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

	GATCTTGCAG TTAACGGTTC TTCCATCAAG GGACAAATGG GCGTACCGAA GCTCTTAGCC	60
10	CAGCCAAGTA TCCACAGCT GCACAATGCT AAGGGTGAGG TAATTGATGT TCAGTCCCAG	120
	CCCCCCGCGG GCTGGCGGCA GGTGCTACTA NAGCATGGCC CAGAAGTATT TCGAAGAAG	180
	GTGCGTGAAT TCGATGGAAC ATTGCTTACA GACACTACAT GGAGAGATGC CCATCAATCA	240
15	TTGTTGGCAA CTAGGGTGGG TACTTATGAC CTAGCTGCTA TTGCACCTAC CACTGCACAT	300
	GCATTAGCAG GAGCCTTTGC ATTAGAGTGT TGGGGTGGCG CTACGTTTGA CGTTGCCATG	360
	CGGTTTTTGC ACGAAGACCC ATGGGAGCGC TTGAGGACAC TGGGAAATT GGTGCCAAAC	420
20	ATCCCATTC AGATGTTGCT TCGTGGTGCC AACGGTGTG CTTACTCCTC TCTGCCTGAT	480
	AATGCGAATG ACATTGCTCA AACAAGCAAA GGAGAATGGT GTC	523

(2) INFORMATION FOR SEQ ID NO:28:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1006RP

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

	NNNNNGNNN NNNNTGTGGG GCGTGGTAGA NTAGTGGGTC TCGTAGACAA TGGATGCCTG	60
40	TAAGCATGTG TAACGGGTAT CGTGGAGGGG TCCCTTCCCG CCTCCGAAGC CTTCTTCGGT	120
	TTCTCAATTT CCCATAGCAA TGGCGACTCG CACCAGTAAA TCCTCCTCTG GGTAGGCTCC	180
	GCTCATTAGT CGAACGGTTC TCCGTAGCCC ATCCTCGTCC AGTTGCGGCG CCGCGAAAC	240
45	AAACAAACAC TGGCGGCGCG GATAACGTCA GTAGCTATGT TTCAGCAGAT TCCGCGGAAA	300
	CGGTCCAACA GATCGTCTGT AACCGGTGCA GATACGTCTG GGCAGCGGGT TTAACTGCA	360
	GCCAGTGCAG ATTTAACGTG CGATGGAAGC CTGCGCGCGG TTCTGGCTGC CCGCCGGTGG	420
50	CTCCAGCGGA GCGAGCGGCG GCGTCGCGAT GCGCGGCGTA AGTCTGTGAT CGCCGGGAGC	480
	TGAGTAGGCG TAGCGAAGGT CACACGGACG CCGGATAGTA GATGGAGCAA GGGGCCCTCTT	540
	TGGACGGTTT GGTACGAAA TNCCTGG	567

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(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1006UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCTCTGTT	CTTTTITAC	CTCTGAAGGT	GCCGAATGTG	TGCGCGTGAA	ACCACTCTTT	60
CGCGATGGGA	TGTTTCTGA	TCTCCCTCGC	GAGCTGTTTC	ATGTACTACT	TCCTTGTAAG	120
GCAATCGCCA	CGCAGGACAG	ACCGAGCTGG	TGCCAACGGT	TTCTCCGGGG	TGCTTTTGCT	180
GAGATGCGTT	CGCATGTTTT	GACCCAGCT	CTGGAATATG	CGCGGGTGC	GATGCTGCGT	240
GTGCTACGAT	GCAACGTCAG	CGATCCCGCA	GGCGGGGGT	GCAGGGGTGT	ACTTCGATCG	300
TAGGCGCTG	TAAATGCTCC	TCTGGGAGCG	CGCTCCCGCC	GATCTTACTG	TCCGCCATGA	360
ACGATGGGAC	AGAGTAGCOG	GGATGGTTC	CTTTGCAGAT	AGGAAATCTG	GAAGAATTIG	420
GTCCCGCTCC	GCCTGATTIG	TTTATACAAA	AAATTGGCCA	TACATTCCTT	G	471

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 518 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1007RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCTTCTCG	CCGAAGTACT	GCACCATGTC	ATTCTCTTCC	GGTTCACCAT	GAACAAGGAC	60
ATCTAGGCCG	ACCTCTCTCT	GGAAGCGGAT	GACTTCTCTCA	ATCTGAGAAT	TGATGAAGTT	120
GGTGTACTCC	TCCGTGGAAA	TGCCCCCTT	TGCATGCTTG	TTTCTGTIGA	TCCGAATGTC	180
CTTAGTCTGT	GGGAAGGAAC	CGATGGTGGT	GGTTGGGAAT	AGCGGGAGCT	TGAAAATTGG	240
CTGCTGCTCC	TTGAGACGCT	CCCCGAATGG	TGCGGCTCTC	GTGGATAGCT	TCTCGTTCAA	300
ACCAGCAACA	CGTTCTCTGA	CAGAAGGATC	GTTGGGTGAT	CGCAGAGGCG	GGACGGGCAG	360
CAATCGAGTC	TGCAATTGGC	TCCAATCTAG	AGGAAAAGTC	TTGCCAGAG	CGTCTTAGC	420
GAGGAAACAA	ACTCATGCAG	TTCTTGTTTG	AAAAGAGAAC	CAGCCTGGCT	TINTGTCCAA	480
GGAGATCGTT	TOCAAGTAAC	TGNNNTGAA	NAAGGAGC			518

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1007UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GATCTTGTGCG AGCTCGCCAT GACAGATGAG AATCCGACAG CACGTTTCAC GGCATTTTAT 60
 GCGCTGGGGC TAATTAGTAA AACGGAGGAA GCGTGTGAAC TATTGGACGA GTTGGGCTGG 120
 GACTGTTGCA TCGATGTTG TCGCCAGCCA GTTGGTATTT GGGTACCAA TAACATCACC 180
 ACCTTTCTCA GTTATCTCA AGAGAGCGTC GAGAAAACAA CCGTTTGGGA AGGTATCGAC 240
 CAATTTGGAC CACCGAATTT CCGGAGGAGG GACTTCCCC CACTGGAGGG TATCACAAT 300
 ACAAGTTGAT ACAATACTCT GAAAAGGTAG GAAAGGGATG TCCTGACAGA CAACCAAGAG 360
 CTTAAATCCA TCCTCGACA CAGGGGTAGA CAAGTGANTG NAAGCGNGA TTGATCTTCC 420
 CATGGAGNTC CAGGATGACC AGCTCCCCAA GATTTCCGTT CGTGGGAANC GGAATCATTT 480
 NTACACAGNG GA 492

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1008I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGAGTCATT TCTGTAGTC CAGTGCATCG ACAAAGTGT CTGCTTCGCC GTTGGCATA 60
 GTTATTTGCG TTCCATACTC GGATCATCA GCGTCTCAA GCGCGACTG AGACAACTCC 120
 TGGCGCAACT TTGTCTGGC GCGAAGCATC TCCAGGGAC CCCTGCATTG ATAACAGGAT 180
 CCGGAGCGAG TCGGAAGTGG CCTTGAGGTT CCGCGAAGA GCCTTGATTT CCTTGTTACC 240
 CCGCGGCTGC AAGGAATCTA GGTGAGGAGC ACGCAGTCGA AGCAACCACT TAAACACCA 300
 ACGGATCGCT GAGCTTTCTG TCCTAACGTC AGAGGCCACC CGCTGGCTCA CGATGACAAA 360

ACAGTTCATT GNANOCGNAT GGAAGNGAT NCATGTGCGN NANATTCTTT NNITCTTTCC 420
 TOGGACCANG NGTNANAAC NACAGTCCCT GACGANTTCC TCACCTANGT CNGCGCAGGG 480
 5 GATNMTTICA AGCGCGNOC GTCTNNCCCC CTGNCNCTCG NNACCTTCT TTGTNNNGG 540
 TTTTCTTTIN CCNNCNCCCC TNNNCNCAC TINGGTTTT NNACNCTC NNNAC 595

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 680 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1008I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TOGAGACCGC ATCAAATATC TGTATTATG TAAATGTGCA TATTATAGAC TTCTATTTC 60
 AGTACCAGGC AATTGTGTCC GATAAATGAG GTGCAATGAG CACCGTCAT CACCGGACGC 120
 25 GATAAATTTT TTTTGGGGG TCAACCATTA AATCTACGTG CATCTAACGC AAGGAGCAAT 180
 TTAGCTAACA ACTCTTCTTA TCTTAAGAAT CGGTATACC TCCTCTTCGC ACATCTTCGC 240
 CTTCCTTAGT CTCGAGTCTT AACTACGTC AACAAATGCA GCTCCGATA AGATGTACAT 300
 30 GTGTATAAC AACATACACA AACTGTGTCA GCAGGTAGCT GGCCAAATTA TGGAGCGTGG 360
 TGACAGACCG GACGTGATTA TCGCCATTAC CGGCGCGGC ATGATTCTTG CAAGAATCAT 420
 CCGTGCTTC CTCAAGGTCA AGGGCCAGAA AAACATCCCC ATCCAGGCGA TTGGGTCTTT 480
 35 CTTTGGTACG AGGACTTGGG TTTGGAAGAC GGGACGAAA GCATCGGCAA GGAAGTTATC 540
 CGGATCAAGT GGCTAGACTT TGGGGGCTT GGGCAAACAC TTTGGACTCA ACTGATTGGA 500
 AGAAGGTGTT GGATTGGCGC CGAGTTGGNC GANACCNGA CACGTCCCTA CGTTGTINAC 660
 40 CGANTTGGGG AGGGGNCAN 680

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 509 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1008RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

EP 0 866 129 A2

GATCTGTCTT GGAGATATC AAGTCTATG CCATCTTCCA AACGTCCTT TCCACATTGC 60
AACAAAATGA CTCTACAAAA TACCAGTTAG TCTTAGAAAA TATGTCACAG GACGAACAGA 120
5 TGCACCTAGC ACATATTACA TCGTTATGAG CACCATAAAT CTCATAGTCT TCTACTTTTA 180
TCTTTAATAT TAATAGTATG TGTATGCCAA TCGGCGCGTT ATGCCCGGGT AACAGTAGTT 240
TCTTTTCTIN GAACATCTGA AAAATTTCAC CCGATGAGCT CTCTGTGTC AATGGGCGAT 300
10 CGAGCTACAA GTGCAGGTGT ACCATTCCACA TCCTATOGG NATTOGGCTG TTGNTAGAGC 360
TGTTAAAATG ATTGCTTCAG AAGATACGAG GTCTTGGGA GTTTTGGGC CGATGAACGN 420
GGTGCATTC CAAGCCAATG CGTGGAAAGG ACTCATTGAA TTTTCANNGA CCNGNAGAAT 480
15 TAANGGNAAA GTCANNGTA ACCNATTGT 509

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1008UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCAAGCGG GAATTTGGC GCAAATGCAC GTTAATGCTC ATATTGTAA CAAGCTGGG 60
GCAGAAGTCC GCGTTTGGG GCTAGAAATT TCCACATTGA AAGGTTCAA TAACACATTA 120
35 GAGGAAGAGA AAGCTCGTC AGAAGATGAT ATTTTGAAGC TGCTAGAGGA AAATCACACT 180
GTGCATCATT TGAAGACTAC CAACGAAGCG TTGACTACCA AGGTAGCGA CTATAGCAAT 240
AGACAAGATA CGATTCTCCA GCTGTTGGG GAAAAGACGG AACGTGTAGA GGAAC TTGGA 300
40 AAATGACGTC GAGGACCTCA AGCAGATGCT GCGGATGCAA GCACAGCAAC TTGGCCGACA 360
TGCAAGAGAG GTTAAGAATT TAGATTCCCA TATCTTATTA ACATTATINA TNCANCGGC 420
TTGGGTTNGT TAATCAACTT CNCCAGATGC NTAGATTGG GTAGTTAGNC ANTTTTTGA 480
45 NTGGNTCAA ATGGNGGCC 500

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1009RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

5 GATCTTCGCT TGGGGCCGTG CGTTCACGGT CTTAGAAAGC AAGCGTGCAA GCGATGTCTT 60
 GCGTACCCCT GGGGGGGGCC ATAGTATCAT CGAAGGTATT GTTCCCTGGC TCACATATTT 120
 10 GTATAGTGCC CGCTTTTCTT GGGAGAGAAT ATGCTGTGTC CCCACGTACT CCGGCAGCTC 180
 GCGGGGACGA AGTTTCTCAC TTAAGGGCAA ATGTGCCATT TTCTGCAGCT CACGCTGATC 240
 TGAGTTCACC GCGCTGTG GACGTGCCCC CTTCGGTTGG GGAGAGTCGT CCATCTCTAT 300
 15 CACCTCACTA TCCTCCATAT TAACGTCCGA GATCAGAC ACCTATCTT CATCTCCAG 360
 CTTATGCTTG CGCCCCAGCA TCTCAGATAC GGACGTGGTC CTCGCTCCTT TCGGCTCCTC 420
 CTGCAGGGAT GCATCTAGAT GGTATGGATG TGATGAATGG AAAGCGTGCA ATCTGGNAAT 480
 20 GGTAAGTCTC CCCCCGTAT CATTIN 506

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1009UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

35 GATCATGCTA GTTCTGCAGC TGAGTTTITA AAAACGAGT ACTGGAGATG TTTCGCTTTA 60
 TGGTATCGCT CCACTAGCGC ACGGACTGAC TTGGTTAAAC GGCTTAGCAC TGATGCGGT 120
 ATTTGGAACG CCGCTCTAA GAAGCTTGAG TTGCACCAT CAATGAAGGG AGCGCAAGTC 180
 40 GAAATTTCCC AGCCTAGAGG CATGTCAGTA GGTCAAATA CGTCTGTTC TGGATCGCTC 240
 TGCATCATGA TATCGACATA GTAGTCGCAC ATATCGATGG AGACGACCTT GCGGGGTCA 300
 AATTGTGTTAA APTGGTTCAA TCCTCAGGC ACTTGGGTGA TAACTCAAG TAGGGCATT 360
 45 TCTTCAGGGA AATGCCCCG TAGGAGGGCA TCGAAGNCAG AGTTNGACGA ACCNCAGGG 420
 GGGGANTCT TTGAAGGGAG AAAGAGGCGG GGAANTGGTA CCACTCGCT CCCCNCANA 480
 AGTTGGCCCC AGCTCAATN 500

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

EP 0 866 129 A2

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1010I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

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TOGAGGCGCT TACGTGGGTC CACCTGAAGA TGCGGCAGAC GGCGCAAGCG GAGCTGGTGC      60
GGGCGAAGCC CACCGTGTTC CCCCTGCTGC TGGCGAAGTT TCTCAGAAAC GATCTGTGCG      120
TGACCGGGGC TGGATGGAG GGCCAGGAAG CGAAGTGCAG CGACGTGCAC GTGCTAGTAC      180
CGAAAACACA CGCGCGCTG GCGTCTCTCC TGCTTGCACA TAGTCCCGTG GCGCGGGGTG      240
GCGATCTTGG CATCACCCCTT GGCGACATTT TATCGTGTTC CCTGCAGGAT GCACTAGACG      300
CGGGCCAGTT AACGACAGCT GAACCCAAAG GAAAGTTAGA GGGTGACCTA GTAAGCGCTC      360
TGGTACATAC AAAACAGCTA GAGCGCCCGG TGGAGTCTTC TACGACTGAA TTAATACGGA      420
GGTACCGACT TGGGACAAA GAGGCGTCTA TGGATGCCCTT GGCTGTGCGC TGGAGATTTT      480
CTGACAGATT TAAAGATGAC GATGAGGTAG AATGACATTT CTGTGCAGGG TCTCAAGTGG      540
GATGAGAGGT CGGCATTTTC GAAGGAGNNT GGTTTATNAN NANATCTTGG ATTTTCTGAG      600
GGGCTNAGN TNCAAGAAAG TCANATN                                           627

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(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 628 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1010I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

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TCGAGGTGGC GGGCGGGAAA CCCTGCGCA ATCCTGGCCT CCAGCGCCCG GCTGACTGCG      60
GGTACCGTCA AGCACTTGAA GTGGCTCGC TCAAGATAAT CCACCGCCTC GTTGGCCCGC      120
AGCCCGCGAC TCCCGTGCAC ATCCCGCGGG ATCAGCTTGA ACTCCCCCGC GCTCAGCCAG      180
AGTGGGTGTG TGCCACCGG GTAGTGTGAC TCCTCTGGCA GCGCTCGCT GCTCATCATC      240
AGCAGAAAGT CGCCCTCTGT GTGCACATC TTGATGAAAA CCTCGCGGCC CTGAGCCCGG      300
GAGAATGCT GCAGCAAGCC TGCCACCAGC GCTCTCTCTT CCTGGGTTG TCCGCGACTT      360
CCACTCGGCC AAGCACCATC GCTTGCCTC CCGCGCCCGG CACCGCCCGC AGGTGCACCC      420
GCTGTACCCC TGNCACGGGT AGTGGTCATT CCACGGCCGG AACACTCTTC AAGCTGAGCA      480

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TGTCTTGGG ATCTTTGTTT GGACGTCATC AAAATTGTCG ATTIGAAAAA CGATACAATA 540
 NAGNGGCTCN GGGTINGAAA GTCACACCNA TCACTCTGGT TCAAAGCATG TCTCAATNIG 600
 CGGGGCATAA CCAATTGCNC GGTANGCA 628

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1010RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GATCCGGCTC GCAAAGGAGA AGATAGAAGA GCAGAAAGAA TACCCGGTGC AGGAGTTTGA 60
 CAAAAAGCTG TATCATAGCA ACCCGCAAG GTACTGGGAT ATATTCTATA AAAATAACAA 120
 AGAAACTTC TTCAAAGACA GGAAGTGGTT GCAGATTGAG TTCCCTCTC TATACGAAGC 180
 TACCAAGAAA GATGCTGGTT CAGTGACTAT CTTCGAGATT GGGTGTGGTG CGGGCAATAC 240
 CATGTTCCCG ATCTTATCTG CAAACGAAAA CGAACACTTA CGGTTGTGG GTGCGGACTT 300
 CTCCCGAAG GCGTGGGAA TTGTTAAAGA CGTCGCAAAA CTTTAACCC TCGAATGCC 360
 ACGGACGGT ATGGGACTTT AGCCAACCC TATGTTCTTT TGGCGATGG TGTGAGCGG 420
 CATTCGGTCG ANATCGNAGN AATGATTTIN GTTTTAGTGC CTNGNGCCC ACAGGGGGCC 480
 AGGNTNIGGT TATTGGANAA AGTCTTNANC AGNGGGT 517

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1010UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCAGGACA GTAGCAGCTT GACTGAGTAT CAGCAGGAAA AGCCTAGCTA ATTGGCGCGA 60
 GTACAATTAC AAGTAAGTGT CTGACTACTT CTTTGGGTGG GATGCCATAT TTTTATAGGAT 120
 GGCCTGCAAC GGGCCGGTGG GGGGOCATC CAAATTTATG GAGTTGAAGA GCTGTTCAAT 180

EP 0 866 129 A2

GGCCTTTATC CCATCTGCAC CGTCTTTATC GCGAACATG GCATGCAACT CTTCAGCAT 240
 GATATCTTCT TCTCGTGCT CTGATCCGGC GTTGGTGGT GFTTGGGCAG TCTTGTAGG 300
 5 CGCCATTTCT GTAATGTTGA AGCTGGTCTT TGGTCATCTT CAGACCCCTC CGTCAGGAAA 360
 TATCAAAGAA ATCGGCTTCA CTAATATCTA CGCCTCACTC TCGAAAAATG TCCGAGGCTC 420
 TTCATCCCCA GCTGAAGGAC CCTGACCAGA AAAATGTCAA TGGTACTCAA CGCAACTTTA 480
 10 ATNTTNCAG AN 492

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1011I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCTGCGCG GCGGATGTTT AGCAGGAGCG CGTATCTAAA CAATTTGAA GTTGTTCAAG 60
 GCGTGAACGT TCCAATAGAC CGCTCTAGCT ATTCCAGTA TGACAAATGG TTAAATGCG 120
 30 TAGATGCAGC TGAGAACGT ACAACTGCGT GGTTAGAGCT GTGGGATGCT TGGCCCTGC 180
 AAAACTTCTA CGCTCAGGAG GCCAGGATGA TCTGCAAAAA AATCATCCAG ACCAATGGCC 240
 CCACATCTTT AATCACTGA GTGTAATGTC CATACTCCA GTACTACCA GTCTTTTGGT 300
 35 TTTCTGGATG TCAGATACCA GACTATGTAC TGAATAGCGA CAACATTAGA TATCTAAAAA 360
 GTCTGTGGT TTACAATCTT AAGGTCGGCT GAAAGAAGAG AAACAATCTT CGAAAACAAT 420
 ACTAAGGCGA ATATATCAAC GTAATATGAC CGCTCAGGCT TGGATAACA TTCCGATATC 480
 40 AGAGGGAGAA GACTCCGCG NGTCTTGNC NNTCNGCGN AAATTGCNCA GTNTTNATCC 540
 CGGNAGCCNC CCACNGGTTT TCANACCCCT TTTINGNGT TCNCGNCAAT NAAGGGNGNC 600
 45 CTCTGCANT TACCCANNA 620

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1011I2

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

	GATCTCTTGC ACCAGTCCAA ATCAGCGGGG TCGTCCACCT TTCTCCATA TATGATTTTG	60
5	CCGATGGTGT CGCTGACAAG CTTCAGGGC ACCAAATCGG GGTGACATG CTCTTGCCG	120
	TTACTGCTCT GTTCAAATAT GTGGTCCAAA AACTTGCTAC CTGGGTGGAA GTCACCATCG	180
	TGGAAGTGT ACTTCTTGGT GAATCCAATA GCGCGAGAC GGCACCTGGC CATGATAATA	240
10	GAGTGGAACC ACACGAGGAT GAACITGCTA TGAAGTTTTT CTACTGGTTT GACATTCTTC	300
	AGTTCTCTG ACTGAGTCGG CCACAGCTCG CAGACTGTGT TTAGAACGCC GGGCTCACCC	360
	TCGTACGCTA TCTTATAGTT CTGCTGAGCA AAGGAACCAC TAGAGGCTTG CTTTGGGATC	420

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 732 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1011RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

30	GATCCAAAGC AAGCCTCTAG TGGTTCCTTT GCTCAGCAGA AGCTATAAGA TAGCGTACGA	60
	GGGTGAGCCC GCGTTCCTAA ACACAGTCTG CGAGCTGTGG CGGACTCAGT CAGAGGAACT	120
35	GAAGAATGTC AAACAGTAG AAAAAGTTCA TAGCAAGTTC ATCTCTGTGT GGTTCACCTC	180
	TATTATCATG GCCAGGTGCC GTCTCGCGCC TATTGGATTG ACCAAGAAGT ACGACTTCCA	240
	CGATGGTGGC TTCCACGCGG GTAGCAAGTT TTTGGACCAC ATATTTGAAC AGAGCAGTAA	300
40	CGGCAAGGAG CATGTGACCC CGGATTGGT GCGCTGGAAA GCTTGTGAGC GACACCATCG	360
	GCAAAATCAT ATATGGGAGG AAAGGTGGAC GACCCGCTG ATTTGGACTG GTGCAAGANA	420
	TCTGCGCGGC GGATGTTTCA GAGGACGCG TATCTAAACA ATTCGAAGTT GTCCAAGGCG	480
45	TGACCGTTCC ATAAACCGCT CTANCTATTC CCAGTATGAC AAATGGGTTA AATCNCTAAA	540
	NGCANCTGCA GAAGGTACAA CTGCGCTGNT TANANCTGTC GGATGCTCGG CCTGCAAACT	600
	TCTACNNCNC GAGGCCAGNA NGATNGGCAA AAAAATCTNC AGANCNANGG CCGCTCCTT	660
50	TAATCCCTNG ANIVINATNT CCAACCNCCN TTNCCCATC TTTTGNVTTT TGTINTTAAA	720
	AACCAAATTN TC	732

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 641 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: 1011UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATCTTCACA CGCACTATTT GTCCAAGGGG CTTCAATGTT CATTCGATTA CACGAAGAAA	60
CAATACTTAC ATGAGAATGG AACAAATAA AACTAAGCGT ATGGTGCCTA ATGATTGTTC	120
AGATGGGCGT TGCTGTTCGT GAACAGTAAA TGCTTGGCAA ACTCATAAGA TGTCCACGAT	180
ATAGCAGTTG CAGGCATGTT GCTGATAATT CTGGGTTTTA GGGCCGAAA GAAACCGGAC	240
CAACCATATG TTTTGTGGAT TGCAGATGCA GCGTTGGGA ATGTGTCAGC CTCCTTGAAC	300
AGCTGACTTT GAACAGAATC TGCACCGCGA ATCTGCAATA CTGTCTTCAC GCAGTCTAGC	360
GGTGTGGGTT ATGGGCGCAC ATGTTGGCGC CCGGATATCC CACCGCACAG ACAATGTATC	420
CAGGGGTTTG TAGCTGGTTA CTCGGATTGA TTATTTTGGT GGATGATTCA ATAAATTACA	480
AAAATTCAC GCTGCGACGG ATTGTTCATA GCAATAGTTG TCCGGTTATG ATTAGAAAAA	540
CGCTTGAAAT GGGCTCGTG GGTCAATCCG CACGGGGCAT CCGCAATGG ANCANITGGG	600
TGAANTGAAC TCTTTGGTGG GNGNNANOGG TCCNNAGGGA C	641

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 653 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1012RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GATCCTAACC CAACTGCACA AAATTGTCAG TCATATGTTG GGAGGCAGTT TACCCCTTCOG	60
CCGCAAAATA CATACTTCTC CTTAGGAAAC GCTCCTCGCT CAGGACTGCA ACTGCATTGA	120
CGAGCAGCAG AATAACGTAG AATAGCTTTC CCAGGCCAAA TATCATCOCT CCACGTACAG	180
TCTATCAGCA GTGTACTCGG CTGTGCGAGA AGTGGCATTC ACAAGATAAG CAGAAGTAGT	240
TCTAAAAATC AGTGGTCACC AACGCGAGGC TGCAAAATCG TGTGTTCAT TCCCATCTCA	300
AAGCATCGCC TGAAAACAAA GGCTCAGAT TGCAGGTGCC CCGCGTGAT AACAGATGAT	360
AATTTATATT TTAAGTTATA TTAACACACA TATACAAAAA GATTTGGTAG TGGATTAATG	420

ATGATTGCT TAATCAGGT TACGTCTTGC GGCTTCTTA GCCAATCTCT TACCGGTACC 480
 AAAGACCTTC TTACCTCTGT TCTTCTTTTG CTTTCTCTGT TGCTTGAAG CCTTCTCAGC 540
 CTTCTCAGCC ATGCCGTATC TGACCAATCT GTANGTTGGC TCGAACTTCT TGGCGTCNGC 600
 AACAGAGTTG TAGATCAAAC CGAAACCGGT GGAATTGACA CCACCAAACT GGG 653

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 650 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1012UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GATCTTCTC GAGCGACCA CGCGCCCCA CACAGACTCC GAGAACCTGC TCTTCTGGA 60
 GGGCACCAA ACATGCTTCC AGATGTTTAC GCAGCAGGTG GAGGTGCGCG CAGGCTCGGG 120
 CCAGGCGAAG ATCCTGGTGG GGTGCTGGA GCGCTTCTGC AAGCTCTCTG TCGAGCGCCA 180
 AAGCCACTGG ATGCAGGCCA TTTCGTCCGA GGTCAGAAG TGCTTCCAGT ACAACCACAA 240
 GTATGAGAAA GACCCCGACA ACATCGCGCA GGAGGAGGAG TGCGCGCGCG GCTTGTGGA 300
 GTACCTCGTC GCGGTGCGCA ACGACCAGAT GAAGCGCGCA GACTAGCGCG TCGCATCTC 360
 GCAGAAGTAC GGCTCCATGG TCTCCAAGGT GCACGAGCGC ACCATCAAGA ACCGCATCGA 420
 GGAAGACCCCT CGACGGCTTC GCAGAGGTGG CCAAGTGAG CAACAGGGC CTCGTGCGCC 480
 TGATCTTGA CGACCTGCGC CGCCCTACG CCGAGATCTT CAGCAAGGCC TGGTACTCGG 540
 GCAACCAGGC GCAGCAGATC GCAGACACCC TCTACGAGTA CCTCGCGGAC ATCCGAGGCC 600
 AGATGAACCC TTCGTCTACT CCACCTCGT CGAGTCCGTC ATCGAAGAGA 650

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 727 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1013I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TOGACGCGGA CAGCGTACTT CAATCTGTAG ACAGAAGAAA CCTTGCCCTC TTGGCCCTTC 60
 TTGGAGCCAC GCACAACCAT AATCTCGTCG TCCTTTCTGA TTGGTAGAGA CTTGATGTTG 120
 TACTGCTCTC TCAACTCCTT GGATAGAGGA GCAGACATGA TCACGCGGCG CTCGGAAGAT 180
 GGCGCGTTGA AGTACGCTT TCTGGCCTTT CTCTGTGG AGGAAACGTC TGCAGACATG 240
 TTAGTACTGT GCGGGGCCAC CAACTTGTTC CAGCACTGG ATTATGCTAG GTCCGCTGC 300
 GCGCTGGGCC GTATGCCAG GTTACCACGG ATGCAGCGC CAGAGACGCT CATTOCCAAT 360
 GTTTCGGGAG CCACCATGTT TCTGTACAT ACCTAGAGAT TGCTTAGCCA TTGCTGATTC 420
 GCGTGTGCT GTGTAAGAAC CTCTGTTTCA NNTGTGNAN AATCTCAATN GTGNAACTT 480
 TTTCAANNITG TCCGCTTAC GCTGNACCCN CTNNNNITG TNAANNCCN NNNNNNNCN 540
 CAANCGTTTC GCTANNVNNN TCCTANANAC NNANANNNT CNNNNNAAN NCCNNNNN 600
 CACNNNTTC NACCNCNNN CAANNNNNN NNNNNNNN NANCCNNNN NATNNTCAT 660
 NCCCTTNC NNNACTNNN ANCCNNNNC TNNNNNAN NNNNNNNC ATNNNAACNA 720
 NAACNCC 727

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1013I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TCGACAAGGT GACCAAGGAG AAGTCCAAAG GTGCTCCGT GCCATTGGAC GTCCACCCAT 60
 CCAAGGTTGT CATCACCAG TTGCACTTGG ACAAGGACAG AAAGGCCTTG ATCGAGAGAA 120
 AGGGTGCCAA GTTGAGTAA ATGCATTCCA CAGGTCAGCC AGCATATTAT AAGTAATTAT 180
 GTTCTACCAA CTCTCTCGA TATATAGTAA GTTCAGAAAG TCGTGTTCCT CTAGTGTTTA 240
 TCAGTGGGCA TAATGACTGC TCTGGTCTC CGCTCGTGG CAGCCATTCT TGGCGGACAG 300
 CCAATGACTCC CGGGACCGAG TGAACAGGCG CGAAATTCG TTCTCGGGC CGACCAACNT 360
 TGGACTCTTA TTGATTTCT TCCGCCCTAA GAAAGTAGAC AGCGCTACA TATATGACAC 420
 ATCCCTGTCT GGGTGTTTAA GGAGCACCGC TCTGAAGAGC AGGGAAAACA CGGAGTCACT 480
 AGGCTCTGCT ACGGCTCGAG GTTTTGAAG TGAGTTTGN ATTATTGTC CNNTGAGAN 540
 TGANAGGGGT GGAGGCGTC ACCCGATCAA CAGACNANCA GGCAATGGTN TGAGTNGNA 600
 CACAGCNCGG CGAGAAGTG GCAANCNTCN ANGNA 635

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1013RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ANAATGGCTG GTAGTATTG TTAACCACTA GTTCTCCTCC GAAGTTGAAG TACTTCACAT 60
 AACTCAGCCC CTCCGAGGGA CTCATCTCCT GTACAGAGG CCTATTCAAC TCAATGCGCT 120
 GCTTGTAGTC CTCCAATGCA TCTGCGCTAT TCCAACCCCT GTNGTCTGCA GAGGCTGCTG 180
 CCATCTCCAG TGTGCGCGCC CTCAGAATTG ACTGCTCAC GACAGACTCA ACGAAGAATA 240
 CTTTACATT AAGAGCAGCA AACTCTCGG CGAGCATTCT GCGCTCTCG CGCATGATGT 300
 TCATCCCATC ATAGACAGNA AGCTGTCCCT GCTCGAAGAA CTTCTTCATG TCCGCTGGA 360
 TCTGGCTAT CAGCGTGGC CGCAGTCTGA TCCCTTCGG CGTAACTGGT CTGGTAGAGA 420
 AGTAGTCCAG CGGTAGNTTC ACCATCCCT GCGGGAACCG NGNCCNCGA TACTGGACA 480
 CANTGAAGGA TTGTGTGNGC ACCCCNAGC ACCCCCGTAT TGGTGTATT GNCACCGNAA 540
 CAANNITTTT GGGTGTCTGT TGNAGGCAC CCAGGACGNA CAAAATTTT TCCGCTTTG 600
 GAAANCCCC CAGNTCCAN NNGNAAAT GGNCCCGGG AATTTTNG CCGTNGGNC 660
 CNCCGNCNG 669

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1013UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATCGCTTAC CAGCCAGTA GTGCGCACA GGAACITGAG GTTGCTATC CGGCTGACAC 60
 GAAGTATATC GACCTTTTG CAGAAGTGA CATATGTAA CCGATTTGC CGCATTTGAA 120
 AAAGCTCGGA GTCAATACCA TTGTGTFTA CTCAITGAT CCAACCAAGC CACATGACGT 180
 TTGCATGGAG GAGTTGAGCA AGCTGGGAAT CTACGTTCTC ATCGATTTAT CAGAACGAGA 240

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CACCTCTATA ATTAGGGAAA CACCAACATG GGATGTAAAA GTATTCCAGC GGTACAAAGA 300
CGTAGTAGAC TCCATGCAGA AATACAATAA TGTTCCTGGC TTTTCTGCTG GTAACGAGGT 360
5 CACTAATGAC CGCACGAACA CAGACGCATC GTCTTTTGTG ACGCGGGCTA TCAGAGATGT 420
CAAAACTAC ATCAAGCAAA TGGGATACAG AACTCTTCGG GTTGGTTACT CACCATCGAT 480
GACCAGGAGA CGAGGGATCA CTGGCCTGAT ACTCCCTTTC GGTNGCGTAT CTNCAGANNC 540
10 TTTTGGCATA ANTTTGTTCG ATTGGGCGCG CATCCACCTN CNGACGANCG TTCAAGAGAG 600
NGGCTTNCNA TTTNNGAACT CCCCCTTGGCG CC 632

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1014RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCAAACTG CCGTCTTGGC GCAGCACGGG GCGCGCGAG TTGGATACGC GGTCCCGGTC 60
30 AAAGGCCACG CCGAGCGCGC CAAACTCCGG GAGGGGCTGG CCGCGGTAGC CCAGTGAAGT 120
GATAAGCACG TCCAATTGCT AATCCAATTG CTGCTCCAGG TGAAGTACAA CCTTGTMTTC 180
AGGGGTCAGG GAGTTTGTGC AGACGGTCAG CGCAGATATC GCGCGGGCGC CGTCCCTGGG 240
35 GATGTAGAGC GCGTCTTGA GATAGTCGGA CACCCAGGCC TTGGAGTAGC CTTCGCGCGG 300
AGGAGGGTAT TTAAGTCGGG ACTTGTCTGC GCGGGCGGGG TACGGCAGCA GGTACTGCTG 360
GCACATGTCA ATGCGCGGTT TGTGCGCGG GTGAGCGGC AGCGCGGCC AGCCTCGGG 420
40 CGTGAAGTGC TCGGGCGCGA TGTGGCGCG CACGCGCAG CGCTCGAGCT CCCACATCTC 480
GCGCAACTCC TTGNTGTGA ACTTGTCTGC GAGGAAGTCC CGGCGCCCGA TGAGACGCAC 540
CTCCTCGAGC GCGCGCGGCC GCAACGCCCTG CAGCGCGTGC GGGTTTGATG TCGGTCTGGC 600
45 CC 602

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 627 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1014UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

5 GATCAGTGTGTT CGGGGCGAGC CGGAGAGCAT ACTGCTGTCA TGTCTATAAC AGGAGCTGCT 60
 CTCGGGGGTC ATTGAGGAGT CCAAGGTTT TGCAGACAGG GACAGCACCA AGCACATCAC 120
 10 AGCCGAGCAC CTAGATGAGG CGGTGGAGGC GTTGCTGGGA GATGTAGACC GAGGCGGGGA 180
 CGGGGCATGG CCTTGATGTA AGTCTATGTA CAGGATATTA GCTTTCAAAA TGCATGGTTG 240
 GGGTACTTCA GCGTTTCCAC CATGGAAAGG GCGCTGGCGG CGTCGTTTTT GTTGAGCAAG 300
 15 AAGAGGCOCT GGAGCTGGCG GGTCGACACT GGGACGCTA GCGCGACGGC CTTGGCGACA 360
 AACTCCGGCG AGAGCGCCGA GTCTCCGGG TAGAAGCGCA GGAACATCTG CTCGATCTGG 420
 TCGGGGTTG CGTTCCCCAC AAGGAOCTTG TAGTCGATGC GGGCCGGGGG CAGCAOGGG 480
 20 GGGTCGAGGA CCTCGGGATG GTTGGTGGTC ATAAAGGTGA TCATCTTCTC ACTGGAGGCG 540
 ACGCGCTOCA GGGCGTTGAG CAGCCCGCTG AAGTGACGC CGTTGGTGTA ACGTCGTG 600
 TTCTTCTTGC GCTTGACAAA GCGCGT 627

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 698 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1015RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

40 GATCCAATTC CAAACGTAAT AACCATGGAG ACTGATGCTT CAAAGACGCC TGGTCTCTT 60
 CATCCATCAA AGAAAAGTGC AATTGTATTA TTTCCTCATC CTCCTCAATC ACAGTAGAGC 120
 TAGGATCCCC CGGGCTGCAG GAATTCGATA TCAAGCTTAT CGATACCGTC GACCTGAGG 180
 GGGGGCCCGG TACCCAATTC GCOCTATAGT GAGTCGTATT ACGCGCGCTC ACTGGCCGTC 240
 45 GTTTTACAAC GTCGTGACTG GGAAAACCTT GCGGTACCC AACTTAATCG CCTTGACGCA 300
 CATCCCCCTT TCGCCAGCTG GGTAAATAGC GAAGAGGCC GCAACGATCG CCGTTCCCAA 360
 CAGTTGCGCA GCTGAATGG CGAATGGACG CGCCCTGTAG CGGCGCATTA AGCGGGGGG 420
 50 GTTGGTGGT TACGGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCGCTCTCTT 480
 TCGCTTCTT CCGTCTCTT CTGCCACGT TCGCCGCTT TCCCGTCAA GCTCTAAATC 540
 GGGGCTCCC TTAGGGTTC CGATTTAGTG CTTTACGCA CCTCGACCC AAAAACTTG 600

ATTAGGGTGA TGGTTCACGT AGTGGGCCAT CGCCTGATAG ACGGTTTTTC GCCTTGACGT 660
 TGAGTCACGT TCTTTAATAG TGGACTCTTG TCCAAC TG 698

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1015UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATCCTAGCT CTA CTGTGAT TGAAGAGGAT GAGGAAATTA TACAATTGCA CTTTTCTTTG 60
 ATGGATGAAG AGACCGAGGC GTCTTTGAAG CATCAGTCTC CATGGTTATT ACGTTTGGA 120
 TTGGATCCAC TAGTTCTAGA GGGGCCGCA CCGCGGTGGA GCTCCAGCTT TGTTCCTTT 180
 TAGTGAGGGT TAATTGCGCG CTGGCGTAA TCATGGTCAT AGCTGTTTCC TGTGTGAAAT 240
 TGTATCCGC TCACAATTCC ACACAACATA CGAGCCGGAA GCATAAAGTG TAAAGCCTGG 300
 GGTGCCTAAT GAGTGAGCTA ACTCACATTA ATTGCGTTC GCTCACTGCC CGCTTTCCAG 360
 TCGGGAAC TGTGTGCA GCTGCATTAA TGAATCGGC AACGCGCGG GAGAGGCGGT 420
 TTGCGTATTG GCGCTCTTC CGCTTCTCG CTCACTGACT CGCTGCGCTC GGTGCTCGG 480
 CTGCGCGAG CGGTATCAGC TCACTCAAAG GCGTAATAC GGTATCCAC AGAATCAGG 540
 GATAACGAG GAAAGAACAT GTGAGCAAAA GGCCAGCAA AGGCCAGGAA CGTAAAAAG 600
 GCGCGTTTC TGGGTTTTT CCATAGGCTC CGCCCCCTGA CGGCATCAC AAAAATCGAC 660
 GCTCAAGTCA GAGGTGGCA AACCCGACAG GACTATAAAG ATCCAGCGTT TCCCT 716

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1016RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GATGTGAATC GATGTGTGGA GAAGAGTGTG ACTAGACACA AGCTGGCGAT GCAGCGAGAT 60
 CTAACAGGAA AGGTGCTGGT TGGGAGAAA AGGTACTACG AAGAGGTAGT CACTAGTGTG 120

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ACCTACAAGC CTACACACCA CCAACTGCGT TACGAAAATC TAAATACGTA CCTCTATCCT 180
 ACAAACTACG AGGTGCGCGA ATTCCAATTC AATTTTGTCC ATCGTGCGTT ATTGAAAAT 240
 5 GTGCTCTGTG OGATTCCAC AGGTATTTGGT AAGACCTTCA TTGCCAGTAC GGGGATGCTC 300
 AATTACTATT GGTGGACAGG GGGCACAAA ATTATTTTTC CTGGTCCAC ACGACCACTT 360
 GTTGGCAGG AAATTAAAGC ATTCTGGG ATTACTGGT TTCCCNNTTA TGATACGGGA 420
 10 ATNCTTCTTT GACAAGAGCC NNNNGCACAG GGNACAGATT TGGNCAAAA GAAAACGTTT 480
 TTTTTCGN NAACGCCCC CANIGGGGG GNAANTTTC CCNNGAGAG GGGGACTTN 540
 NNTCCCNNA GANNINGGN TTTCTINGG NNTNNGNGA NGGNTCCAC CCNGCNNGG 600
 15 GGGGCCACN NCCCCNCNN NNGNNTTTT NNGNNNTTN TTTTACAAA ANTTNC 656

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 435 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1016UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GATCCATCGA ACGTCCATTT TATACGAGA CATTTTTATA CAATTTTTAT TTAATAATGA 60
 GGATTTGGCA TTCCCTCAA CTCGCTGACT AGAAGTTAGC TGGTGCTAGT AGTGTAGCTG 120
 35 GGCTAATGTC GACTGAATTG CGGTGCGG TGCTGGAGGA TTATTTGTG TCCGCAGCTA 180
 ATGCCTTCCT GCCAGATGAA TTCCAGTGA AAGAATTGCA AGATGAATAC TATCGAOCCT 240
 GGGAAACGAT TGTGAGTAAT CTACCCGCGC TATTGTTGGC GGCACAGCTG CCGGATGTGG 300
 40 TGGACCAGCT GAAGGTGCTG GAGGTGAAGA AGGAGCTGTT CGACGATATT TCGGCAGGTT 360
 CGGCGCGCAT ATTGCGGTT GGCCTCAAC GTCAATGCGT ATGTGTGAG CTACGACGAC 420
 GCGTTCGACA CGATT 435

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1017I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

5 GATCTTCAAA TGGGACAAAT GCAAGGCTAT TGATCTTATT CCCAGCAAAC AAGTGCGACA 60
 TGTATGGTGT ATTTTGTGTG GGCAACCGAC TGCTGGTGAA AACGGGCTTA AAATCTGAGC 120
 TAGTTTTAAA GGCATCCTTC CAAAGTGTC AATGTGGTCC TCTCGACACT GCAAGCAAGC 180
 10 CCATGTCAGA GATTTTCACA TTGCTTGCTG GTATAGGCAG GTTTTCAACG GAATGTAAC 240
 CCTGAAGTT OCTGATATCC CACAGTCTCA TGGACTTATC TGCTCCGGTN TGTAGCCATA 300
 TAGTAACCTT GCCTATCTAC CGGACACCA GTGACGGGCC CGGTACC 347

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG101712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

30 GATCTTCTTG GGTGCGGCA TCAGACAGGC GTAATAATT TGATCATTCC TGGTGGGGT 60
 GAGGCTAACT ATGATGCATT GGAAGTTAAT CTTACGAGA CGACGAAGCA AAGGAAAGAG 120
 CAGGAGGTTA GATCGCTACT GAACAAATTA CTTGCTGATT CTATTGCATT AGATCCAAAT 180
 35 GTGATTGGTA CGTTCGACAA GCGTTCGCG CAGATTAGAT TGACCGCCAA AGACCTGACC 240
 CAAATCGCAA CTGATGAAGA CATGAAATCT AAGGAGAATA GAGACATTCC AAAAGCAAAC 300
 OCTGCTGTGA AGAGTAAGAA ATTCAGGTCT GGTACATTTC CTCGTAAGA AGACGCAGAA 360
 40 TGTGTAGAT GAGAGGAAGT TGAGAGTACA GAAGCAGTTA GAAAAAGAAA AGGNGGCCN 420
 CTGCGGAAG CANGCTG CTGAGGAG CTANCAGAG ATNCGANCTN CCTGNOGAN 480
 GGTGAGCA GTCCACTGCG MNTNNCTCA CCNNNATTC TTCGTNNCN GANTTCACNC 540
 45 CANNNCNCT CCGNNCTNN NCTTNNCCN NCTNNNTC ACCNNNCNC TCCNNNTCC 600
 NANCCACNC CCGNCCNC MCCCCNNCN CCCCCNNAN NNNNNCCCC CTCTNCCCN 660
 NCCCCCNCT NCC 673

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1017RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GATCAAGGTT	GAAAACGAGC	AGCGTGATAA	AAAAGAGCAT	GACGCGGATG	TCCCTGAAGA	60
GGAAATTTAAG	ATTAAATATA	CCTCGACCTA	CTATAAGGTT	GAGAATATGA	CGCGTGTAGT	120
ACCACAGCAA	TTAAAATATA	TTGCATTTC	AAAGGATGAG	AGATTTACTC	CGCTCGCAA	180
GTTTAAGGGT	AGCAATGGCG	TTATAGTGCT	ATCGGACAAA	ACTCCTGACG	AGCGGCTGGA	240
AGTAATCAAA	ACCGCTAGAC	AGGAAAAAGA	GACGGATGCT	CCTCTGCGTG	CTCCCTTCAA	300
GGTTCAGGAT	GACTTAGAAT	TCTGAAGTGA	TAATTAGGAA	GCGTCGATTA	TGTTTCATTAG	360
GAAAAAGGGT	ATTTTCTCTA	GAAACGAAAG	AACCTACTGA	TTGCAGCTCT	CTCTAAACAA	420
GTATATTATG	AGGTGATTTA	TTTCAACTGA	ATCTGGCTAA	CGCCCGGCAA	CTAGGTCTTA	480
TCTTCTGTGA	GTCACCTAG	AGGTGGTGGT	CCCCAANCG	CNC		523

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1017UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GATCTCCATC	CAGTTTGG	CCTCGTTCCT	GAGCTCTCT	GTGACTTCAT	CCTTGATAAG	60
CGCAATTAAG	CCAGGCGCTC	TGTATGCGTA	CGCAGTGTAG	AGTTGCACAA	AGTGCGCCCC	120
CGCTTTGGCA	AACTCGATGG	CATCCTGGCC	ACTACTGATA	CCACCACATC	CAACCAAAC	180
CAGGTTGCTG	TCCTTTGTGT	ATTGGTGTAT	CGTGGCGCAA	GCTTTTAGCG	CAAATGGTTT	240
CACGGGCTTG	GCGGACAAGC	CGCCTGCGTG	GTTTTTCAGC	TCCTCATOGA	CAGTGTACAG	300
CGAGTCTGGC	CTTTGGATAG	TAGTGTGGG	AAAGATGAT	ACCCCCAATA	CTCGATTTC	360
TTGGGCGCGC	TCTGCGATCG	ATTGGAATCC	TGGCTCGGTC	AAATCGGTG	CGATTTTAAC	420
AGGAAAGTTG	GTTATGGTTA	CTGGACCAAG	AAAATGCCNC	CGTGGNCAAA	GATTGGGTTA	480
GCANAACAAG	NIN					493

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 523 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1018RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GATCATCGTC	GAGGAGTACA	CGCACTCGCT	CTGCGCGTGC	GTGAACTTCG	CCGCGTGACA	60
CCCGTACTTC	TTGACGCCA	CCGTGTTTCTAG	GAACCGGCAC	CCGGCCCGGT	CGTACAGGTG	120
CATGTTGTTCG	CACGCCGTTG	CGCTCAGAAG	GTACTGTCCA	TGGTGTGCGA	ACGACAGCGA	180
CGTGATCGGG	CCCTGTTCTT	TCGCGCCAC	CTTGAAAGAC	TTGACCGCCC	GGAACCCCGC	240
CAATGTGTCT	TTGTTGATCC	CGATACTCAT	CCCGCTCGTC	TTGCAGCTTC	CGGTCCCTGG	300
CCCTCTCGCC	GCTGCTCTGC	ACTGCTGGCT	AGCAGAGCTC	ACCAAAATTT	TTATAGCCAT	360
GCCAGGCCA	AACCTTCACTA	ACTGGGGAAC	CACACGACCA	CAGCAAGCAA	TGCCCTCAGT	420
ATGTCGGTCG	GTCGACCGT	CCTGGGATCG	CTACTAACC	GCACAGCTCA	AGCAGATGGT	480
GCACCTCAGC	GCCGACCTCG	CGCTGGTGGC	GATGGTGCTG	GCC		523

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 770 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1018UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GATGCGGTGT	ACGACTTCAT	GCGGATGCAC	TACGTTATCA	CCAGATGGT	GGTGGGGGC	60
GACTTTCGGT	TCATGGCGGA	CTACCTGGAG	GTCTGGGCG	GCGGGCTGA	GCAACACGAG	120
TTGTGCGATG	CCCGCATGTC	TGCCCTGTG	CAACGGGACC	ACATTGCCCG	ATACACCGAG	180
CTGCTGATGC	TGTATGCGCG	GAAGTCTGGG	GATGAGAAAA	TGCTGGCGGA	GCTCTTTGCC	240
TCCTTGGTCG	ATAGTCTGCC	TGCGGGGATG	GGCGGAGCCA	CTCTTCGTCA	GCCATTGCAT	300
GAAGTCATGA	CGTACCTGAT	CAGCGAAAAC	CAGCCGCAAC	AGGTGCTGAA	ACTGGTGGCG	360
GGCATGGCGA	AGGCGGAGCC	CAATCGGCGG	CCGGGCAAAT	CCTCCGTTCC	AGGCACCTTG	420
GCGCTGGTTG	TTTCGGCGTT	GCGACAGTTC	AACAATCCTA	ATCTGTGCTG	GAGCTTTATT	480

GTGCAGGCAT ACAGAAAGAC GCAAACGAGA GTGCTGCTGG GACAACTCGG GCTATGGTCT 540
 CTGGCATTTT ATGGCCGGGC TGTTCGGCTC TCTCCCGAGG CGGCGAAGTC GCGCAGGAG 600
 5 CTGGCGCAGA TATCGCCTGT GGACCTGCCG AAGGAGCTAA TACTGAAGTC CGTACCTGAC 660
 AGCTGATAAT GTGCGAGCTC TATCAGCGAA TCTATCCGAG AAGCGATGCG AGGTGCCCCG 720
 GGAGGAGTAC CCGAGATTTT AATCCAGCTA TTTCGGCTTT ACCAGGACTT 770

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 735 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1019RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GATCCATGAC CCATGCTAGG TGAAGGAGC CCTTACCCGC TAACTGGAC TCCCTCTTCA 60
 ATTGCCTTAT CAGTTTGGTA TCCACAGCAC CCACGTGTA CAACAACCGC CCCATCAGG 120
 TAGACTTGCC CCATCCACA TGGCCTAGAA CAACAAACGA CATATGGGGC TTCTTCTCAC 180
 30 GTACATATGC AGGGATGTG AATGGGTTCC GCGGGTTAGT GGGCTGCACA ACCTTCTTGG 240
 CCGACGGCTG TTGCGCCTCC TTGCGCCCGG AATCTCTCTC CTCGTCTCG TAGTTCTTGG 300
 GGGCCGGCTC CTGTGTGTG AATTTCAGAT CGGCCACCTT CTCGGCCACC TGCTTAATCT 360
 35 CAAAGGCTCG CTCTCTGGAT TCCAACACCA CGTCATCCGG CGAGGGCTTC ATGAAATTGG 420
 CACTGGCCTG CTCTTAGCT GCTTTATAGT TGTTAGGATA AAAAACTGAG AACACCTCT 480
 CCACTGCGCT CTGAGCTGG GTTTTGGGTG GTTCTGGCA TCTGTCTGT CTCGAGAGGA 540
 GCACGCTCGA CAGCTGCAGT GCAGGGCGCG CTGCAGGCTT GAAGGACGGC TGACGCTGCA 600
 40 GAAGAGCCCC CAGGGCCATC CACTGGTCTT GCGTGCCCTC CGTCTTGGG GGGGGGGCTG 660
 CAACAGGCTT TGCTCAGCG TCGCCGGCGG ACTGCTTCGC AGAGACGACA GCGTCTGCAT 720
 45 CAGCGACGCG CCGG 735

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 740 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1019UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

5 GATGCGAGAT TCATCATGCG TGTATACCA GGCTCTATCT TCCTCGAGGT CCTCGGGACC 60
 AAACGGGGCG CTCTCTGTG TGCCAAGAGG TGCAGGACCC TGGCGGAT CCTCGGCCAG 120
 CAGAGTGGCA ATCTGGTCTT CATCGCTAT CGCTGTCAGC TTAGGCACAA AAGCCAGTTT 180
 10 TTCCGTTTTG TGGCGTGAT CATCTGCTC GAGGCTGCTC TTCTGATCTC TGGACCCCTC 240
 TGCAAACCTCT TTGAGCTGCC TTGCTGCTGC CTTGTCAAGT CGCTTAAATC TCAGCGTTT 300
 CTGTTTCTGG CCACCGCTCC CCAAGCTCTG GTCCGGCTCC AGTGTGTGTT CCAGTTCTGTC 360
 15 GTCCGAATCT TCGAAGCTCA GGGGACCAA GTTCTTGAT GTGTTTCCCT TCAGGCGCTC 420
 CCCGTCAAGG ACAGCCTCA CGTGGTGTG TGTGGCTCC TCCTGGTAC TCCGAGGGA 480
 TACTAGCAGC TCATGCAGGA ACTTCTCTC CCCTTAAACT TGCCAAGGC CATGCAGCTC 540
 20 TTAGTGAAT TCACTGGATC GTATGCATGC ACGGCGCTA TATGTCATAT CGGCTGCACA 600
 AACTTTCTGT GACATTGGAT GCGGATGTTG GTGGATCACT CCTTCAGCG GGGTCATGTT 660
 CTTAGCTCT ACCGTACTTG CTCTCTCAGA TGCATGATGT GTACCATCGC ATCTTCAGCT 720
 25 TGACAGACTT CCATATAAGT 740

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1020RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

40 GATGTTCTCT GTTCTGCGG GCAAAGTCA GAATTGACCT AGTGCCAGAC ATGACAGTAT 60
 CGTTCAAACCT CCTCGGAGAG TTAGCCTTGG ATATCCACCA TGAAGACAAA AACCAGAGAC 120
 45 CAACAGCGGA TCCTACCAA ATGGCCAGAA TACCGAAAA CCAGTCAAT TCTCCGGTTG 180
 CTTCACTTG GACAGTGACG TTCATCCAA ATAGACCCGT AACAGATTG AAAGGAATA 240
 ACATTGTTC AATCATAGTG ACCTTTCCCA ACATTTCAGT AACACGATTG TTACACCGGA 300
 50 AGGACTCAAC TTGCAATTGT GCCAAGTAGT TACCATGTGA ACGGAGAAA ATCTTCTCAT 360
 AGGACAGTAA ATTTTGAAAC ATCGGAGGA CATGGTCTG AATATCTCCC AAATAGAGCG 420
 CTATATCAGC TCTTGGTTGA GTGGCTGGA CATGATGATG TTGTATGTTG GAGCTAGCC 480
 55 TGCCAGACAG AGGGTGTGT CGCTAGCT GCAAGTTCG AATGTTTATC TCGAGGT 537

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 563 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1020UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCAGCACC GTGCCCTTCG TGTACGCTTG CTGACATG GTGTGGACG ACCGTGTGTC	60
GCATTTCTTA CACGTGAAAG CAATCATCAT CATCGGCTTG TCACCTTTA TAGACCGAT	120
ATGCCGAAAC TCATCTGCAA TAGGCGTTT CTGGCTGTTT TGCAGCTGG GCGAACCGCT	180
GTGGAACCGA TGAGCTACCA AATGCCCCC AAACACCGA CCCAGCAGT ACTGCATGCA	240
GTTACGGCTT GGGCGGAGTA AACCAGCAAT CCTGAGAGG CCCATOGAAC GTCTAAGCAT	300
TTTAAACAGT TATACGTAGT CAGCGGTTT CTTAAACAG GACATGAGAG TGGTTCGAAA	360
GAAGGGTCA TCTCAATTT TTCACTTTA GAAGCGCTG CCGAAAAGC ACCGTCACCA	420
TTTATCTATT ACAAGATGAA CAGTTAGTGG TGGCGCAAT TGTGTCAGAT ATATGTCCT	480
GGACATGGAT ACAAGACACT CTGOCACAG AAGGAGCAG AGATAGCATC GAAAATCTTG	540
CAGAAGGCTG AGCTGGCTCA GAT	563

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1021I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GATCTCACC TGCGCACCAT CGACAACCT GCATACGCG GCGGTGAGGT CATCGGCAAG	60
GCCCGTGCC GCACACTCGA GATGCGCTC AATGCCCTGT CCGCTACCAA TGGCGGGCA	120
CGAACCTCG AAACCGTGC TATGAACATA CGAAAGGCA TGGTTTCCAA GCACCGCAGT	180
CGCATCCGG AGCACGAGCA GCTGGCCCG GACTCCGGCA CGTCTCTCG CAAGGTCGT	240
CGCGGAGAGT TCCGAAGAT AGACGCAACC TACAAAAAG ACATCGAGCG TCGCATTGGC	300

ACGACCATCA AGGCTGCAGA CCGTGCCCGC AAGAAACACC GCGATC

346

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 562 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1021I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GATCTGCGCC	GGATGGCTGC	GAGTTGAGCG	CGGGAAGAT	GTGTGACTCC	TGCAGAAAAC	60
GCTGGAGCTC	GATGTCTGT	TCCAGCAGCT	GCTTCTCGTC	GGGTCCGCC	GGGCAGATT	120
TGGGCGCGG	CTGGTCTCT	AGGCCGGCG	CCTTGCCCT	GCGGATGGG	CGCAGTTCTC	180
GTGGAGAAG	CCGCTGTAG	GCATCTGACG	GCGCGGGAA	CGAGTCACG	CGCGCGTAT	240
GGGCGCCTC	GTGTGGGAG	CTGGCTGAG	CGCGTCCAT	TTGGGACTGC	TCGTGGGATT	300
CAGACTGTCC	GGAGCGCGG	TGCGCCTGC	TCTCGGGTC	ACTGTGCTC	TCGGAGGCG	360
TGGTGCTTGT	GTGCTGCTT	TGTGCAGCAC	GGTCTTGTC	TACATATCC	ATATCCTCTA	420
GGGAGCCAAA	CTGGGCTCG	AAGGCCCTCC	CCTGGGNC	GACNIGCTTG	NATTTATCTT	480
CAATTGTGCG	TCATCNGGG	GGTCTCTTG	GCCCCANGA	GINININANC	AGGAANCCCT	540
AGNANNANGG	TTTTCAAATT	CC				562

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 611 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1021RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GATCCTGAG	TTTGTGCGG	GCGGGTCCG	CTCATTTACC	TAATCTGTC	TATAGTAAAC	60
ACGTTGTGT	ATCTACATAG	CGCACTGTT	GTAACTTACG	CTGCAAGCAT	GCGCGGGCG	120
ACGTCCCCA	CCAGCGCCG	GTAGAACGCC	TGGCCCGCG	GCCGCCGCC	CAGCATGCAC	180
AGGCGCAGC	ACGGTTTCAT	CGTGATCAG	AGGCCAGTCC	ACAGCGGGCC	CTGCAACAGC	240
GCGATCAGCA	GGACGTCCG	CACCAACC	TTGGGAGCA	CCAGTGGCT	GATCCCGTC	300

TOGCGGTCCG CCGTGGGCTC GGGCTCCTTC TGTCGGCGCA GGTGTGCTG GCGGCGCTT 360
 TOCTTCGCCA GCGCTGGGCG GAACGTCTTT TTGGAACCTG ACGTGGGTA TCGTTATTC 420
 5 TTGGGGTCCA TTGGAACGCG TGTCGGGGT CAGAGGGAGG ATTCTGCGC TGGTTTGGTT 480
 TTTACGAAGA CGACCTCGG TGAGAATGTC AGTTTGGCCA CTNGGCAGCC CCAGGAAGGA 540
 CCGNGAATTC AAACCACTG AGTNGGGCGN CGNGTAAAA ACGCTAAGTT AGTGCNNTGC 600
 10 ANACCCNCT C 611

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1021UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GATCGGGTG TTTCTTGGG GCACGGTCTG CAGCCTTGAT GGTGTGCCA ATGCGACGCT 60
 CGATGCTTTT TTGTAGGTT GGTCTATCT TCCGAATC TCCGCGACG ACCTTGGCGA 120
 30 GGAAGGTGCC GGAGTCCCGG GCAGCTGCT CGTCTCCCG GATGCGACTG CGGTGCTTGG 180
 AAACCATGCC TTTGGGTATG TTCATAGGCA CGGTTTCGAG GGTTCGTGCC GCGCCATTGG 240
 TAGCGGACAG GGCATTGAGG CGCATCTCGA GTGTGCGGC ACGGCGCTTG CCGATGACCT 300
 35 CACCGCCGGC GTATGCAGG TTGTGATGG TCAGCAGGT GAGATC 346

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1022RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ANNNNNNNN NNNANGGTGG GCGTGGTNG AATAGTGGT CTTTCTGCCG GGGTCTGTGC 60
 AGAAAACGAG ATTCTGGGA GTATCTGAAA TTCTTTGTTG CCGCGAGCCG TCTGGGTCTG 120
 55 CGTCAACGA CAGCGAGTTT GCGACAGGAA CTGAAGCTAA TTTCGTTGCT GGAGGTGTTT 180

TGGGGCTTCG CGTTTTTCAGC CTTTCAGGAA ATCTAGAGGG GCTGTGTGCT TTGAGGCTGA 240
 AATCAGGGGA ATAGCCTGAA TTTGCGAGCG TGAATTGAGC GGTTATATGG AACTGTGGTA 300
 5 CATCGNCACA CTGTACCAAG AGGACAGCGA ATATCTGACA GTAGGGGCTC CTTCGTAAAG 360
 ACACAGTGTA TCGCGTGAGA TAGGTGTGTA TTGAGTCTAG CGTGCTAGGT ACTCTTTAAC 420
 TTTCACTCGG TGTTTTTT 438

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1022UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GATCCAGCAG ACGTTTTAAT CACCGATTTT TTCGGTAACA TTCAAAATAT AATTCTCGAT 60
 GACAGTGAGA TAGATGGTGA AACTCCAGCT GGACTTACGG AATCTGGCCG GACTCGCAAT 120
 CTGCTAGAAT TCGCAAAAGC GAAATTTTTT GGCANIGTAG ACGCAGAGAC TAATGGCAGC 180
 30 CATAAAAACG TGATTCCAAG CTATCCAGTG GTAAATGAGG ATTTACTAAG TGGGGNANCA 240
 AATGCATCCA CAAACAAAAT GATAAAATTG TGGGGGATTA TCATCTTCTT GGCCTAAGC 300
 TCATTAAATGA TGAAGTACGC CAACACTGAA AACATATCGG GTAGTCGAGC ACTATTATGT 360
 TTCTCTTAGA AAAATGCTTC ATGCTTCATG GAATTAAGGC GGCAACAAGT GCAAGGTAA 420
 35 GAACGGAATT TTAATATAGG CGGAAATTT GTATATATTA T 461

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1023I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTCGAGAAAA CAGAGCTTGA GGTCCACTG TTCTTTTTC A CTGCGGATGT CTCTGTCTGC 60
 TCCACGACCC CCACTTTCAG ATTGTGGTGC ATCAAGCGCT GCAAGTGGAC TTCGAGACGG 120
 55 GTGTCTGGGA TGGTGCACTA CGAAACTTC TTGTGCTTGT GATCAGCGGG GTCTGTCTCG 180

TGTACCGTAA GCTTGCCGGG CACCAGCTTG ATC

213

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 725 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1023I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GTGAGGGGAA GTAACCAATA TATTCAAGAG GGCTACCTAT GGCATCAATG AGACGTTGG 60
 AACCAAGAT CGTCGGGTCC TGGGTGATAG CGCTTCTGTG TGGGGTCTTG TGTGCAAGCG 120
 ACAACCTTCA TACACGGGAT ACTTCCTGGT TAGTGTTAAT CTCAACAGCG GTGAAGTTAT 180
 CTTGATGAC TTCAAAGAGG AGCGTTTCT GACGGAGGCT TTGGAGACGC GAATAAAATA 240
 CACAAACCCG AGTGAAGTTG TGGTCGGAGA TGGCCTTGGC TCAGAAATCG AAAAGGTGTT 300
 TCATACTTCA GATTCCGATA TCACTCTAAA TAGGATCGAG CTCGTGGGGT TGTATGAAGA 360
 AATCTTCAGT GAGCCGCACC CAGCCTTTAG GGGCAACGTT CCTCTGCAA CAGCGCTCAT 420
 GCTGGTGCAT GGCTACCTAA CAACTTCAA AAATGAGAGT TTA CTCTTCT TCAAGGAAAA 480
 CTTTAAACCA TTCTGCTCGA AGACGCACAT GATTCTTCCC TTCTAGGCT ATTGGAAGCT 540
 TAGATATTTT GGGGACAGTA CAGATAGGAG CAGTAAAGGT CCGCTGTAT GGGTNTTAGG 600
 TCAANCTAGA ANAACTAGGG TTAAGGACTT GGAGGACTGG NTTGAAAGGC CTNTTAATTT 660
 GGTCAGTCA ANAGAGTTGN GGNNGCCAAN GATTACNAG GNGGNATIN TCATGGCTCG 720
 GAATT 725

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 659 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1023RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TGCCCCGCAA GCTTACGGTA CACGAGACAG ACCCCGCTGA TCACAAGCAC AAGAAGTTTG 60

EP 0 866 129 A2

NGTACTGCAC CATCCAGAC ACCCGTCTCG AAGTCCACTT GCAGCGCTTG ATGCACCACA 120
 ATCTGAAAGT GGGGGTCTGT GAGCAGACAG AGACATCCGC AGTGAAAAAG AACAGTGGGA 180
 5 CCTCAAGCTC TGTTTTCTCG ACCCTAGGGA TAACAGGGTA ATACAGATAT CAGATCTAAG 240
 CTTCCTCTGT CCCCCTCGG TCACCCGGCC AGCGACATGG AGGCCAGAA TACCTCTCTT 300
 GACAGTCTTG ACGTGGCAG CTCAGGGGCA TGATGTGACT GTGCCCCGT ACATTTAGCC 360
 10 CATACTCCC CATGTATAAT CATTTGCATC CATACTTTT GGATGGNCGC ACGGCGGAA 420
 GCAAAAATTA CCGGTCTCTG CTGNAGACCT GCGAGCAGGG AAACGCTCCC CTCACAGAG 480
 CGTTNGATTG TTCCCCACGG CGNGCCCNCTG TNGAGAATNT AAAGGTTAGG ATTINGCAATG 540
 15 AGGTNCTCTT TTCANTTNTT CCGTTTNTAA ATCNTTGTNG GTCAAGTCNT CANATCAAAT 600
 TCCCAACATT AACACCNCTG TTAGGGAAGT TCANNTTTCN GGGGCCNNGA TTANTTCN 659

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 646 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1023UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GATCTCAAAC CTGAGAATAT TCTACTTCAT CAATCTGGTC ACGTTATGCT TTCTGATTTT 60
 35 GACCTGTCAG TACAGGCAAA AGGAACAGA AATCTCAGG TTAAGGGAAA TGCCAGTCT 120
 TCGCTGTGCG ACACAAAAGT TTGTTCTGAT GGCTTCAGGA CTAATTCCTT TGTTGGAACG 180
 GAAGAGTACA TTGCACTGA GGTATCAGG GGAAATGGCC ATACAGCATC CGTGGATTGG 240
 40 TGGACATTGG GTATACTTAC TTAAGAAATG CTCCTTGGGT TCACTCCTTT CAAGGGCGAC 300
 AACACAAATC AAACGTTCTC CAATATTTTG GAAGAATGAC GTTTATTTCC CAAACAATAA 360
 CGATATATCT CGCACTTGCA AGGACTTGGA TTAAAAAGTT ATTGGGTCAA GAAAGAGAGT 420
 45 AAGCGACTTG GTCAAAGTTT GGCGCAAGT GAGATTAAAA AAGCATCCCT TTCTTTTAAG 480
 ACCCGTCCAG TGGCGGTTA TTGGAGGGAA CCAGGAACCT CCGTTTATC CCGTATTA 540
 CCGGAGATGG GTACGACTTT GGAAAGTAT CACATTAAAG GATGTTAAAA AGGCCGGGAA 600
 50 TCCGGCCAC CCGGTTAGT CTCATATTCA AAGCCNGGT TCNNNN 646

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 557 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1024RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

10	ATNNNNNGNN CANNNGTGGG GCGGAGOGAN TAGTGGGTCA GCANGGTGGG CTCGGTGTGT	60
	GCGCAGCCGT TGGCATGCTC GCGGATCCTC GCGTCCAATA TACCAGAATG CATCATGCTT	120
	CGCTGGCTCT ATATTGACCT GGTGGCCATA TATGAAAAGG CGGTCTTGA AGTTTGTAG	180
15	AAACTCGTCT GCGTGAGATG GCGTAGCGAA CCCAAGGAAG CATTATATGC GGCATTACG	240
	AGGCCTGGAA AACTAACTA CCGGTACTT CTCATCTAGC AGTGAAGGG GCACGTCTGC	300
	GGAAGGAAGC GGCTCTGGCA ACGTTTCTC CCGGATAGA GCATATGGT TATCCTTGTT	360
20	GATGGACTTC AACAGTTGTC GAGCATATTC TATCCTGGAG GCATTTGAG CTGGCAAATT	420
	TGACAGGTAG AACTGGATG GCGCGTTAG TATCGAATCG ACAGCAGTAT AGTGACCAGC	480
	ATTACATAC GACCGGACGC ATGATATTAC TTCCTTGNGN ACTTAANNTN CCAATCTTN	540
25	NGCCAGATTN ATTTTGG	557

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1024UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

40	GATCTAAATT CCCAGCCGC TGCGGGGTT TCTCTGGAG TCTTTGCCGT GAAGCACGAC	60
	ATAATCGAGC CCAACACAG CAAGATCGCA GAGAATCAAG CTTATGTAAG TCTCAGTGA	120
45	CTCGANGCGT GCAGAACGGT ACGGTGTGC ACTGCAGGTG CCAGGCCATG TCTCACATGG	180
	TTGTAACAGC GCGCGACCGC GGTTCGGAAT ATCAAACAAA CATATGTTTG CCGCAAAGG	240
	GACTGGTTCC CGCAGCTGCC ACCCGCAGGG GCACAGCGCG GCAATGCAGA GTCGGTTAG	300
50	GGTGCGGTGC CCGGATGGG GCAGTGTGCG CCGC	334

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 621 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1025RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GATCAGCCCG TTGCGCCCGC CGCCGTTGTA CTTCTGGTTC TGGATGGACC CCGGCGTGAT 60
 GCGGCTCTCG TTGCGGTACT CGTCGCTGCT GCGCAAGTCG CACTTCAGCG CCACTAGCAC 120
 CAGCTTCACG CCTCGCAGT GGTCCGCAAT TTCGCTCACC CACTTGTCTT TGACGTTCTC 180
 CAGCGAGTCC CGCGAGTCCA CCGAGAAACA CAGCATAATC GTGTGTGTGT CCGAGTACGA 240
 CAGCGATCCG AACCGGTCAA ACTCCTCCTG CCCAGCAGTG TCCACAGGC TCAGCGTGAT 300
 GTGCTGGTTG TCCACGAAGA TGTCAATGAT GTAGTTTTCG AATACCGTGG GCTCGTACAC 360
 CTTCCGAAAG TACCTCGGT GAACACGTTT AACAGCGACG TCTTCCCGCA AGCACCGTCT 420
 CCGAGGATGA CGATCTTGCG CTCGATAGGA TGCTTCGACG ACGAGCTCGA CCACACAGAG 480
 GCATCTTG TG TTTGTAGAGC TGGTGGTGGG AGCTCCTCTG ATGCCAGTCC ACGCTACAAA 540
 TACAGCGTTT GAGACGAAAT ACTAGCTGCT ACTGTCTTTT CTCTCTGACG AGGTGCACGG 600
 CGCATCCCCG TTATAACTGT C 621

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 522 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1025UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GATCCCCATG AGAATGAGCG CATCTTGGAT ATGGCGGCGG CACCCGGTGG TAAAACCACC 60
 TATATATCTG CCATGATGAA GAACACTGGT TGTGTCTTTG CAAATGACGC CAACAAGGCA 120
 AGAACGAAGT CCTTGATTGC GAATATTAC CGTCTCGGCT GCACGAATAC AATTGTCTGC 180
 AACTACGACG CCGCGGAATT CCCTAAGGTT ATCGGTGGAT TTGACAGAAT TCTACTTGAT 240
 GCGGCTGCT CAGGTACAGG TGTATCGGC AAAGATCAAT CTGTGAAAGT AAATCGTACT 300
 GAGAAGGACT TTATGCAAAT TCCACACCTG CAAAAGCAAC TGATATTATC TGCAATTGAC 360
 TCTGTTGACA GCAACTCCAA GCACGGGGT GTCAATTGTCT ACTCTACTTG TTCCGTTGCG 420

GTTGAAGAAA ACGAGGCOGT GGTGGAATAC GCTACGGAA GAGACCTAAT GTCAGCTGTT 480
 GAAACCGCT GGTATTGGT AAGGAAGGCT CACTAGCTAC GA 522

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1026RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GATCCAATTG CTGTCATAC ATACGCATTA ACAGATTTTA TTACTATGTA TOCAACGTGA 60
 ATTGCTATAT GTACCTTATT ATCGTTTCA TAAAGATGCT TTAATTTCTT ATTCTGAATC 120
 GGAGTCGTTT GACCGGCGCT TAGACTGGTT ATGCTCTCTG CCATCGTTT TCTOGAAAAT 180
 GAAAATTCTA GCTTCACGCT CGGTCGACG CTTAGTCGTA TCTGCTCAT TGTTAGTTCT 240
 CCTATGACGG TATCTGGGA AGGTATCCCA CTGGAATTTG TGCGACCTCT CAAGCTTTAA 300
 ACCATGCTCC TTGGCAAGTA CCTTAGGCTG CCAAGAATCG TATGGATCAC CGGCAAATAG 360
 GGACAAAATG ATCTCCCCA TATCATCAGA TGATTGTTCT TTTTCTACT TCATATCCGG 420
 AAAGATGGGC AACAACCTAC TTCTTATTCG CCAGCTTGAT AGTTGTTTAC AGCTATCAAA 480
 AATATCCCGA TAGAGCTCTG AGCTCTCT 508

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1026UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GATCTAGCAG ACTAGACTCT CTATGCATC AAGTTTCTGT TTTCAAGTCT GGGTTTCTTG 60
 AGCAACCTGG TGCCCCATA CTTGTGTCAG ACGCACAGG AAGCAGAGT CTATCGAOGA 120
 TGTCGAACCT ACAGACGAAA AAACAGCGCC CGCCAGCTAT TOCAGAGGCA GACGTATCAC 180
 TCCAGGCTAT CAAGAAGCGG CGCATGTCCG CCAGGTCCTC TACCTCCCGT AAGTCGGGTT 240
 CTGCCACAGG TATTAGTGTT GTGCCACGGG CGCAGCTTC AGAGTCATAT GTGGTTCCAC 300

CTGCTGGTGC TCCTCTGAAG AAAGAGTCTG CGGATGACTT ATTTCAAACG ACTGCTTCCT 360
 5 TTTATGAACG TTACTACTATT TCCACACTGA AAGAAATACC GAAAAACATT GCAGATGAGG 420
 ACTCTGCCCG ATATACCGTT AACGAGGATA GCATCACTAT GGCTGACCTT TGCAAACCTC 480
 TATTCCCGAT AGGTGAAGTA TCTGATAATT TCACCGGGCG AAAGAAGCTG CAAAAGCCAA 540
 10 GATGGAAGCT CGGAAGAAGC GCGCGAACT CGACAGATG GCTAAGGCTC AATC 594

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1027RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CATATCGACG TACTCTGGCG TTGTTCTTTC TTGTCAGCA GGAACGCGT CCGGCATAGG 60
 CTTACTGACT TTCACAGACA TGATTCTTTT GTCGCAAGTA AAGTATATTAT ATGGCGCTGT 120
 CAAAAATGGT AATAGTACGG AAAGAGCAAC CTGAGAAGCG TCCAGGGCCT GCGATAAGCC 180
 30 GTTTTACCT AGAGCAGTGG ATACAGCTAA TGTGGAATC AATGCAATGG CTCGTGTCAG 240
 AATTCTCGT TTCCATGGGG TTATAGTCCA GCGTATATGG CCTCCGCATA CTATTGTGCC 300
 AGCTATGGTA CAGACAAATNC CTGCCGATTG GCGCGAGATT AAGAGTGGCA GCATGAATAT 360
 35 GGTACCTGCC GCTGGTGCCA AAGTGTGGA TAATAGGTGG TGTATCGTGT ATAGATCGCC 420
 ATCGATGGCT TCCGGGGTAT CATACAGTGC GCTA 454

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1027UP

(x) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GATCAACGAG TAAAAATGCC AGGTGTTTCC GTTAGGTACG TGTATGAGT GCTAGTTTAT 60
 55 GGTTTGGTAC GGCTGCTGGG GGGCGCTTTC TGGGAGGTTC CAGCGCTCAT ACGTTATGTG 120

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AAGATGCTTC GATCGNGAGG GTTGGGAGAA GGAATGGGAA TGTGCCAAGC AGGACTTGGT 180
 GATTGGTTCC AGAACGTGCG TGACTGTGTC AATATGAAA TCATTGGGCG AAACCTAGCT 240
 5 TGCTACGGAG TCCAGCATGC AGAACGTGCG GCCGAAGCTA GCTGAGGCTC GATGAGACGG 300
 TGGCGGAAAT CCTTCGATCC CAGGCCAAAG CAGAAGTACC TACCAGCTTT TAATGTGCCC 360
 GCCTACTAAC ATGATATACA GAGAAGTTCC AGCTCAAGAG TTCATCAACG CTTACGCTTC 420
 10 TTTTCTTGCA AAGACAAGGT AAGTTG 446

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1028RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GATCATGCAA ACGGAGAGAA GGAGAAGAAG TCTAAGAAAG AGGGCACTAA AGAGAAGAAA 60
 GCCAAAAAGC AGGAGAAAAA GGAAGTGAAG AACATCATTTG AGGAGTCCGT TGAGCAAAAT 120
 AAGCTAGCAC TGATAGAAAA GGTGGAGGAA GAAAGAGGCC GCAAGAAGGA GAAAGACCTT 180
 30 GACATCAAGT TCAGGTATCG GGAAGTTTCG CCAGAAAGTT TTGGCTTGAC CACCCGTGAG 240
 ATATTTATCG CTGACGACGC TGCTTGAAT GAGTATATTG GCCTCAAGAA ATTTGCACCA 300
 TATAGAGCAA AGGAGTTGCG CAACAAAGAT AAAAGGAAGG TCATGAAGGC TAAGCGTCTA 360
 35 AAAGAATGGA GGAAAAAGGT GTTCAATAAC GAAAATGGGT TGGCCGATGA GGATGAGGCC 420
 CTTGATACCC AGGCGGCTCC TAAAAAGGAG AAAAGCCGTT CTAAGCACAA GACAAGTAAG 480
 TAATATTACC GTCTTTATGT ACGTCTGCG GTAATTATAT TTGCTATAC ATATATATTA 540
 40 ATTTAAACTT T 551

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1028UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GATCCGGGCC CGGCACAGGC CTGGCAGCAC CCATGGCCGC ATGCTGTGCC TAAGATGTCT 60
 CAGAATTACG CGGCCGCTCA GGGGGGGGCC AGCCCTCCA TGCTTTTGGG CCAGGAAGCC 120
 TTCCACGAGC TGGGGGACTC GCTTGGCATG TCAATGTACA TGTCGCCCCA GACCCATAGG 180
 CTCAAGGGCA ATGGGGGTA CCTGTTGCCG ACGCTTCTA TCTCCGACC TTGGGTGCTC 240
 GGTGACACCG GCGCCCTCC GTCTTCTCAG TCATTGACAT CGCACCTTCT GGTACCCCG 300
 AACTTTAACA TGAATGACTA TGTGCATAAC CTTTTCAGCC CTTCAACCAAG AATAGACCCG 360
 CCAGGTAGCT CTGGGAATAT ATAGGGCCTC GCACACATT AGGCACAGT ATACTAGCTA 420
 ATCCTACATT CTCTGTCATA GTAATGCCTA TGTGAGCACA CCTGCCGTAT AATTTCATTA 480
 TTTCCTGTTT CATAAATGCT GACATATGTC ACGTGGCTGG ATCAGCACGT GATGGCAAAA 540
 TTCTTATGAA TGAGCCTGTT CATCTCGTCA GACAATACAT TATACACGCA TCCATCTCTC 600
 GGTATGATAC GGACTCTCTC ACACTGGA 628

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1029RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GATCGTAACA CTCTGGAGAA GTGGAAAGAG CTAGTCCCTC CGAGCTGTAA ACGATGCATG 60
 GATGCGCTTC ATCACAACCG GTACGACACC GCGAGTTTC CGGAGCACAC GCTCGAGGAT 120
 GTGGGAAAAG GGGTTCCGCG CGATGCACTG GTATACCATA TTGGGCCACT GTGGCAATTT 180
 CGATGGGAC TGGATCGGCG CGTGTGCAG AGCTCAAAGA AGGTTTGTTT GCTATTCTCG 240
 AAGATCGATA TGGTGGTGCA GAGACGTCG CACATGCCG AGGACGTAGG TGCATTTTTC 300
 CAGAGCTTGC TTTATCATGA CCTGCATGTC AAGATCAGCA ACTTCGCTT CTTTCTGCG 360
 CTGAAGCAAT GGAACATCCA GACGGTGCGG AACGCTCTGA GTAAAGAAAG TTACTTACTT 420
 GGGGGCCAA ACGCGGGCAA GTGTCATTG ATCAATGCC TGATGAAGAC TGTGTGTTAC 480
 GAAAGTCGCG GTCTCGTATC CTCAAAGCAG TCCTCTGGA CCGCTGCGA CTTGCTTCCA 540
 AAAGCGCAT TGGACATCCA TTCTGCGGT GTGAGCACA TACCGAATT CACTCGCCAA 600
 CCCAGCATTA CGATATAAAG GGCAAGATCT CCACGATTTC CAGGCTACCG CACAT 655

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1029UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GATCTCGTGG	TGTTTTCGAA	CTTGGTGCGT	GACGGGATAT	CTCAGGCTTT	GCGTCTGAG	60
CATGATTATG	AGGTGAACAA	GATGCGCCGC	GCGCTCTCCT	TACTCCAAAA	GCTGTATATT	120
AGGGATAGAA	GGACCAATTT	CCTCTCCGCG	GCCAAGGGGG	ACGACTTCTG	GGTCATTGCG	180
GATACCACGG	TGAAAACTG	CGACATTACA	TCTCTCCTTC	TTTACTTTGA	TGAGTICTAC	240
AGAGAACAGT	TGGATTTGTT	CCTGGGCGAG	GCGCGTGCTC	GGCAGGAGGT	CCCCAGGGGC	300
GATCTCGTAG	CGTGGGAAAA	CGATATAAAA	GTAAAGTTCT	TTAGCGAGAA	GTCATCGAAG	360
CACGCTTCGT	GGGGTTCCCT	TGCCCTGCGG	AAATTGGAAC	TGGTACTGCG	CGCTCCGTTT	420
CTGTTGCCCT	TTGCGGAGCG	GGTGGCCTAC	TTTGAAACGC	TGATACACCA	CGACCGACCG	480
CGGTTGCAGG	GACGCCACAC	AGGACCAGCC	TTGGGCGCTC	CGACCTGTA	CTTCCCGTGG	540
TCGGGGCGGC	AGCGTGGGAT	TATCTCCAGG	AACAACATCC	TGGAAGATGC	ATACSAGGCG	600
TATTATCCGC	TGGGCGAAGA	CTTTAAGGAC	CAGCTGGC			638

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1030RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GATCTGCTTG	TTGCGCAACG	CTTCCCAATC	GATGTGCTG	AGAAAGGGGT	GGGCGGGGAC	60
CTCTGGCGCG	TGTTGACCG	CACCGAGGCG	GTGCTTGGGA	TTGCGGTTCA	AAAGGCCCTT	120
GACAAAGGAG	CGACCTTCCG	GCGATAGCAC	GTCCCTGGGG	AAATTGACCT	TGCCAAACGC	180
AATCTTCTGG	TACATCTTCT	GGTTGTCTTC	TGCAAAAAAA	GCGACCCAGC	CACAGCACAT	240
CTCGAATATC	AAGAGGCCCA	GCGACCAGAA	GTCAACCATT	TTGCTGTAGC	CGGTCTCATC	300
GAGCAGCAGC	TCGGGGCGTA	GATACTGGGT	GGTACCGCAG	AACGTATTGG	TGCGATCCTT	360

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TAGGTCCGCT TTTGAGAGGC CGAAGTCACA TAGTGCGATA TTGCCGTTGG CGTCTAAAAG 420
 GATGTTTTCT GGCTTGAGGT CGCGGTACAC GATATCATTG TOGTGAAGGT ATTCCAACGC 480
 5 AAGCACCAAC TCGCAATGT AGAACTTTGC CGCTCCTCC GCGAACGAC CTCTTTCTG 540
 AAGGTGCCAG AAAAGCTCAC CACCGNTCAG GAAGTCAGTC ACCAAGTATA AGTCTGTGGG 600
 CGTTTGAAAA GAAATTTTCA ACCAACAAATG AAGGACACG ACTTTGAGCA GTAAGAACGA 660
 10 GATGTTGCGC TCACCAATAG TATGTGCA 688

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1030UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GATCGATTCC CTGAGCATGT TTTTCCCTAT GCTGCAGGTT TTACATGGTG ACATTGCGGA 60
 TGCCGAACCTA AAGAACCTTA TGCTTTTGAA ACTCTGGAAC ACTTACGGCG GAATTCCTGA 120
 30 ACGCTGGCTA TTCACTACTC TCTACAAGAA ACAGCAAGTT ACGGTAAATG ATACCGTGCA 180
 GCTCGAGTGG TATCCTTTTAC GGCCAGAGTT TGTAGAATCA ACCTATTCCC TTTACAGGGC 240
 CACTAAAGAC GCATTTTATC TGAATATCGG ACGAAGCATC CTCAGGCTC TATCAACGGC 300
 35 CTTTAAACG AAATGTGGGT TTGCGGGCAT ACAAACGTC ATAACGGGAG AGCCACATGA 360
 TAGGATGGAA TCGTTGTTT TGGGCGAGAC CTTAAATAT CTCTATCTCC TCTTTGACGT 420
 ATCCAATGAA TTGCATACAC AAAAACGCAC TAACCAATA TTTAGCACTG AGGCGCATCC 480
 40 ACTGTGGTIG ACTGCTCGA TGAAGGCTCG CTACGAAAAG AACAAGTACT GTGAAAACGA 540
 CGTGTATATA CAGAACTTGC GTGGCTACA GGAGCTTGAC CAGCTGAAAA GCGTGCCAA 600
 TTCATTCACT GCAGAGGAAG CCATGATACC AGCTTCAGAT TTCAAAACAG AAGACTCGA 660
 45 GGAGTCCTTG AAGGACCGG TTGCAGCGCC ATACTAGAGG OCTACAGTA GATACGACAC 720
 GTTCGTGGAA CATGCAGACC TTTCGGACA A 751

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1031RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GATCTTAGTA	ATGATCACGT	GATTGGATTA	CCGCTTGTC	GTTTGTCTCT	COGCAAAGCG	60
ACATTTACAC	GGGAAAAGCG	GTGAACCTCC	GOOGAAACCC	AAATACTCGT	ACACTATGAC	120
TATAGACGAC	AATGTGATG	ACGTGAGCAC	AGTTTAACTC	TAGTGTACAA	TCACTGTCAC	180
ATACCTTCTC	TGCCACCCAC	ACATTAACCA	TTTATTTGTG	GTCACGTGAA	ATGAATCGAT	240
GCATTTTATA	ACTGCAGGTT	AGTTGAGCCA	TCTCGCCAAC	GATGTCTGTC	GACAGCATTG	300
GGGGCACGGC	GCGTCATGAG	TGATTGGAAG	GAGGCACAGG	ACTCCACGGG	GCGTGTTTAC	360
TACTATAATT	CGAAGGGGGA	AACGTCATGG	AATAAGCCCA	ACGACACGCC	AGTTGAGCTG	420
GAACCGGAC	TGAAGAATG	TGGCTGGAAA	GTGGCAACGA	CGGAGGACGG	TAACTGTAC	480
TATTACAACA	GGGAACTGG	CGAAAGCAGG	TGGGAGAAGC	CGGAGTTGGA	GCCAGCCGAG	540
GAAGTGCCCC	GGGAAGARGA	CGAACGCCCG	CCGGAGGARG	AGAAGAACGA	GOOGTCCGCT	600
GCTGARGAGC	COGGGGTCCG	GATCGAACTG	CTGCTCAACT	CAAACC		646

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDELNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1031UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GATCANOGAN	CAGCACCGAC	AAATATAACA	GCAGCACGGG	CATTTGTCTA	GTCGGCTGGT	60
GYYTGTGTC	CACCGTGACG	CTGGCGCTGG	GCTGGAGTGC	AAAAACCGGA	GCCACAAGCG	120
TGCGGCTCCG	ACGGGGAAAG	CTGCGATCGT	GGCAGCAGCA	GAGAATGGGT	GCGGGAGTGC	180
YAGAGCGGTG	CTGGGAGCGC	GCGGACGCGC	GCAOGCTGCG	CGGGGCCGCG	CTGATGCTGG	240
GCGGGGCATA	CGAATCAAG	AAGGCACACG	CGGGGGGCGA	GCTGGCGATG	CAGGTGGCGC	300
GGCTGCSGCG	CCTGCGTGAC	GTGGGGCTGC	GGCGGGGGCG	CGTCCCGCTG	CTGGCKGTAC	360
ACCCCGGTCT	GGTGAACCTC	GCGTAC				386

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 775 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1032RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GATCTTTAAC CTCTGGACTT CAATCTTCTG GGTAAAAGCA CAAGTTTAGA GATGTATGAT	60
CCAAGCACCA AACTACAGTC TCGAGACAGC AAAATAATCC TACTTATATA AACTGAACGT	120
TGCAATCTTT TAAAAAATTT ACTAACTTGG ATTAATGCGG CGCCGGTGAG CGCCTCTGTT	180
ATTAGCTGAG TCATGCTGAG GGTITGGCTA GGAAGCATCC GCTCTTACTA CGTAITTTACC	240
AAGGCACAGG AAAATGTGGT GGTATTCTTG ATTTCGGCGG CGTTTGTGAC ATTACTCCAT	300
AGCTCATGGT CAGCAATCCC GTTCAATGGA CATTTGCTCA ATCGTGAGTC TTCCACTGGA	360
CTTGAAATCC CGCAGGGATT TTGGCTCCTT GGCTCAACCA GGTCGCGCGG ACACCTACAG	420
CCGAAAAAAT TGCTGCTTGG ACTAGGTCCG CTGACGTGGA CATGCGAGAT GACTTTAAAG	480
TGATACATTA AAACCAGGCG TGTATGAAGT CAGCAAAGGT CTCTTTTATA CAGTGTGCAT	540
ATAATATTTC GGGCGCTTGC AATTACCTCA TGCCAGGTAC TCGTAAGATT CGCCGTCCGC	600
GAGCGCTGTA GGTATTCCTT GCTAATTAAG TTGTGATGG CCTTCTTGAT AGAGATACT	660
TTGCATTGTA CGGTGTGAG ATTGGCTAT GCATTGTCA CCAAAGTGGC ATGAGAGACG	720
ACCGTTTGC TTTCATAATT CTGACGATAC AAGCTTCAGA ACAATTGCTT TCTTG	775

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1032UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GATCCCGAAA ATAGACTACA TCTGCCGCAA GCAGCGCGCC CTATCTGCAT TTCTCTTCTT	60
GGTGGTTGTC ATGTGGGTCA TCACGTTTAC CATTAGCATT CTAAGGGTAG TGGAACGGGT	120
GAGTTCACCT TCACCCAGAT AAAAGTTAAC AGGACAAGTG AAAAAAACC GGGATAAAGG	180
CATCAGTTAT GTAATAAAGA GCTATACGGC AATAAACATT TAAGTAACTA CCATGGTATC	240
TCCAGGGTAT TACTAGGTTT CCTGAAGTT TCGAATGTGC CTTGGTTACC CGGTGTTTAC	300

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GCAGGCTAGC GGGACAAGAA AAATGCGGTC CCACCCATTC CACGATTAGC GGTGGCAAAA 360
 GTCTTAAAAG TTAGGCAAAT AAACACATAA CCATCCCTCA AAAAGCGCTT GAGCAAGGCT 420
 5 ATCGGGGGTC AGAGCAGGTG TAATATACAT TAGAAGTGAG CGATGAACGA TAAATTGCOG 480
 AGAGCAGATG ACTTGAAGC CACTTGAAC TTTGTGGAGC CCGTATCGG GCAGATCCTG 540
 GGGCGGGATG GGTGCCCCA TGCAGGGGGA GTGCAGAAAC TGCTGTCAGC TGGATGTAC 600
 10 ATGGATGTCT ACACGGCTAT CTACAACTAC TGGTCAACA AGTGGCGGTC CACCGGGCAT 660
 TTTCACTCGG ACTCGGGCA ACGGCAGTCG AACCACTCAT CGATCTGGT CCGAGGGAGA 720

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 602 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1033RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GATCTGTGTC AACAGGTGCG CCCGTCGCG CAGTCCATC GCGATCCATA GGTACTCAG 60
 30 TGACACATTG CAGTCCAGCA CCTCACCAC ATGTGCGTGC CCCGCGCACC GCGTCTGCAG 120
 CACCACTCG CCGTCAGAT CCTGTCGCT CATCCCTGCG GCTTTGCAGC GCTGACGTG 180
 CACGAACCTC ACAGCCACTA TCGTCTGCGG GTCTGCGCGC AGCGAGGCGG TTTTGAAGAA 240
 35 CCGGAACGTG CCTGCCCCA TGTCTCCCC GAGCTCTAGT TCCTTAATCT CCGGCAGGCA 300
 TTCAGCCTGC GAGCACTCCA TAGTAGCCCA AAGTCGTTGG ACGGCCCTTC AGGTGGCCTC 360
 TAAGTGCTGG TGATGGTTGG TTGAAAAGTG ATGCCCAAC AATAGTGTA AAAACGGCAA 420
 40 AGTGGGCTT ACGGGGGGAA CAAAACAAGT GCTAACTACA CGGAAGCAGG AATTAAATTG 480
 GGAAGTGGC TTGAGCAGC GTATAGGAGT ACCGAGGTG GATATGAGTG TCGAACAGGT 540
 GTCTGGTGG CACGCGTGC AAGAACAGGT GGCACGGTTT GAACGCAATG TGGAGGCGCG 600
 45 GA 602

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 683 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1033UP

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GATCCGCGTC GTGAAAACA GGTCCTTGGG GTGCGATACC GCCAGCACCT TGCACGAGT 60
 CCGCACCCAGC TGGTCGTGCG TCTCCAGGCG CGTGATGATG TCCTCCACCG AAAACACCTC 120
 10 CAGCACCGTC TCAAACGGCG CAAGCTTCAC CACTGTGTCC AGCAGCGACA GAAGCCCGCT 180
 ATAGTCCAGC CCACTCATCT CCCCTGCCGT GAGCACCTTT TTCATGCGCG AGAGTAGTGG 240
 CCGTGCGTCT GCGTGGAGAC GCACCATCAC CCCAGGTG AGCTGCAGCA TGTCACCAG 300
 15 CCGTTTACC GACCCACGC CGTGCTCTC GGGCGCTCC AGCACATCG CCAGCTGGCT 360
 CATTCGGTCC TGGATCCTCC ATTCTCCAT CGCGATATCG ACTCTTCCA AGTAGCGTTT 420
 TGGGGTTTGT AAAAGTAAAG GGCACTTTTC CAGCACTTGG CCACCTAATG TGTGAGGCA 480
 20 CAGAACCGGG GCCCTATGTT GCGGAGTCA AGGCTTGCTT CGCTATATTC CGACTTCAGG 540
 AAGCTGCAAG AGCTCAATCC AGATGGGTTC CAGGCTAACG TTCTAACATG GAAAGACCAC 600
 CTGATGAACA CAGTGTGGCG GGACGAGCTT CTGATAGAAG GGGGCGACAA GCTGCTGGAG 660
 25 CGATTGAGCA CCAAGGAGAC GGG 683

(2) INFORMATION FOR SEQ ID NO:98:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 653 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1034RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GATCATATTG GTCTTGGGCG CAGCATGCGC TCTTCTGGTT CTGAGCCAGT AGTATGATAG 60
 CATGCCGCCG ATGAACCTGG CAATGGAGAA ACTAGGTGAG TTGTACATCC CGACGCCAAG 120
 45 GGCAACGCCT GAGGGTAACC ACTGGGCGCA TCTGTACTTG TCCTTATCAA TACAATTCTT 180
 TACGAGGGAT ATGACTGCAA AGATGCTTCC TAGGATGATC GAACATTCCA GTGCGTATGG 240
 TGGGAGTGCC ATACCCATGA CCAGACGTGC GCAGTCTATC CATACGAACG CAGTTGGGAT 300
 50 CCGGAATTGC TGGCTGGGGA TTTCGTAGAC CTGTGTGTAA AAAATGTACA TTACGCTAGA 360
 CAACACGATC GACCAGCTGG CGCGATAAT CTGCGCGGTA AACTGAGCCC TAGGAGAAGC 420
 ACGATTAAA TGCCCTGTCT TAAGATCTTG CATTAAATCG CCGCTTGCT GAGGCGCCGC 480
 55 CTCAGCTATA CTTCGGCAA CCAAATTTAT TAATACAGCG GCCTTGTGAT CCCTGGGTAC 540

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ACAAGAGOGA AAATGATTTG AGCCAGCTTT CCGATGCCGC TGAACGGGTT GAGATCGGTT 600
TCCCCAAGAC CCGGACGCC AAAATCGATA GAAAGATGCT ATAAGGAGAG OCA 653

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 670 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PAG1034UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GATCAAGCAC AGCGGACACC ACCAAGCAG AACCACGGTA CCATATCTCT CACACACGGC 60
TCCCACTAGC ACAGCGCCTC CACCTGGCCG CCCTGGGCTC GGGCCCCCGT CGGCATAAGC 120
ACGTGGGGGG ACCTATTTAG TTCCAAAAT ATTGTTGTAA CAGTAATAAT ATCTTCATTG 180
AGGACATTTT AGTTGTGTACA CTGAAAAGAA CAGATACTAC ACTTGATCTA AGCCAAAAGG 240
CAAAGAGATT TGGTTTCTAA AAGAAAGAGA AACATGCCTG TAAGAGGGAG GGCATCGCA 300
CATTTTTTCT CTCCTTATAT ACCAAGTAAA ATTTAGAAAA AGAAACGACG CGCTGCTTG 360
GTGGGCGCGG TCTGCCTGGG ACTCCAGAGG GGCTCACGCA GGAATCCTGC ATCCAGGGCG 420
ATGOGATCAA GCTCTGAACG CCCATAGCTG CCGCCATACA CGCGCCATT CGCGAGCTTT 480
CGTTGAGTTC GTAAGCCATG AAATCACAGT ATACGATTCT CGAGCGCAAG TTAAAGAGAG 540
CCCACTGGGC ATACTGCTAG GCTTACAACG GCGCACCAGC TGCGAAAGCG GAACTCCAAT 600
AGTTAAGGGC GGTGGCAAT AGTATCTGCT GCAAGCAGCT TCTAGAAATT GTAGATGAG 660
TGGTTTCATG 670

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 558 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PAG1035I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GATCTTTTGT GGAACCAAGA TCACCACACA CGAATATGCG ACGCCAAGCG CCGGAACGAG 60
CCACACATGG GCGCGGCGG TAGCGGTGGG CCCAAGCAAG CGTATTTTGA GGACCTGACG 120

EP 0 866 129 A2

TGCTGTGGGT GAGCAATCCA GGGCATACTA GGOCCAGGTT GTCAGCTGAA AGTGTGTTAC 180
 CCGGTATCGG TATTACCOGG CTCGTATAAA TGTTACCOGG ATATGGTGAA GCCAAAATTT 240
 5 TCCACGGCGT AAACAACAGG AGAGTGTACG TGCATATGGC GGCAGCAGCT AGTGTAGCCT 300
 AGTGAGAAGA AGGNCCTGTGA GCTAAGACTA GCGAGGAGAC GAGGATTGGG CACTGATTGC 360
 GCGATGTGGA TATTCTCTAC GCGCTGAAG AGCAATGTNG NATATNNGGN CGGCTNGTN 420
 10 GGCAACCNGN GGNCCNGNGG AGAGNACCGA GNTTGNNTNA NGGNGNGGCG CNCANAACCA 480
 ANNNVNNCCN CAATCNCCTA CNATCAANNC CAANTTNCCN CNNNCANCCC CNNGNNNNAT 540
 NNNNATTCNN NNNNNCN 558

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 604 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1035I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GATCCTTAAA AGCTGGCCTC CGCAGATAGA CCTTCTGCGC AGAGGCTGGA AACCTCAACT 60
 AGCAAGTCGC CACCOGAATC AGATAAGCAC TAGAGTCGTT CCAGTAACAG AGGAAGCGAT 120
 CAAGGAAGAT AGTAGAAGAG GACACTGCTG CCAGGCTTGA TGGACAGAG GGTTTAGCTT 180
 35 TCTGTTGAAT TTCAGAGTTT CGCGCTTTG TTTACTTCGC TTCATTCCTT CGTGTAAGA 240
 AGCTGTTTGC AGGATGTCAT CATTTGCCAG TCGCCAGGTA GGGTATTGCA GGGCCGACGG 300
 AGTCGGTGAA ACAGAGTCAG GACCGAGAAC GCGATAGAC AGGCGTTTGG TTTGTAAGCG 360
 40 GTGAGAGCTG AAGCAGCTCA AGAGGCCCGC CTTGCTCAGG TTGTGCGGTG GCGGTAGAGC 420
 ACAGCAGGGC ATCCCTGCTC GTTGGAGCGT NCGGNCAGNA GCCCAGGCGC NTOGAACAGG 480
 GGGTGTTTAT NANGANCNAC CGACCACAAA CACGCTNINA TTCGNACCGG CGGOCAGTTN 540
 45 CCTCANCNTG GTTCCCGNGA CTGTGTTTNN GAGCCNATCC TTGGCNCCTC GGCNNAGNAA 600
 AAAA 604

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1035RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GATCTTAAAT TGTTGCATTG TGACCTGAAA GTTGCCCCGT AGACGCTGCA TATTCAAGGT	60
TTCCATTTC ACGGGACGTA ACCTAATCCG CTGCACCTTC GACAAACGAC TAATGTATCT	120
GTTCCTGGAC TCTGGGTCAT TCGCATCCCC ACTCCACTGT ACTTGTCCTG ACTGTAGTTG	180
TTGAAGCTTG AGGTTATCTG CCTCGAATGA CTGCAGTAGT AGTGATTTTC GTCTCCCAAT	240
CGTTTCTATG GACCGCCTGA ACACCGAAGC TGCTCCGCC TGAAGGACT CGAAAAGCCG	300
CCGCTCCTCT GCAGAAGGCG GGAAATAAGA CATAACTTGC TCATCGCGTA GGTAAATCTA	360
CGTCATTATC CGGCTCCACC ATGTTCCGCT GGGATAAAAT GGTGTTTCCT CCAGGGGGCG	420
GGGAATACCA CCCACTCTCC AATCCTGCC CGGTANIGA ATNGVTTTNT TNATGGGGNN	480

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1035UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GATCTGGCGT ACGGTACCGA TATATTCAA CTGAGGTATT CGTTAGAACA GCTACCTTCA	60
GTGGTCCAC GCTATATTGC GTTGCAAATA TGTTTGGTGA CCTTCTGGC TTATCAGTGG	120
CAITAAAGAG CGCGCTAATG GGGACTATCT CTTTACTGG GCCAGTGGTC TCCAAGAAGG	180
AAGCATTCTC AATATATTTT CGTGGTTTTC TCAGGATGCC ATAATCTGGT ACACTCACAA	240
ACAATTTATG TTGCACTGGG TGAGATGCAG GGGTATTAGT ATTTGGAATC ATGTGGGTGA	300
TTGTCCCGGA TGGGGTGGC TTCAACAACG CAGAGGAAA AATATCCCCA GGGGGATATT	360
ATTTGTCGAA GCAAGAATCG CTTCAGTAG GAATTGAAGA TTCTTCTTG ATACTTAAAG	420
CTGAATTGGT TCANATGGGG TCCAACGAAN GANTAGNTG GATGNNCOCT TNGGGGGGGG	480
CC	482

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 645 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1036RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GATCATATTT CAATGCAAGA GCTCATTAA TAGGTATTGT CTTGAGACAT GCGCTCAAGT	60
CATTAATGTC ATGGGAAAAA TGCAACGTTT CACCTOCTAT CTCCAATGTA TATTTTAGCA	120
TTTCAAAATC ATGTTTTCCTG TTTACTATAA AGTGCAACCC ATTCAAGTCT GGGCTTTCT	180
TAGTAAAGOC TCTAAAGGCG TAATGCTGCT CTTGTATACT GCGTAGCTGT GGGTCAAAAT	240
CGGTACAGG CTGTGAAGA AGAGCGGTAA ATTGTTTCAG AAATTCGAGA TGCAATATTG	300
GTATGCCTTT AACAAGTGCA AAACAAATAC TTTTTOGGAA TCTTGGTCAT CTTCATGGGG	360
TCTTAATAAT ATGATGTGTA GTGGGCTCC GAAAAAGAGG TCACCACTCG TATTOCTAAC	420
CCTTAATTAC CTCAGCAAA GCAGGCTTC TTGTAACAAA GTTTCGGGAC CTGGACTOCC	480
CATGGGCCCC TCCAATNIGA TTGGNCGGAT NTGNNOCCCT TCNGATANA GGNCTOGATG	540
GCCANOGGAA NCCNTOCTAG TGATNTCCCN CCCCTTCAGT GNNNCCNCTN GAGGTTTGA	600
NGGCNNNTTT TCCNIVINGCG GGNVIVICTG GNAACCNCCC CCTINT	645

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 613 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1036UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GATCCOCTTT GGTAAAGAGA GGTGTGGCT TGTATTCAAC GCACATCGTG GGCTATTTGT	60
CATTACTCTG GCOCCGTCC AGAGACCTAC AGGTATAAAT TCCCATCAA GTGOCACCAG	120
AAAGATATGC TATACTGGTT TTGAGCTTGA GCGACTGTTA ACTGCAACCA GCGGGACCGA	180
ACGGGGTAGC TTTTACTCAT TTATTGAGGC TAAATTGGAA CCAGACATCA CAATTCTGCT	240
TCAGTGGGAA ATGGACGCAT ACAATCCAAA ACGCCAGAAG TATACTGAAA TAAAATCCTC	300
TGTGGACTTC AATGTACGAA ATGTCCGCA CCTGAGCAAA CTGCTTAAAA TATGGGAACA	360
AACAGGGGTG GTCCCATOCA CTGATATCTT GTAGGGGTCA GAGACCATC AACCATGTG	420

TTGAAACAGN CGGCOCTTAT GGGTGGTCAA ATCGNAGGAA AATCTTTTAA GGGTCGNOGN 480
 NAGGCANCAC TTTTITTAAT TATCOGAGTG CAANATGGAA ATAANCATCG TNAATTTGGA 540
 AGGTATTTCC CGGGGGAAC CANGCNCNC AANNMTTITN NGGGGTINGAA AGANTCAAAT 600
 TAAATNGGCC NGT 613

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 606 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1037RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATCATCATT ATTTCTCGG TTCGTGCCGA CGATTGGAAG GGGGGGGTGG GTTCTTTGAA 60
 GGATTTTCAGG CGTATGAATG TTGCTCTCAC CAGAGCAAAG GCCAGTCTCT GGATCCTGGG 120
 TCACCATAAA TCTTTATACA AGAACAAGCT ATGGATGCAT TTGATTTTCTG ATGCGAAAGG 180
 GGGTACTGC CTCGAAATGG CATGTCCGGG CTTCTTTGAT CCACGGAACA GAGCGGCCCA 240
 GGATGCTCTT CATAGGTTC AAAATCAACA TAATTATATC GAGAAGCAG ATGATTATGG 300
 GCGTGAACCG GTGATGACTA AATCAAGAGG ACGCAATAGA TCATCCAGAA AACGCAAACA 360
 TATGGAAGAT AATCCAGATG ATAACATAGA TCCGTTGCT GAATTCAAGA AGGAAAATCA 420
 AAGAGAAAGC AACACAGGCA CCGTGGTTA CCGTGGGAT ACATCTAACC ACAGATTGGC 480
 ACCTGCTAGG AACGATAGCA AGAAGGCCAA GAGTGCTCC AATGCGCGCG GTATTTCCGA 540
 GGCTACTTCA NARGATGGTG ATCGAAGTCA GAAAGGACAT GGAACCTAAGA AGATCTTCC 600
 ATATTG 606

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 653 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1038RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GATCAAAAAA AGAAATTACA ATTGACTGTT GCACCCACAC ATTCAACGGT TGCACCCACA 60

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CATTATGAGA TGCTTGATTT GGGCGAAGT GGGCTTTCCA ACTACAGTCC CGAGACTTTG 120
GGTGCCAACC GAAGCAGACT TCAACAGTGG TGATAACCAT AGTGTGGAAG TCTAGCGAAT 180
5 CTAAGGATAA TACCAAGAGA CAAAGCATAA TGGTATGTGC ACAGGATGGG GCGAAGTGTG 240
GTCTAGAGCT GTCGGTGCGA GCAGAATACG GTGCGGGCAA TGAGGACGCC GCAGACGCCG 300
AGCGTGTGGG CAGCTCACGA GGGCCGGAGC GCTTCCAAGC GGTCAGACAG AGTACTAAGC 360
10 CATTGCAGAC AAGATGGCTC ACGAAAAGT TTGGGGTCTC CCACCCNNAN AAATAACGGT 420
AAGGGTCCC CCAGTGGCGG TGTCGGCTTC GCTCTTGTTT GGTCAAAAG TACGGGTTCG 480
ACATCTTCCC CAATGGTTC AAGAGAAGGC CACGACATTG GTTCCCAAAT CCCCTAAGAG 540
15 GGGGGGGGCC CTTCCTCTCT TNCNAAATCC GGGGGGGGTT TGGTTTNCNG GAGGTTTNT 600
TATTTTTCNA NACCCCNVTT TTTANITTTA NNCNCGGTNC CCAGNGTTT GGN 653

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 609 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1038UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GATCGGTTCT CGGGCTTCTT TAGCTGCCCG TTATTCAACG AGTCATCGAC TGAGAAAGAG 60
35 ATAAAAGCGG TCGATAGCGA AAATAAGAAA AATCTCCAAA ATGATATGTG GGGCTTTTAC 120
CAGCTGGGTA AGTCGCTGAC CAACCCATT CACCCGTACC ACAAATCTC TACTGGAAAC 180
TTTGAGACTT TATGGAGCAT TCCGAGATCG AAAGGGTICA ACGTCCGTGA TGAGCTGCTG 240
40 AAGTTCTACA AACGGTCATA TTCTGCAAAT CTCATGAAAT TAGTGATCTT GGGCCGCGAA 300
GATCTAGATA CCTTGGGTCA GTGGGCATAT GAGCTGTTCA AAGACGTCCC TAAOCATGGG 360
ACCAAGTGG CTGAGTATCA CGGCCAGGGA TTCACGGCCG AGACCTGATG AAGGTAATTA 420
45 AAGTGAAGCG GNTAAAATCT TAAGAGTGTG GAATTCATNC GNGGGGAGA TTGGTTAGN 480
ATGGAGGCAG CAGTCGTATG NGGATTATC GGCAGAGGAA GGTCTCCCG NTCTGGAGAA 540
AAAGTGAAN CGNCNCCGT NGGNNTCCCC TTNAAGGAA AATNCCCNC AANNGGCTTN 600
50 ANNAAGGNT 609

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 643 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1039RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GATCATTTCT	CTTCAATCCC	ATTGACGTGA	ATGATGAACC	GCAITATCTT	TTTAACAGCG	60
ACAACATGCC	ACGGTATATA	ATTGTCTCTA	CCTCGTGATA	TGCAGAACCA	GGTGTTTAGA	120
CTGGCAATAT	COCTAAACTG	GTGTAATATG	GTCTTCAAAA	GTTTTGTGCT	GTCCGAATGA	180
GGGCAATTTA	GTAATTTAAC	CTCGAATTTG	TCTAAAGTAT	CGCCACCGGC	ACATCTTTTA	240
AACCGCACCA	GCGCGCGGCT	TTTTATTGCG	CATCGGCGCT	GIGAATTAGC	AAGTTGTAAA	300
GGGCTACTGA	ATAAGACGCC	ATGCAGCTCT	TCATCGATAT	TCACAACCTC	GTAATCATCC	360
AATTGGTTAG	CTTGGATTTT	GGNGGCATA	TCTCTTATCC	CTAAAAAGTG	GGTTGGATGA	420
TGGATAAAAC	TGATCTTCAT	CATATAGAGA	AATTTGGGCT	CGCCCCAAGC	CAGACACAGN	480
CAATGTAGTT	TCTGTGGCA	NAGTTNGCTN	CGCAGGNATT	ACTCGCANCC	GGGGAGGINT	540
CACCCCGGAG	ACAAAAATTC	CCCTTTTCT	NIGGAAATCG	TNGTAGNNCC	TANCAAGGAT	600
GGGTCAAGGA	CCTGGTTGCC	ATTCCAMTTT	ACCAITTTTIN	CCC		643

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 635 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1039UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GATCCTTCCA	ATAACGGCTA	AACATCCATG	TGCTGGTTTT	AACTATGAGG	GAGTTGGAGT	60
AATTTGCGGG	TCTCGCAAAG	TAAATTGACA	GAAAACCTC	AGATCGGTAA	CGAACAGCT	120
GAACGACGGA	GATTAAAAGG	AAGAGGCAAA	TAAGCTATAG	ATAAGATCGA	TAAATATTGA	180
GGGGGGGATG	GATATATTAG	AACTAGCTTT	TAGACTTGAA	GATGTGCTTT	CACGCTATTA	240
TAGAGTTGAA	AAGGTGGTGC	GAGTCAATTA	TCAACAGTTC	GTACCGAGGA	CTCCAGATGA	300
TCAATGGTGT	ATCCAATCCG	AGCTTCTTAA	TCCGCAAGAA	GGATCCGAAA	GCGCTGGTGG	360
CGCTTTTTC	GCGGGAATC	TGGTGCTTTT	AGCATCAATG	ACCAGGACTT	ACCAITTCOC	420

GGGGTTGGAA GGGATAGGCG AACCCCCCNC CTCGAGAAG AAGGGCCACT TTACGGCAGG 480
 GTTTTCCAAG GCNAACCTGC AACGCCNNITG GATCTTTTTA AAGCNITGGG GGATGNTCAA 540
 5 TAANAATTCTN GAGGCGNAGA ACCTTTGGCA ATTGGAAAAN NNNTTTCOC C GNAAGAAAGC 600
 NNAGGGANCC CCCCCGGNCN NATTTTGGGA ATGNC 635

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 648 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1040RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GATCCAGTGT ACCAGGTAGC GTCAGGCACT TCTAGCGCAA GGGCCGCCGT AAACCTTGGC 60
 25 CTCTCACAGC ATTTGGGATG AGTATGGGCC ATCTTETAGG CAGTGAATG ATCATGATGG 120
 GTACAAAAAG AAATGATTTT CCCCAGGATC GAACTGGGGA CGTCTCGGT GTTAAGCAGA 180
 TGCCATAACC GACTAGACCA CGAAACCACT TTCTGCAGGC TCTTATTGGA CAGGTGATGT 240
 30 TAGCGCAGAA GAACATGAAC GTGATAATAA TTCAGAAACC TCTTATGCTA AAGTGAATTA 300
 CTATTGCTTA ATAACCTGAA GGAATAGGC ATTGCCAGTA TTGAAAATCG GGCTTTGGGT 360
 TTATTGGCTA ATTATATTAT TNNCANTATA TATATATAAC AACAGGTGA AGAATGGNTG 420
 35 TCGNTGGTTT GGGGGCGATA CCNAGAACC AAAGTAGAAG TTGACAAGTT GGTGGNAGNG 480
 GTTCAATTCA GNACTTCATG GCAACNTTTC CNATNNTTIN NTNAGAACC CCNATTANTC 540
 TTTNNCTTCG GGGGGTCTCN NCAACCGGA AACAATNTIN CNGAAGTGA TTTGGGGGAN 600
 40 GTTCNTCGGT NTTTTCNCC TTGGGTCCA AATTGGGCCG GAANCCCT 648

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 613 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1040UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GATCAGCAAC CTCTCCGCC GTCTGTGTCC TGCTTTTACC GAGGATACGA AAATAGCCGC 60

GGCTCTGTTT CAAATGGCGA TGCTGACGAG CAAACCACGT CTTCTGATGC AAGCAGTACT 120
 AGTTACATTA TTCTAGAGAT GGAGCAATG OGGACAGCTC TGCGTCAGTA TTTGAGGGCA 180
 5 ATCTGCCAAG ATGCAGAGGT ATCCGCCAGT CTGTCCCTAA CGAAATTCCT ATTCAAGAGG 240
 ACGATAGACA AGCGTGCTTT TACGCCAGAA ATCCTGGAAG ATATTGAATC TCGGGAGCTT 300
 ATGGATGTAT ACAACCTCGA AAATCAAGTT AAATTCCAAA AAATGGGGT TTGGATAGAA 360
 10 CTGTGAAGCT ACAAGTCTC GCTAAAGTCC CTAAAAGAAA AAATCTTGCA AGATATGACT 420
 ACATTATGAG GTTTTCNCC AATTTAAGEA GAGGAGGATC CCAGNGACNA TTTAGCTCTC 480
 AGAGATTCTT GGNITGGGAA AATTTTTTAG GTACCNATNC AGGTTCCCGG AATNAATGIN 540
 15 NATINTTTAC ANTCGGCNG AAATATGCTC ANAGNNAAG TTTGGGCACC CCCCCNCT 600
 ATGANGTTTT GTC 613

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 649 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1041RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GATCCTCCAC CAGAGCGTGG GCGTCCATA CCTCTGTTC ACGCAGTGGC GCGTCTTGT 60
 35 AGAAAACGCC CAACAGTTGT TTGTAGGTGA ACTCGTCGGG GAATTTCTGG GCGCGAATTC 120
 GCTCCAGCTC CTCTTGGAA AGCTTTTCAC GGCGCACCA GCTTCTCATC CGGTTC AACC 180
 AGCGCTTTTC GTGAGTGGC CGCTGTCCG CCGCTTCTGC CGCAGCAATA TCTGGGCGCA 240
 40 GATGCGGTAC GCGCTCGGC ACTTCATGAC GGATGACGCC CTGCGGCTCT TCTGTGAAGA 300
 ACTCGTAGTC CAACCCAGCT TGAACAAAC AACTGCTTCA CGTATGCGG CCATAC TTTC 360
 ATCGACGTCT CGAGATAGTC GCGCGGAGGA GGGCAACAA ACAACGGAG CCGCGGGGT 420
 45 TTGGGCGATG TGTGANGTG GCTGCGCTG GCGCTTCAAC AACGACGAAT AATGTTGGAT 480
 TTNGCCCTNG TCCNTGGG GVNCAATCA GAATGCGGN TCAACCNAN CAAAAGGGAC 540
 AATNGCCGG AACCAAGCG GTTCCANGCC GAAAGTGT TTATNNCCNAC TTTCCGGTA 600
 50 NAATTTTTNT TTNCTG GNVGTGNT NACCNCACC CCNAAATAA 649

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 645 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1041UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GATCTGCTTC	CTGAAAATG	GCGTCTCTGT	CTTACTGGTA	CTCTCAAATA	GCTACGTCTA	60
GGTACAGGGC	CATTTCGGGA	TCCAGCCAC	GGTCCACTG	CAGGAGGTAC	AACAGGATAT	120
CGCACGTCTC	GCCCTGCGCA	CGTCACTTGG	AGCCTCCCGT	TCTCGTCTTG	ACGTCTCAAT	180
AAGGTACGCC	GTTTCTCTTC	GCCGATGGAC	TGCCCTAACT	GTATGGCCTG	GCTACAAGTC	240
TGTTGGTTTC	GAGCAGCCCA	CTTCTTTATC	CACCTCAAG	GTTTACCGCA	ATCCAGCAAT	300
TTTGGGTCTT	GGCAGACCG	GATATCATGT	GACTTAATT	CGTCAACGTT	CAAGAGTTGG	360
GGGCGGGCGC	AGCAAATTTA	ACGGGGGCGN	CGGTGCTCCC	CCCGATCGG	GGGGGGGGGA	420
GGENATTANC	ANTCCANTGC	CGGCCAAATC	TTNGTTTACA	NAAAGCAAGC	ANANTCATAG	480
TGATTTGGGG	GAANANCCCA	AGGTINNGGC	CNCCANGGNT	CAAANTCNCC	CNTTNNTTTT	540
TGGGTTCCTG	NOGGAAAANN	CCATTCTCCG	AGGGGCCNAG	GNCCGGGAAT	TTTCCCGNGT	600
TNNAGGGGAG	TCNNTTNGGG	GGGGANNNGG	CCANAGGAAG	GNGGT		645

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 682 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1042RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GATCCGTGCT	GCGGACAACC	GCCAGAGCTC	GCCTACAGCC	CGTATATATA	CGCCGGCTGC	60
CGGCTGCGG	CATGCGATT	GTCCACCTC	GCTCTGCTTC	GTCCCGCTG	CCGTTGCTCC	120
ATGGGACCTT	TCATTTAGTG	TCTCGGAAC	GTTTGAATG	TACCTATOG	TGGTACCAOG	180
TTGCTGCGG	TGCGTTACT	ACATCTTCTA	GCGGGACTG	AGTCACATGT	CTGCGCGGC	240
ACTCTTTTC	TGTAGATAGT	CAGACGACAG	ATAGTCGATA	GTTGGAGATT	TGGGCAACAA	300
TAGCGGTGCG	CATTACGCT	GCCATTGTT	CCCATGTCAT	TGGGAGGCTG	GGNCCACCC	360
ACGGGAATC	TTCGCGTTT	AANCTNANA	GNCCNGGGA	ATGNAAAACN	CTTCTTTTNG	420

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NCNGCNGCAA ACGGGCCTNN AGNGATTTC TTGNOGATT NGGGANGCAC TGAGAATCCA 480
 AGTNGGAAGG GGGCTNNAAA AATNGCTCCG GGCCANNCT NCCCAAAGGT TINAAAANCN 540
 GCNTAAATINA GGCNCAGAAG AACNCGGGA GGAANCANAC ANAAANINGG CCCCNCTGA 600
 AGGAAAGGGG CNGNNNITGGG GNOGAANCCC CNGNAACGNT NTTTCTTAAA GGANAACAAA 660
 NGGTNCAAAA AAAATGGGGG NC 682

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 649 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PAG1042UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GATCGCGTCC TCGAGCGACT TGTGAGGGTG AAGCTGATA CGGTGATGGT GGTGGTGATG 60
 GTGGTGGTGA TGGTGGTGTG CTCTGCCCTG CGGTATGACC TGGGCTGTTG GCGTGGGCT 120
 GTTGCTGCCG ACAGCAGCAC CTGTATCGC AATGCCGAT ATGCTAGAAT GGAGCAAATT 180
 AATGGACTGG TCTGCATTCT TGCAGAGCG AGCCTGCAC ATGCTGGATA TGCTTACGAG 240
 ATCGCCGGAG GATCTTTATG TCTGTTTGC TATTCAACCAC GTGGTGTGG CAGTGTGTT 300
 GTTTCATGAC CAGCCCGTAT CTTCANAGGA GTCGTAGTTC ACGCATTTGT GGCCAAAGCC 360
 AGTCGAAGGA GGCCATCCTC CAGGTCGGG GAGTCCCGG GGAAGTTTC CACAAGCCAA 420
 GGTACCTAGA AGATGAATCT TTTTGTGANT ANCGTTGGG CCNCTNGGCA ATTTNAAGTC 480
 GNAANTGNIG AACTTCGGAA AGTTGGAAAT TGGNCCNAGG NCTTCTTCCC CCCNCCNCT 540
 TNGGNAAGCA AAAANAANA ATTAATTGNN CCCCCCCCCG CAAATTTGNG GTCNGAGAAA 600
 TTCCAAACC TTGGGTTAAT AGTAAGGNC CCGTGNCTG GGCCCNCCC 649

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PAG1043RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GGATCGGCGA TGGGATATAA AGAATTGCTC CCTGATTGAT TGTTGTTGGA AGGAGATGCA 60
 GATGGATTGT CCAGAAAAAC CGGTTTTAAG ACTCGTTCAT CAAACTTGTT AAACCATTTG 120
 5 CCATCGGCTT GCAGTATATT GCGCAAGGTT TCGCGGATAT TTCTCTGTC TAATGATAAT 180
 CGCCCCACAG GCTGGTACG GCGTGATGCA GAGGCGAAG AGGGTGGGTC TATCATAGGA 240
 GGAAAGCTTT CTTGATCCGG GGAGCCGGTC GGGCTGTGCG TTAAAAATGG AGGTGCGTCT 300
 10 AATGAAGACA TTAGCTGGAC AGGTCTAGGG GCTTCAATAT CAAATTCATC ATCCGTTTCC 360
 TCCTGTCTTT CTACGCACCC TGTCCTTATG TTTAAGATCT CAAGCATACC CGCAGGAGTA 420
 CCTCCAAATA TGATAACGGT GAGAACCACA ACTACCAGCA CAGTGGCCAG AAGAGGGGAA 480
 15 CTTGGANCTC GCGCNNGGA CCCTAGCCA GNGNCACTCC AANAGNAACC CCNANCCCG 540
 NCCNNNNGG NAACNNCCTN NNTTTNGNNT TGGATNTCCC CNANNANINN AAAACCCCCC 600
 CCGCGGGIN TTTNNGGGNC CCNNNNCCC MNNAANGGN AAAANNNC 648
 20

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: 1043UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GATCAGATTG TCTTGATGAT GAGAAGCTGG CGCATCAGTA GAGTGACAG AAGACCCATG 60
 CGGAACAACT GTACCACCCA GGGACTGCCG TCTTCCCGGA ATGTTGGGAA AAACAACAGC 120
 ACGGCTGAG TCACTTACAG TCGAGTGGG TTGGAGGCG GACAGATTAA AAGAAAAGCG 180
 40 CTCGGGGTTT GTGAACAGNT CAGACCAAAA CCCAGGTCTT GGCTGGCGGA ATTCTTGCT 240
 TACCTTCACA TNCAACTTAG TGTGTTGCT GTCCNAAATA TACTCCAAAA TCTTGATCGG 300
 CGCACCTCTG TGGTTCATGT CTGCACAAG TTGACCACTG TATTCCAGTT TGACATCAGA 360
 45 GGGCGAAATC ATCAGTGTGT GCGTTCACA GAGCAAATAA ACTCCTTTAC TTCTGCAC 419

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1044I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

5 GATCTCCGAC TCCGCGCGTC TGTACCCGTC ATGCGCCCTCT GTAGTCGCGG TCATGCTCAT 60
 OCTACCCAGC CGCACCAACC AATGCTCGAT GCAAGCTCAA TGCTCGCAGC CGGCGACTGC 120
 10 TGTATACGTG CTGGCTTAGG GTGGGGACGT CCTTTCACGG CCGGGCGGCC ATTGGAGTCC 180
 AGCAAGCGGG GAATGCTGTT GTGACTGTAA CACCCATACA TTGCAGGCGG TACATTTCAA 240
 CGATGGGACG CGAGTGGGTG GGGAGCTGGA CGGAGACCGA ACGGGGGGAG CCAGGGGGGC 300
 15 GGGGGCAAT CCGCAGGCGG ACCCAGCGGC CGACCAAGCG GCGCTAGGC CGAGGGCAGC 360
 AGGCCAGAGC CGCGGGCGCG GTTTTTCATG AAAAATATAG TGGCTACAAG AGGGATAGGT 420
 TGGATATACC AGAACTCACT CGTAAGAGAT AATTAAGCAG ACGAAATGGT TGTTTGGAGG 480
 20 ACGTTGSTAT CGCGAATCAC AATAATTGA CAAAAGGTTT TTGANTCGGG GAGGTGNTG 540
 TTGTTGNGGG NCGNAGACCG CCNTATTANA NGAAGNGAG GNAACNCAAG ANNGGGGCAN 600
 GGGGTC 606

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1044I2

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:120:

40 GATCTACAGA ATGCAGGAGA CGCTGCTTGA CACAACACAA ACGGCTGAGA CGGCAGGCGC 60
 GGCCGAGCGC GTGCAGGAGG CGGACCCGGA CGGACAGGGG GCGGGCGTGG ACTGGGGGA 120
 GCTGCTGGAG GTTGTGGAGC GCGACTACGG GCGCGGGCGG TCGCGGCTGG GGACGATACG 180
 45 GTACGAGGCC GCGCGCGCGG GCGGGCTGAC GCGCGGGCGG GCGCGGGCCC TGCGTTTTC 240
 GTACGAGGTG GGGCAGCAGA CCGTGCCGGT GCGGCTTGCT GCGCGCATG GGCACGGCAG 300
 CGATCCAACA GGCTCGTGAC GGTGGAGCTG AGCGCGGAGG ACCTTGAGAG CGCGCTCGCG 360
 50 ACGGGCGAGA ACGCAGGGGT TGCGCAACCC GGAGCTTTTG TGGGTAGNCG TGTTCAACTN 420
 AGANTCGGGA CCCNVTINCT NNTGCTNNG NACTNNGNG TGTNNACGN NGAGCTGAGN 480
 TGCAGGCAN GNNAGNNNC CNNNCNNGN ACGCCCNCA ACCCNNGAN CCCNVTITTT 540
 55 TAGNNNGNT TAANNCCNC CCCNNNTNN GNGNGGNT CCCCCTGNT NNNNNNNN 600

ANTTNTTCATT TTCCCCCCTT CGNAGGNITIN NT

632

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 626 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1044RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GATCGGGTGC CTAGTGGGAC CTCATGCACC GCTTGGAACT GCGGCCCCAC CCATGTCAGC	60
ATCTTTATCT TGCTCGAACC TGTGACCGAG TAAACAAGCA CGTCATCCA CGTCTCAGCC	120
TTCCACATG GATGTTCAAA CAGCCAGGCA TGGTCAATGC CTCGTTTGTG AACTATCTTG	180
TGTAATGTT GTAAGTTGCT CGAATGAAGT AGCAGTAAGC ACTTGGTGTG GCGGACGAAT	240
ATTGTCCGCA GCGGTTCCGA GTACAGCAGC TCTTCTACAC CATAATTCCG GCCAAGCAAT	300
TCTGTATATG TCTGAAC TAG ACCCAGGCCT CTCTCGTCCA TACTGGAGTA CACCAAGAAG	360
TCCTATTAT TTCCGACCAC CACAAGTTGT CGAACGGCAT CAACCACAGG GACACACTGA	420
GCACCTTGGG ACGGAATGGG ATTTACTAGC TCAGCCCTAA GCATCTTATG ATGAGGGCTG	480
CCCTTAGCTT GCTGAGTGCT TCGGGCTGCC TGCTTGTTGGT TGGTGGGTCC TTTCTTAGAA	540
CGATTGTTCA AAACCATGAT GATGGGGTTT GGTCCGGCCN GGTGATTTGA AGATTTAAAC	600
CGGTCACAAG GAATTGACCN TGGGGG	626

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 545 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1044UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GATCTCCTTG ACCGCGGGTG GCGCTCTCTT CTGAAGGTG ACACGGTGCA ACTGCTACTG	60
TTAGTATGG TCCGGTCTGC GGCTCCGCTC CAGCAGCAG GGAGCCCTGC TCCGCACTCA	120
ACATACCTC TTGTGCAAGT TAATGGTGTA CTGCGAGTA ACAACGTCTT TCAAACCAGC	180
CATTTGGCT GCTTAATTAT CTCTACAGAG TGAGTTCTGG TATATCCAAC CTATCCCTCT	240

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TGTAGCCACT ATATTTTTC A TGAAAAACCG CGCCCCGGGC TCTGGCCTGC TGCCCTGGGC 300
 CTAGCGCCCG CGTGGTGGC CGCTGGGTGC GGCTGGGGAT TGCCCGCGCC CGCCTGGNTC 360
 5 CCCCCNNOGG CTCCNNCCAG NTCCCACGA NTCGNGCCA TNGNNGAAAT GTACGGNTTG 420
 AANGNTGNT GTNAAAGGCA NAAAAGAATC CCCNNTNGT GNTTNNAAAN MNNGGCNNNN 480
 10 NNNNAGGGAN GNCOCACCN ANNNAGAANT TTAANAAGNG NNNNNNANA TNNNTGATN 540
 NANAA 545

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1045RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GTGGATCCGT AATGTGGGTT TGTAGGCAG AGGGGATTCG ACGGTGGCTG GGGGCCATTC 60
 TGCCCGTTAA TTAGATGCCA CCAATGTGT TTCACATCCC AGGCGAAGGT TOGCATACCG 120
 30 CCCACATACT TGGGTAATTC ATAATGCGC CACATGACGG GATACTAAAC AAAGCAAAGT 180
 GTCACATICT TATTTTCTGT TGTTGTCAA AATCGGGGG TAGGCGATCA ATTTGCATAT 240
 ACAACACGAA AGGGGATCGG AGATTTCTAG GTCACAGGAC AGTTTGGGGT TTTTATTTGG 300
 35 TGCTTTGTG AAACCATAGG CACTTGACAT AGGAGCCCTC TTTAGAGTAC AATAAGCAAC 360
 TGSCAGCAGC CCTACAGCTT GGCTAAACT TCTCATTAT GTGAAACGGG AAAGACGACA 420
 ATGCTCTGA ACGCTTTTAC GCACTTTTTC GTGGCCCAAT TGCATNGNTT CCGNAANTAN 480
 40 NNITTININN TNGGNTTTT TTGNNNAAA AAAACNNNA AAAAAGGGG GGGGGGNTNA 540
 AAACCANGA TNNITTTTTT NGGNGGGG GGGGCCCCCT TTTNNAAAN CCNNCCCCC 600
 CNNNAAANN GNNNTTNNN GNNNAAAAA TNNNNNNN NTTTTINGEN NNCCNNNITT 660
 45 NCCCCCCNA NNGVCCNNC CCNNNITTT TTTTNNNA NNAANCNCC CNGGGNGG 720
 CCC 723

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1045UP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATCTAATAA CCACCGTTG TATATTGGG CGGTAACTA TATATGGGA TCATATAAGT 60
 10 GCTTAAAAAC ACCTCACCCG CAAGGGGGTC ATCTATAAAC AAGCCATAGT GTGTGTATCT 120
 TTGCTACAT AGCATCATGA CTATGTTGCG CACGCGTCAT TTGCACTGTT TTAGCATGTA 180
 ACTGGCAGAG CCAGCAACGA ACAGAGCTAA TTTTGGAGGC TTACCATACT GTTGTGCTG 240
 15 GATGTTGAAG CACGCTGTT GTGGATAAGT TTAGAACCG TCGCCAGCAC ATTCTATACC 300
 TGAAACTACC AGTTCAGGG GACATGTTCT TGTGGCTTT GACAGAAITA TTATTGTAGT 360
 CCAGTTAGAT GTACTACCAT TGTGCGCTA ACATAATCAC CATTGTCTC TCTGGAATCA 420
 20 CGTGTGCCA AGCATATTAA TGTGTGTACT TAACTCGGT ACTCCCTTTA TCGAAAGGCA 480
 TCACGGAATC GGCCTTCACT AT 502

(2) INFORMATION FOR SEQ ID NO:125:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1046RP

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GATCGCGCGC GCAAGCCCGT GCGCGAGCTC GAGCAGGTTT TCGAGGTGCG GGGGCAGCGC 60
 40 GTCACACGAG TAGGCGTAGG GATAGAGGAT CTCCTCCGAG TACGAGTGCA GGTCCAGGTA 120
 GCGGTAGATG TCCAGCTCGG CCTTGTGCTT GTTCACTAG TCGTTCCAGC TGCGGCGCTC 180
 CACGGCCTCG AACGGCTGCT GGCGCTATA GTCGCCCGAG CAGGGGTAGG CGTGCTGGCC 240
 45 GGTCCAGTGG TAGTGAACG AGTGGTCAAT GTCGACGCA TCGCAGCCG GCATGTACGT 300
 GGGCTGCCCG TTCTTGGCGC ACAGGCGGTC GTGCGTCCAC GTGTACGGT AGCGGTCTGG 360
 GTTGAACACA GGGATCACCA GGAAGTCAG CGCGTCCAG TAGCGGTCTT CCTTGGGCGC 420
 50 CCGCCATAC CGCGAGAGCA GACGCTCCAC GACAAAGCAC GCGGTGCTCA CGCCAATCCA 480
 CTCGCGAGCA TGCAAGCCGT CCGTAATTAC CACCG 515

(2) INFORMATION FOR SEQ ID NO:126:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1046UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GATCCGGGAG CTCCATCATT AGAGGGTCTG GACTTCGGGA AGACACGCAG TGGTATGTCT	60
GTAACCTTTC AATTTCAAAT TAATTCCTCT TTCATCGTAG TTCGGGCTGC TGGGCGATCT	120
CCGACACAAA CGGCTGAGTC GCTGACACAA ACAAAAATC GACTACGGAA AACGACTAAG	180
CGTCGCAGAT GCTATATATA TACAACCTGG TTCCTAATTA GGGTTAGATC CTTGCGAGAA	240
ACAGACGTTG AGCTTGTGCA CTTTCAAAAT TTAGTCCCGT CTCGGAAGTT TCAGGCAAC	300
ACGAATAACA ACACATATIG CCATGGCATC GGTAACGTTT AAAGACAATG CGGAAGTGAT	360
AATGATAGGT GAGCAGGATC GGAGAAGAGA GCAAGGTATG GCCAGGCCCT GGATAACGGG	420
ATTTCATCGAC GCGGATATCA TGTTGGCAAAA GGACGGTCCG TAACTCATAG TAGACATCGC	480
CAAAGAGAAC TTCGACAGCT TATATTGACA TTCGTCTCTT TGCTCTACAT TGTGAGGCA	540
AAGATATAAG AGAGTATGGT G	561

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 685 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1047RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GATCGAGTAG ATGTTCCGCA GCGCTGGCAT CTTGAGGTCC CGGTACGTCA GGATGAACTC	60
GCCAATGCTG GTATCCAGCG TGAACCCGTT GAGGCCCTGC CCGTCTGTTA GCATGACGTG	120
CGTGGACGGC CCGTACATCG CGTAACAAGC TGCCACGATC TCCCGGCCCG ACCGCAGCAC	180
ATCCTTGATT GTCCCGCTCG AGTCCGGAGT CAGCTTGAAA ATCGAAACGA TCGTGCCAC	240
CGACACACCG GGTCCAGGT TCGACGACCC GTCAATCGGG TCGCAGCACA CCGCATACGT	300
CCCACCGGTC TCCGGGAACA CGATCAGGTC CTCCTGCTCC TCCGACACCA GCACCTTGAC	360
GTTCCCGCTG GCCTTCATCG CATTGATGAA GATTCATCG CCCAGCACAT CCAACTTTT	420
CTGCTGGTCC CCAGTCGGT TAGACCGGCC GGAGAGCCCA ATCAGGTTCA CCAGCTCCGC	480

GCGTCTGATC GTCTGCGAGA TGAACITGAA CGCAAACGAC AGTGAGTTGA GCAGCAGGTT 540
 5 GAACTCGCCC GTGCGGTTTT TGGCCGAGCT GCGCTGCGAC TCCAGGATGA AACCGGCCAG 600
 CGTAATGATA TCCGTGTGGA TAGCCTCTGC GGAGTCGCGT CTCTGTGGGT TCACGGTAGC 660
 CATTTCTGCT TGAGTGGGCT GTGGT 685

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1047UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GATCACTCCC CTCGCTTGAA ACAATGCGGT ATAGCGGAAT CTGGCCGAGC ACCAAGAAGA 60
 25 TCAGCAGCGA GACGGCTGTC CAGATCAACT TCTGGTTGTA TGGCACTTTG CGCTCGGGCG 120
 CGATCACCTC GGGCAAAAAA GCTCGAAGG GTTTGAATAG ATCCAACAGA CGCCCACTCA 180
 30 TTTCAGGCTC ACAATGTTTG TAGGTAGCTT GCTGGGCTTG GATTGGCTAC ACAGTTGGAA 240
 CCACACAAAG TCACTATTGG GCGAGATGGT ACTCTAAATG ACTGCAAGGA GAACTGGTCG 300
 GTTTOGTTTC CTGAACAGCT TAATTGGACT GAGTTGCAGT AGCTGTACTG AAAGGAACAC 360
 35 GTATCTTGAA AAAATTATAA ATCTCAGTAC CACGTGACCG GATACGAGGT GCTATTCCAT 420
 CTOGCTAGAG GAGCTATATG CCTAGTCGGC GTACCCCTGG TGAGTAAGAA TAGCTCTCTT 480
 GGACAATAAT CCGTGATGAC CTTATTATGC TATAAAGCTA TTTTACATAG CAATGGATCT 540
 40 CCGTGTTTAG ACCTTTGCGC CGCCAAAAGA CCAAGTACAT CAGCACCGAG AACAGCAGGC 600
 AATCGCCAGG CGCTTGTGGA GCTOCAGAAG ACATGCTGGA TGCAAACCGG AAGAACGCGC 660
 NTCGGAGTAC AGTTGGCG 678

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1048RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

5 GATCGTCATA GTCCGCTCG TGTATTTGGT TCCTTCTGG CCGGCGCTGC ACCGGCATA 60
 CCATCGCGTC CACCTGCATC TTGTCATCCG CGTCCATCTC GTCGTCCAGA AACACCTGGC 120
 TATCGTGGAG CATCCTGTCC CGGCATTGA GCTGGGGGTC GATCGGTCCG CCGTCCGCCA 180
 ACGACAGCTC CTGTGCTCC GGTGTGTCCA CGCCCTCATT TTCATAGAAG TCCTTGTGTC 240
 10 GATTGGGGGT ATAGTCCCGG TACATGTGCT CGCCACCAG GTCGAECTCG TCTATGGGCT 300
 CTTCTGGGTC ATCCAGGTCC TCTTGCAAAC TCGATGGGCT CGTCGGGTC GGTAATCGGG 360
 GTTCTCGAAG TCGATCTTCG TCCCGGGGAC CCCAGGGGG ATTATTCCCC CATAAGGGAA 420
 15 GCGGGGCCCC CTCCCAACTT GTGGGAAGAT AGTGGGTGCT CCGAGGTCTT TTGACCTGC 480
 TGTAAATANTC CNCTGTCTTT TTCGGTTCAA CINTAGCCCT CNGGGCCNGG TINACCCCC 540
 ATCCCGTATG GAAGCANCA ATAACAAATG CCTCCGAAAA NTTTGTNTT TTCNATTTT 600
 20 GGAANAAGNA AGTTCTNANA ANGAATTTIN NANITNNN 638

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 621 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: PAG1048UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

35 GATCCGCTC CTCAGCCATG GCTTCTCTA ATAGTAACAC ACGCCCTGCT TCGTAGTGT 60
 CGAGGTGCAC ACCTACCCG GCAAATAATG CCTCATCTGA CAGCTGCACC TGGTAGAACT 120
 40 GTGAGCACCG GAAGTGCAGC TTGCTGCAGA AGCTTGTGAG ATATTGTAG GGGTGTCTT 180
 GTGTGAGAAA GTTGCTCACC CGTGGATTCT CGTAGGGATC ACGGATACGA CCTTGGCTCT 240
 GCGGCGACAG CCGGTACCCG CATAGCTTGT TTAGATTGCG CTCATCTATC AAGTCTGAAT 300
 45 ATGTGGGCTT GGGGAAAGAA CCTTCCACG TATTTTAGTG TCTGGGTGT GCATTCTTGT 360
 CTTGCGAAGA GCAGTTCGGA GCAATTGAC CGTCAGAAG TCCCCCTCT TTAGTGAAAG 420
 NNGCGATGTT GGTGATAGGA ACTTAAACCC CGTTTGGNT TNCNCAATA GNAGCCANNA 480
 50 CCTTANGTAC GGTNINCCGT TCTTAACCCC GCGGGTCCC NGGGNGGTTT CAAGTTCTTG 540
 GNGGGANAAG GTNCCGVINC CCGGGGGINC GCTACTTAA GNGANGCAN AAGGNAAAAG 600
 NCCCCNGAA AAGTGGNTT T 621

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG149RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```

15 GATCTTTCAG CTTTGGCGTG CTATGGCAGG CAGCCTGCGC CTTTATGGCC TCAATGCCTC      60
   GCTGACGACT CTCTGTGCC TGTGGGCAAT CTGGTCAAGT GGGTACTATC CAGCGAAGGG      120
   ACTCCTATATG GCTGTGTGAG ACAAGAGGAA ACTCAGCATG CTCTACGTGC CCTACTTCCT      180
20 GATTCTCTCTG CGCCTGCTCT TGTGTGTGAGG TCTGGAGCAA TCAGAAAGTG CAACACTCTA      240
   TATATAATCA CCTGACTATG TACCTATTTC TGCATAGCA CGTTACGTTT TGTACAGATT      300
   CCAGTCAGTT AGCTGCTCTG AGCAACCGGT GAGCTCCGAA AAGGGAATTC GCTACAAGGT      360
25 CTTAGGCGCAT AGNCTGCAA CTGGCTTTGG CTAGGTCAAT TGGTTTTCTT GGAACCAATC      420
   TTGGTATAGA CTCGTGGTGA TTGATGGGCG TGAGGAGTGT TTGNGGNA GNCAAACACC      480

```

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1049UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

45 GATGCTCTCC TGGGCGACAG CGCTTCTAG ACCCTCGACG GCGACACCT TGATGCTGCT      60
   CTGCTCTCA AACGTACCA GACCTTGTA GTAGGTGACG CGTTTTTCT TGAAGAGCAT      120
   CTCAATACCG CCAGTCAATT GCTTCACAAC GGTGCTCTTG GCTTTTGGG ACTGGGGCAT      180
   GTTCACAGTG ACCTCGCCTT TGAAGTGGAT ACCGCGCTGC TTGGCATGGA GTTGCATCTG      240
50 GTGCAGCAGG TGCGAGTTGT TTAGCAGCGC CTTGGATGGG ATACACCCCA CGTTCAAACA      300
   GGTTGCACTT AGACGGGGCG GCTTCTCCAC AACCGGGGG TCGAAAACCA GTTTGTGTGA      360
   GCGTGGATG GCGGCCACNN TTAACCAACG GGGACNCCA CCCATCAACC ACAACGTGGG      420
55 GGTTTTCTTT TGTGGGAAT TCAACCAGGC CCNCTTTNNT GGGACGACCN CTTANNC      477

```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1050RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

NNNTTNTTGG TGGGGCGTGT AGANTAGTGG TCGGGGNGCC GCTCCACATT CTCCATGCTC      60
ACCACCACGA CAGACTGGAA GTACAGGAAA AGCGACATTG TCGTCGCAGA GATGTGCGAC      120
GCGGGGTTCG AGTTCOCAAA AGCAGACAGC GTTGCGGACG CCAGCAGTCC AAGCCCCGCA      180
ATTGTGCGCG TCGCCACTTT CACAGGTGTT TGGGCCACGG TCGGGCGGTT CGTGAAGTGC      240
GTCTGGATGC ACGACACCTG GTCGTTCGAC TGGGTTTCGT GTACCATCAC CTTGAGGTAG      300
GGTCATTGT CCGGCACCTG GTACGTCACG CCGGGAATCT TTTTGTGTT CTCGGGCTC      360
ACATACTGCA CGGCTGGAT CTGAATGCA CCGGGTGTC CAGGACAAA CTGCTTCTAG      420
CGATCCCAT ACATGTCCTT CGC                                         443

```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1050UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

GATCCTTTCG TATGAAGTAT GCAGCTGTGG ATATGCTTAG TTAACITCTG CCCAGCTATT      60
TAAGCTGCAA TTGAATCGGC GGTGACTCAG CTTGCAAAGG GTAGCAGAGA GGACGGGATG      120
GGTTTATTCG GAAAGGATAG AGGTGAACGG ATAGCTGAGT TTCCGTGTTA CCTGCTAGAG      180
ACCNGAACGC ATCTGGTGCC GNTGNCAGGG GATTCTATAC AACCTTGTA TCGAGGGGAC      240
ATATNGGAG CCGATACTAG GGCAGNTCCC TGGGATAGGT GAGGCTINTAG ACGGGGCGCT      300
GACGGGCGCT TTTGAGGCGG CAGAGGTACC CCGCGGGTT GCGGAGGTGA TGAAGGGGTT      360
CCAGGAGCGG TACGACTCCC GGGGACAAA ACCGAGGCCC                                         400

```

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 713 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1051RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

15	GATCAAATTT GACATGTAAT TAATATATTG AGGTAAAATC TAGATAATAA ATACTGCCAG	60
	CAGTGTCTGAC CAACTTCCAT TAGCAAGCAT ATAAGAGGTC TTAAATCAGC CGAAGGTATA	120
	TGCGAGGGAA GATAGATCCC CCGGGCTGCA GGAATTCGAT ATCAAGCTTA TCGATACCGT	180
20	CGACCTCGAG GGGGGGCCCC GTACCCAATT CGCCTATAG TGAGTCGTAT TACGCGGCT	240
	CACTGGCCGT CGTTTACAA CGTCGTGACT GGGAAAACCC TGGCGTTACC CAACTTAATC	300
	GCCTTGCAGC ACATCCCCCT TTCGCCAGCT GCGTAATAG CGAAGAGGCC CGCACCGATC	360
25	GCCCTTCCCA ACAGTTGCGC AGCCTGAATG GCGAATGGAC GCGCCTGTA GCGGCGCATT	420
	AAGCGGGCG GGTGTGGTGG TTACGCGCAG CGTGACCGCT ACACTTGCCA GCGCCTAGC	480
	GCCGCTCCT TTGCTTTCT TCCCTCCTT TCTGCGCAG TTGCGCGCT TTTCGCTCA	540
30	AGCTCTAAAT CGGGGCTCC CTTTAGGGTT CCGATTAGT GCTTTACGGC ACCTCGACCC	600
	CAAAAACCTG ATTAGGGTGA TGGTCACGTA GTGGGCATC GCCCTGATAG ACGGTTTTCG	660
	CCCTTTGACG TTGAGTCAC GTTCTTTAAT AGTGGACTCT TGTTCCAAAC TGG	713

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 703 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1051UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

50	GATCTATCTT CCTCGCATA TACCTTCGGC TGATTTAAGA CCTCTTATAT GCTTGCTAAT	60
	GGAAGTTGGT CAGCACTGCT GGCAGTATTT ATTATCTAGA TTTTACCTCA ATATATTAAT	120
	TACATGTCAA ATTTGATCCA CTAGTCTAG AGCGGCGCC ACGGGGTGG AGCTCCAGCT	180
55	TTTGTTCCCT TTAGTGAGGG TTAATTGCGC GCTTGGCGTA ATCATGGTCA TAGCTGTTTC	240

CTGTGTGAAA TTGTTATCCG CTCACAATTC CACACAACAT ACGAGCCGGA AGCATAAAGT 300
 GTAAAGCCTG GGGTGCCCTAA TGAGTGAGCT AACTCACATT AATTGCGTTG CGCTCACTGC 360
 5 CCGCTTTTCCA GTGGGGAAC CTGTCTGTCC AGCTGCATTA ATGAATCGGC CAACGGCGCG 420
 GGAGAGGCGG TTTGCGTATT GGGCGCTCTT CCGCTTCTCG CTCACTGACT CGCTGCGCTC 480
 GGTCTTTCCG CTGCGGCGAG CCGTATCAGC TCACTCAAAG GCGGTAATAC CCGTATCCAC 540
 10 AGAATCAGGG GATAACGCAG GAAAGAACAT GTGAGCAAAA GGCCAGCAAA AGGCCAGGAA 600
 CCGTAAAAAG GCGCGTTTCG TCGTTTTC ATAGGCTCCG CCGCTGACGA GCATTACAAA 660
 AATCGACGCT CAAGTCAGAA GTGGCGAAAC CCGACAGGAC TAT 703

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1052I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GATCTCCGCT TCAAACCAGC TAGGGACGAC CCGAGGTCGT TCCAGAGAAA GTCAACAATC 60
 AATATCCTGG GTAAAGCTAG CACCGCCGAA CTACTTGCTC TTGGCACCAC CGCAAAGGCA 120
 CACAACGAAA ACTGGGAAGA TGAAGTGAAG AAACAACAAA CCGTCACCGT TGATGACCAG 180
 35 GTTGTMTCCG CAGAAGATTC GCGCTTTGCA GAGCCAGTGC AGGAACCAAA GACCTCAGTG 240
 TCCGGCTACA TCAAGAGGAA ACTATCCCTC AAGCGTGATA AATCCACAAG ATCCAATCGT 300
 TCGCAATATG ATAGGTTACA GGACTAGATA TGGATGTTAA GTATAGAAAA ACTGTATATT 360
 40 ATTTGACGTG CTGGGCGTTA CGGAAACATA TAAAGATTTA ATTACTCATG GGCGGATGGT 420
 ATTTTTCAT GGGCCCCACT GGACTCCATT TGGCAGTTG GAGGACGAAG TAGGAACCCA 480
 ATTGCTGGTT ACAAGCGCTC GGTTCATGT ACCTATACA CAAGTATCCA TTATTNGGGC 540
 45 TTATTGATTT GTGTCTNIGG GCGGACTTT TANTTTCTC ACTGGGGGAN GTCTT 595

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1052I2

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

5	GATCTGGGTT GCGGTGAAG ACCACCAATG CGATGCACAC GAGTATCATG ATCAGCAAGA	60
	TTAAAGAAAA GACAGCGTTC AAAATAAAAA ATACCCATGC CATAATGGAG CTGACGCTTG	120
	CAGGCTGTCC AAAGAGCCCT GAGAAAAATA AGAAGAGGAA CGAATTAACA AGAGTAACAC	180
10	TGGATATCAT AATGTTGAGG ATGTTAGTCG CCGGTCGAG GTACGGCTG CATTTAGCCA	240
	GAGCTGCGAG GTATATTATT TCAATGACAA ATAGAGCGAC GGCTGGGTT TTACCGGAAT	300
	TGTGGGCAAA TGCAATAAAT ACGCTTTTCA ACAAATATG CGCGAGGATC ATGCAGGACC	360
15	ACCACTAGTG TGTCGCACTG TACATTGTTG AGAAGAAGCC GTATTGTGTT AGCACATTTT	420
	CATTGCCGCA TAGAATGGCA GCTGGGTTTG AGTGACACAC AATGGAAGCC CTTCACNGT	480
	AGATAGTGGC GCAGGCAGCC CACCCATAA TTGACAAGAT AAANGTNGAG CTAAGNCTGC	540
20	CAGAACGACC NCCGCCGGG ATCANCCTTC ANTGATTGCC CACCAGCAGA GATCGCNATT	600
	GANTGACCCC GGCAGTTTNN CGCAA	625

(2) INFORMATION FOR SEQ ID NO:139:

25	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 486 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

30	(ii) MOLECULE TYPE: DNA (genomic)
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	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1052RP

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

	GATCGCGAC GCGTGGGCGC AGAACCTGGC GTGGAGCATG GGGCTGATCC GAGTGAATT	60
40	CATGCAACGC ATCTTCGGT GGTACGTCCA GCGAGCGGC GCGAGCCGT CGCTGCATTT	120
	GACGTCAACG ACCACGTCG TGCTTGCCCA ACGCTCACTG GATGCGCTAG TGGGCGGGCC	180
	CGTGAGCAAG GCGACACAGT CGCTATTTGC CAGCACACAC ACGATGATCT TCAGAGGGAT	240
45	CCGTAGACTG GCCTACCGTG CGAACATAGA GAGCTCATCG GTTGTGTGTA CCGGGCTAAC	300
	GTTCCTCCTT CTGTTGGCT ATTTGGATTG GCGTGGCGT TTACATTTGT TCAAGCGGG	360
	CTACTCGGAG CTGCTTATCC CGCATGAAG TCAATGAACC CAGGTCCGG TCCCTAGACT	420
50	TCCAAGAAAA ACGTGGGTGA TTNGCTCAA AGGTGTTCTT TTGGGGTANA TCTTCCCCG	480
	NGTTCA	486

(2) INFORMATION FOR SEQ ID NO:140:

55	(i) SEQUENCE CHARACTERISTICS:
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EP 0 866 129 A2

(A) LENGTH: 468 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1052UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GATCCAGCTC TTGCGCGGTA TGAACCTTTC CGCCCGCACC GGCGCCTCGC ACACCGAAAT	60
CGACCGCACC TCCGTCTGCG TCTGTAGTTC CCAATTTTCC GGCGCCCCCG AGTACAGCGT	120
GATCAGCACC CACGGCTCGC TCGGGTGAAA GTCAATGCC TTACCCCTGT CTGTCTCGA	180
GACAAACGTT TTCTACTCAC GTTAGTACTT GCTCCGCGCC CTGGATAGCA TGGTCGAGCT	240
CTGCGGGTCC GCCCCCTCCG TGGGTGGCAA AGATGGTCTT CAAACACACC GTAATAGGCC	300
GTGCGGACCC ATGCAGGCC CATTCGTCTT CGGACACACA CATACTTCG TTTCCTAACT	360
TCATTGGTCC CCACTTGGGA TTCTAGTAG CTGTTCAACT CGGCTTTTGT GGTCTCTGTG	420
GAAAANTAAT ATTCCCTGCG ATTATTTTAAA TAGGGGTCCN TTTTNTTT	468

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1053RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GATCATAGTG ATTGATATCG GGAGAGGGTT TGGTATGIGA CAGCCTGTAT TCACGTATCT	60
GGTCTTTCAC TTCATATATT TCTTGTGGGA GCTGTGAATA TATCTCCATG CGTTCTCTGT	120
TOCATTTTTC GTGCAITTTG TGAATGCAG CCCACTTCTC GTACGTTGAA GTAGGCTTGG	180
GTACTAACGA TCCTGAACA GGGAGGAGGC ATGTTGCCGAG GGAGAATATT AAGGAATCAT	240
ATCTCAITTT TACGTCTGAG ATAACCTAGTA CTAACCTGCA TCGGGCGTCC AAATACCCGT	300
CGTAGTAATC GTATAGGAGC AAAGCTTCAT CTCTTATAG ATGTGGAGTT GATTGAGTCC	360
ACTGCAGCCC TTGGTATTTA GCCAGCATTC CATCATATTT GGACTGATAA TATTGGAAGT	420
TCTTCCACGC GTCTTATAC GGATCAATTA CTGATTTTAC AACATCGAGT AATATGGAAA	480
GATATAACTC TGGATTGCC TGTATGACTT CCAGCAGGCC ATGGAACATA TCCCGAATGC	540

EP 0 866 129 A2

CGTCGCGGCA CTGAGAGACT AACTTTGGCG TGTATATCTG CTCTTCGACT GTCCCATGGT 600
 TGAGGTAGGT ATCTTCAGGT AGAATGAAGT CAATGAGCGA TAAACTGACT TGCTTGAATC 660
 5 GTCCCAAAGA GT 672

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1053UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GATCTCGGCT CGCTGCTGCG GCTGAGGCC TACTGGGCAG AGCGCTACCC AATAACAAC 60
 GCCCTAATCG GCGGTGCAGA TAAATTGCAC AAGCTCTACT CAACCGATT TGGGCCCATC 120
 GTGCGCGCCA GGACTTTTCG CTGTGAACCTC GTGACAAGC TTGGACCGCT GAAAGACCTC 180
 25 ATAATGGCAA AGGTCAGCGG CCCAAATTAA TAGTCACGTG TACATAAAGG TTTTCCTAAT 240
 AGCTATACAG CTTGCCCCCG TCTTCAGCTT GCAGCGCGCA ACCGGCGTGC AGCATGAGC 300
 GTCTACTTGG AAATAACCAT TGGGACCTT GTAGTAGACC TGGACTACAA GACATGCAGC 360
 GCGAGAGCT ACAACTTCCT CAACTCTGC AAACTCGCT TCTACGACTG TCAGTGCATC 420
 TACCGACCTC CATCTGAAG GCTCAGCAG CCTCGGCGA TCCACAGGTG GCGTTTGCAT 480
 TCGCACCGA TTGCGCTGTA CACAATACT CGATGAAGG CCTGCGCGAC ACACGGGCGG 540
 35 TCACCCCGAA GCTCATTGAA GCTCCGTTG CCGTCAACC CGCAGAGCGC TTGGACAGG 600
 TCGCTTTG 609

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1054RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GATCGTGC CGGTCCGCA ACGACAGCTC CTCGTCTCC GCGTGTCCA CGCCCTCAT 60
 55 TTCATAGAAG TCCTTGTTC GATTGGCGGT ATAGTCCGCG TACATGTGT CGCCACAG 120

EP 0 866 129 A2

GTCGACCTCG TCTATGCGCT CTTCTGGGTC ATCCAGGTG TCTGCAAAC TCGATGCGCTC 180
 GTGCGCGTCTG TTATCGGGGT TCTCGAAGTC GATCTGTGTC GCGGACCCCA GCGGCGAATT 240
 5 ATTCCCCATA CGCGAGCCGC GCGCGCTCCC AACTTGTGGC GACGATGGTG GGTGCTCGTA 300
 GCTCTGTGAC CTGCTGTAC TACTCGGCTG CTCTGTATCG TTTTCATCTC TAGCCCTTCT 360
 GCGCGCGTGT GAACCTCCA TTCCGTTATG CGAAGOCATA CCCAAATTAC CAAATTGCCC 420
 10 TTCTGAGAT CTTGAATACT ATCTCCAGA TGTITGACAG ACGCGCAGCT TCTCAGATA 480
 CGAAATATCG TGATTTTACG TGACTTTCAA TACCTCATTT GGATTGGATT GGTAAGCAT 540
 AGATTTTCAG TCATATTGAA AAATTATTTT CAAACAGGC AATTGGATGA GCTG 594

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 545 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1054UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GATCGTCGCG TTGCGCAGGG CTGCCAACG AAGCCTTGAC ATGTCAAAC GCTTGAAAGA 60
 AGAGGTGATA TGGGCCACCC ACGAGGCCAA GTGGGAGCAA CTGCTCGCTA CTGGGACCT 120
 TCCCCAGAT GGGGCCAAAA GCGACTGGAA GCGTGGCCGA GCATGGCTGG AACCATATGA 180
 35 GCGCGCGTTT CGGAACCAGC TTGCAAATCG CAAGCGCAGC AGCCAGAAGC TCAAGCGCTA 240
 TAGTGCCAA ATCAGCAAGG TACACCTCCC GTATTACATT AAGTGCAGTG CTGCTATGCA 300
 TACCGTTCGC GCCAAACGCT TCGAGTGTIT CCAGAAAGAG CTCCACACCG TTAATCCATT 360
 40 CGTTCCAGGC AGAGATCTCG GTTCCTACT CTCCAAGTGG CGAATGGTGA ACGGAAAAAA 420
 CTACTATCGC TGAATGTATA TAGTTTATAG TCCTATTCTT TCATCAGGTC TCCCAGCAGA 480
 GCGCGCGCT CGGTCTCAAC TATGCGCACC TCGCTCAGCC ATTGCTGAG GTCCTTCTGA 540
 45 GTTCG 545

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 532 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

EP 0 866 129 A2

(A) ORGANISM: PAG1055RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GATCCGTCGC	CGGTCCGCCA	ACGACAGCTC	CTCGTGCTCC	GCGTCGTCCA	CGCCCTCATT	60
TTCATAGAAG	TCCTTGTTGC	GATTGGCGGT	ATAGTCCGCG	TACATGTGCT	CGCCACCAG	120
GTGACCTCG	TCTATGCGCT	CTTCTGGGTC	ATCCAGGTGG	TCTGCAAACT	CGATGCGCTC	180
GTGCGCGTGG	TTATCGGGGT	TCTCGAAGTC	GATCTGTGTC	GGCGACCCCA	GCGGCGAATT	240
ATTCCCCATA	CGCGAGCCGC	GCCCCGTCCC	AACCTGTGGC	GACGATGGTG	GGTGCTCGTA	300
GCTCTGTGAC	CTGCTGTGAC	TACTCCGCTG	CTCTGTATCG	TTTTCATCTC	TAGCCCTTCT	360
GCGCCCGTGT	GAACCTCCCA	TTCCGTTATG	CGAAGCCATA	CCCAAATTAC	CAAATTGCCC	420
TTCTGAGAT	CTTGAATACT	ATCTCCAGCA	TGTTTGACAG	ACGCGCAGCT	TCTCAAGATA	480
CGAAATATCG	TGATTTTACG	TGACTTTCAA	TACCTCATTT	TGGATTGGAT	TG	532

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1055UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GATCGTCGCG	TTGCGCAGGG	CTGCCCAAG	AAGCCTTGAC	ATGTCAAACC	GCTTGAAAGA	60
AGAGGTGATA	TGGGCCACCC	ACGAGGCCAA	GTGGGAGCAA	CTGCTCGCTA	CTGGGACCC	120
TCCCCAGAT	GGGGCCAAAA	GCGACTGGAA	GCCTGGCCGA	GCATGGCTGG	AACCATATGA	180
GGCCGCGTTT	CGGAACCAGC	TTGCAAATCG	CAAGCGCAGC	AGCCAGAAGC	TCAAGCGCTA	240
TAGTGCCCAA	ATCAGCAAGG	TACACCTCCC	GTATTACATT	AAGTGCACTG	CTGCTATGCA	300
TACCCGTGCG	GCCAAACGCT	TCGAGTGTTT	CCAGAAAGAG	CTCCACACCG	TTAATCCATT	360
CGTTCAGGC	AGAGATCTCG	GTCCCTACT	CTCCAAGTGG	CGAATGGTGA	ACGGTAAAAA	420
CTACTATGCG	TGAATGTATA	TAGGTTATAG	TCCTATTCT	TCATCAGGTC	TCCAGCAGA	480
GGCGCCGCT	CGTCTCAAC	TATGCGCACC	TGCTCAGCC	ATTGCTGAG	GTCTTCTGT	540
AGTCTGTCAC	CCG					553

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs

EP 0 866 129 A2

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1056RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GATCATCAGC GCGAGCTTCC AATTGTGGG CTTTCTGTG ACATACATCC TOCACACCTC	60
GCAATGCGCG CGCCAGGGCT CGGCTTTTG CCTCGGCTG ACCCTCAGG GATACGGGTA	120
CAGCATGATT CCTAGCGAGC TGAOCAGCAA GGTCGGCAAG GACCGGACA TCGCGCGCT	180
GSAGCTGGAC GACCCCAACG AATTGGAAGA TTGCACTG TACTGCGCG TGGGCGAGC	240
GGCGCAGGAC CGCTTCGAAT CACAGCTCTC GCACGGGCTG ATGGAAAAAC GGCGCAGAAT	300
TCGCGCGCTC GCGATCGTGC TAGAGATTTT GGGGCTTGA ATTATGTGCA AAAGCGTGT	360
CGACTACATT GTGGTCAAGC GCATGGAGCG CGCATCTTT ACTGCGAGCG ACAGCGAGAG	420
CCCCGCATAG ATGTTTATAT AACTTATATA TCCTCATTG ATCTTCGCTT GGGCCCCGTC	480
TAGGGAGCAG ACCAGCAGTT TCCTCGTTG CCTTNAAGTC GATGCCGCCA GAGAGACCAG	540
ACGCCCCAGC GGGTA	556

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1056UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GATCCAACCC AGGACTTCTC GAAAGATAGA ACTCCGAACA CAGCCACCG CAGGAACCTC	60
TCATCAGCTA GCAGCAATAC TAAGCAGACC TTCAGCGAAA ATGAAGAAGA ATCTGATGCT	120
GAGTTCGAAG ATGTATAGTT GTACCCGTAT ATTGCATTTT TTTTTTTTTT TTTTTTTTTT	180
TTTTTTTGGG GATGTCAAAA GCTCATCTCA ACTCCATGAC CAGCCAGTAG TGAATAAGC	240
AGTGTGTCTA GTTCTTCTAA GTGATTTTAA GGACTATGAG CTTTAATGAG AAGGTGAAGT	300
GGTACTAGG CACTGCTGTT GCGACTCTAG TTAAGATAAA GTCTGTGAA GCCGTATATC	360
GCTCTATGC AGCTAAGCAG AACACTAGCA GGAGCATTTT TGGGGAGGAG AAGGACGTAA	420
GACTGGCCAA ACGGATTCGT GAGTCTAGG CGTACGATGA GGAATTATAT CCGGAGCAGT	480

TAGCTCGGAA CTACGCATTT TGGGCGAAGA CGGTATGGCA CGACTACAGG AACAGTACTC 540
 ATATGGTGGG 550

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1057RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GATCAGGGCC AAATCACTGC TAAGTACAAA CACAAAGGCG CAAGTATTAA GGTGAGAGAG 60
 CGTTACAGGT GCATTGATAA TACCGCAGGT ATATATCAAG GCGCACAGTG AACACATTCT 120
 GCAGACGATA GATATGTCTG AGACGAAGTA GGTGAGATA TTTACGCACA AGCCTCATTT 180
 GTAAGATAAA TGGTCATTAC TAACGTTTTT GGGTTTAGCA GCAGCAGGCG GAGCAACAAC 240
 GAGGGGCAGG AGCACGGTGG TGGTGGACAG GGTCCAGGAG TCGAGGATGG CGGGGAGCCA 300
 CCGGCCAGGG CGAACACGCG CAATGTGACT GTGGCAATCC AGTACTCGTG GCTCCACGAC 360
 ATGAGGAATG TCGGGGGAGA GGGCGAGGAA CCGGACAGGG CCGGGGGGAG AACGGAGATA 420
 CGTTCTGTGAT GAGCTTCACG GACGTGCCGG ACTCGACGTC GAACGATCGG TTTCAGGAAG 480
 TGATCGGCAT TCGGGCGCAG TTTCATTTGA GCGCGTGGC GCGGCGGATC AGCCTCCTGC 540
 GGGGGCTCTC GAAGGAGTCC TTGAAAACCT CCTCTCAGG AAGCTCAGCG AGCTGGACAG 600
 CGAGCTGTGC AGTATATGCT ACGACGACTT TGAAGACGAC ACGTCGATCG GGT 653

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1057UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GATCTAGGGG TTCTTCTPTGC CCGCTACGG GCGCCCTCG CAGCCTCGG CTGGCTCCCG 60
 CCGGAGAGGG GATCGGCAAG GCTCCTCGCA GCGGCACACT GCGTCTATGC CTGGACCGTC 120

CGGCGAGCCG GACAGCCGAG GAGCAGCCCC GCGATGTCIG TCTCCCCGGC GGCGCTTACT 180
 CTGGGGCTGG TGTGTAATTT TCTAAAACT GGTGAAATG TACGGGCTCG CTGGAGCCCC 240
 5 CGCCTGTGCA TTGTACACGG GAATAGCCGA TCAATTGGAT GGGGACGCCA GTGTTACCCC 300
 CGAAACCGTG CGCAGCGGCT GGCGGGCCGA GGGCTGAGGT GCGCTGCGG CGCAAGGCGC 360
 ATTTGCTGTC GACTGCAGAG CTGCAGGAGC TGTGGAAGC GCAGGACAAG TTGCAGCTGT 420
 10 ACGTGGCGGG GTTGTGCGAG AGCGAGGAGA CGCAGAAGCG GGTGGAGCAG CAAOGAAAAC 480
 AGCTGGCTGA AATACGGGAA ACGTTTGCGG GCTTGAAGG GGAACGACAG CGCGTGCAAG 540
 AGCGGCTGGA CGGGTATCAG AGGCTAATGT TCCGTACCA TGAAGCGTGG CAGGCGGTAR 600
 15 ACGGGCGTGC CGGGCCCGTT ACAACGACGG GTTCTGCGCG CGCGGCTGCA CAAGAAATGC 660
 GCGCTGGG 668

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 614 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1058I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GATCTTCACA TTGCAATGCA GGTCTCTCTT GTTTTATAGTA GCACCCCTCCG GCGCCTTGTT 60
 GGCCCTCAAC TTGAGTTTCAT CGCACTTTGG CTTGATAAGA CCAGCTTTCA AGTACACCAT 120
 35 GATGTGCTCG TCATCACCGT GCTTAAAGCA ACAGCGCTTG CCATAGCGGC AGTAGCCTGT 180
 CTTACTCCAA TTGATACATG GCTTGTGCG GAATTGTGCC GACCGCTCCT TGAACCTTAA 240
 CTGTGGAGA CCATGGGCAA ATTGGCACTT GTTATGTTAC TTGCAGGCCC CCGTAGTCCG 300
 40 AAATGATTTC CATAACTCTG TCTTGTAAG CATCTGTGTG ACCTTCTCCT GCGATGGCTG 360
 TGGCTGCTGC TTGTGGGTGG CGGGGGGGG GACTGAACCC GCAAAAAGTT CGGCTCCGGC 420
 TGTGCGGCTG CTGCGCCCTG GCGCTGGGT CTTCCGACG GATGCTGCAG GAGCGCAGGT 480
 45 TTTCCGGCGT CAGGGTAGTA TCCATTTGT AGGCCGNTAA TGAGAGTTTA TCGCCACCTC 540
 NAAGGTAGGT TCCCGTTCC GAGGGGCCAA GGGVAATCAN TNGCCGCCA AACCGTNAAC 600
 CCCCCCNCC CNGC 614

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 634 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1058I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

AAGCTTGCAT GCCTGCAGGT CGACTCTAGA GGATCTTGCA AAGTATGGCT TGGTAGTGIG	60
GTGATGGTTA TCTGCAGTTT CAATTGCTTT GTTAGTTAGT GTATCACATT CTTCTGGCTT	120
TGGCCGATTA GAGTGCCTGG CCTCATGGAT GGGGATCTCC GGTGTATACA CGTATATTTA	180
TTCTCTTCGC CCAAGTGGCG GAGTACAATT TTCTCTAGC TGGACCTATT TCGGTTGTAT	240
TTCASTAGTG AAATAAACT ATCAATTAAG TACAGCTTTC GTATGACTCT GCCACAGGAT	300
GAGAGCAGAC ACTCTGCAAA GTACCGGATT TCAAATAAAT GTTTAGGAAT AAAATCAAAG	360
GCGTACAATT ACATAATTAT AAAATGCTCT CGTAGCTATG TCTTTCGGGT CTTTTTTTTA	420
TCCTAAAGTG AACATCGAGT CTTGTCCTTC TTAGGTGTTT AGATGACAAG CTTACATGCC	480
TCNGNNGNIN AAACAGTTNG TCGAATCCCT CGGATCCTCN CCANGTAGNA AGGNANTACG	540
NNCAGCAGAG TCATTACCN C NACCCACCG CTTGCCANCC NANTTNCCTN GGNGNAGNG	600
GGNGGNGNT TGNACCNANN TTGNNCCNT NGCC	634

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1058RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GATCATTCCTT GAGAATGCTC ATAGTTATGG TTTAACGGTT CTTCAAACGG AAGAGTATCT	60
TCAATTACAG AGTAGTTTGG AGAGAGAACA GGTAACGTCC TACAACATTG CCGAGAAAGC	120
AACTACAATT GGCTACGTTG CACTTCCAAG AACCGAGTAC GATGAACTTG TAGCTTCGCA	180
AGCTTCTACG AAAGAACAGA ATTTTGAGGT ATACGGCGCG GAAAATGGCA AGGTCATAGT	240
GGATAAATCT GAGTATCAAG ATTTGAAGAT CAAAGCTATC CCAGTGATTT CACCATTGCC	300
TCAAATGAGC AAAGAGCAGA TGGTTGAAAA GGCCAAGGAA CTTGGAATGG TAGCTTTGCT	360
CCATTGACGA GTATGAGAAG TTAAAGAGCC CTATTTCCCG ATAACGCTTT GGATTGCAAC	420
AGCGAAGGAC CCGGAAAGG TTGGTCTCCT AAAGGAGGAG TACAACCCCT TATTG	475

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1058UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GATCTGGGCG CCGACAGCC TGCCAGGTG CGCTGCATC CGCCGCTCCT GGTCGGGCTC 60
 GTCGAGCCCC AGCTCCTGCC GGAAGCTAGC CCTCCAGCTC ATGTACGACT CATGCGTTAC 120
 CTTCGTTCCG CGGAATTCTT TCTGCTCTTC GAGCTCGGT TOGCGTAGCT GCCGCTCGTG 180
 CTCCTTCTCT CGCGGCTCAA GTCCTTCTG AAACCACGAC TCCGCTCCT CCTTTATGA 240
 CGAGATCAGC GCAAAACACA TCTGTATTCC CAGCAGGATG TCTCTCTCA CCTGTCCGAT 300
 GGACTGGCTT GGAAAGACCG TCCACCTCGC CGGTCAAAAT GAAATGCTTG TCCGAATAT 360
 TCTCCAGTTT CGCAACACAA GGGTCCCCC GTGCTGTCC GGACTTCCIN GTTCTCAAT 420
 CCCNCTCAA CTGCTCGGN TTTCGGGGG GAAGGTCGA NCGGCTTAA TGTCAC 476

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 644 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1059RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GATCTGTTAC GCTGCAGGC GAAACCTCCA ATGCTCTGG CCAAGGTTGG CGGCTGGGAT 60
 TCTTGGGCTC ACTGCATGCT TCGGTTTTCA AGGAACGACT GGAGAATGAA TACGGCTCGA 120
 AACTCATTAT CACACAACCC ACTGTTCCAT ATGTCTGTGA GACTCCGAT GGGACCCAGA 180
 TAACAGTAAC AAATCCAGAT GACTTTCTCT ACCTGACACT TCGGCGAACC AAGATAAAGA 240
 ATTTCCAGGA GCCATATGTA GAAGCTATAA TGACTCTTCC ACAGGATTAT CTCGGAAGGG 300
 TTATCACTCT CTGCGACGAC AACCGTGGCA TACAGAAAGA GATAACGTAC ATTAACACCA 360
 CGGGGCAAGT GATGCTGAAA TATGATATCC CATTTGCCA TCTAGTAGAC GACTTTTTTG 420

GTAAGCTCAA GTCGTGTCAG CATGGTTATG CTCCCTAGA CTACGANGAT GCAGGCTATA 480
 AGCCGTCCTGA CATGTGCAAG ATGGAGTTGC TTGTAAATGG AAAAGGTGTG GATGCACTTG 540
 CACAAGTGAT GCATCGCTCC CAAACCGAAC GATGGCCAA AGAATGGGTT ANGAAGITCA 600
 AGCAATATGT CAAATCCAG TTATACGAAG TGGTTATCCA GGCC 644

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 649 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1059UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GATCGTGGCG GACGTGTTTG TGCGCACCGC GGACGTGCTG CTGAAGATGT CGCGGTACGA 60
 RGAAGCCAAG GCGGCGGCGG ARCGCGGCCT GAGCTGGAG CCGGACCACA TGAAGCTGAA 120
 GCGCGTCAC CTGGAGTCTG TGCGCAAGTT GCGCGACTAT AACGGGACA TCTAGTCCGC 180
 GCGCGCGGCC CGCGCGGCA CCACGGGTAT ATATACACAG CCGGTCTCCG CGCGCCATGC 240
 CGCCCGCGCG GACCGCAGAC ACAGGCCCCG ATCTTGGGCG GCGGCGGCG ATGAGCTGGT 300
 GCAACCTCT TGGCCCGTAC CCTGCTAAGG AGGTAATCT CCCAECTCAG TACTATAAAA 360
 AATTTTAAAG TTAGCCACTT TCGAGTTACA ACTCCCGGCC TGTCGGGTAA CGGATCTCAA 420
 CTGTGAAGC CCTAACGCT GCTCTACTCC TTTTGGGCTA AGGCAATATC CCGCCATGTC 480
 TTGTCGGAT ATCAATGTCA CGGTGATTC GTTTATGAT AGGTTGAAGC GGAAGCAGAT 540
 TACTGGCAG TACAATGTGT CGCTGGAGAC GTTACAAATT CTGATCGGTT ACGTATCTGC 600
 CATCCGGTGG TGACGAAGG ACGARCTCAT TGAACAGATC CGTCTACTC 649

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 641 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1060RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GATCTGCTCA TACTGAGCG CCAACTGGTC GTACTCCGTA TGCAAAACAT CTGTGGTTTC 60

CTGGAAGTGC GCCACCTTGA GCGATATCTC ATTAAACTTG GTAACCAGCT CTCCCAACTG 120
 ATGATTGACT GCACTGGTTT CCGTCAGCAG GTCCCTCCAGT TOGCCAGTTC TGGTGTCCAC 180
 5 TTCCGCCACG TATCCGCTGT ACAATGTATA CTGTCGTTC GCAGACCCCA GARCAGAAGC 240
 TCGCCGCCAC TCTGGCGCCA GCAGCTCAAT TACCTGAGGT TCAATCTCTG TTTCACCGT 300
 TGCCAACAGA GTGTCTACTT TTTGGCGTAA CGAACTATCC CCAAAAAGCG GAGGCAGCTC 360
 10 ATCGTGAGAR GARGCACCGG GATTTGCCGC TACATCCTGT ATGACTGART TCTTCCGGCT 420
 CCTAAGCATG GTGCAGTTGC TGCTCAACG GCTTTCTTCC TGGTGCAAGT CTGCAGTGGT 480
 TOGTGCTTAT GCGCAAGCAG AATACCATGT TGAGCCGGCG AAATCTCATC ACGTGATCAT 540
 15 CATCTTGCAA CGGCTCGGAR GACRGTGATG CACTGTTCCA TAGGCTTAGG GCGCAATTAT 600
 ACGCTAGCTA GTTATATTGA TAATATGTAC ATGATGCCTT C 641

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 649 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1060UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GATCTTGCCG TCCTTCTTGT CCAGCTGTAG GTCCGGATGA GGGTACGCCT CGCTCAGGTA 60
 35 CTCCAGCCGC AGCTGCGCGC TCTCCATGGA CGCCTCCAGG ATCGAAGGCG CCGGCACAGC 120
 CTCGGAGGGG AGGGGCGGCT GCAGGAGGGG CATCTCCTGT CGCTCCTGGT GCATCTGCAG 180
 CGCCGCAGCG CTCGGCTCCA GCGCCGGGTC GAAGTACTTC ACAITGTGCA GCGCCGACTT 240
 40 GTACAGATTC AGGATGCAGC CCTTGAGCTG CGCACGGTGC AACCGGTACG CAGTCGCGAC 300
 ATACTGGTAC CCGCTCGTCC CCCCTCCCGT GAAGTGCGGC CGCTCCGATC CGATCGAAGA 360
 CAGTGACGCT GTTGGCTGGT GGCTGTATCG CCCCTCGCGC GCGGCGGCTG CGCCCTGCGC 420
 45 CTGTGTCACC CACCCGAGCC GAAACACAGT CCGTGTGTAC GTCTCCCGGT TCAGCCCGCC 480
 TCCAGTGC AC CGGCGGARC CCGCCGGCTG CGARCAAGC GACACCTGCT CCTCGCAGCG 540
 CGACCCCGCC TTCATGTCTT CACATGTACG CGTCCGCTTG TGCGCTTGCC CCGTCNGCAC 600
 50 CTGTTAACTG CATCCGCGTC TGTTGGCTGC TGCTGCTTGC TGCTTGCTT 649

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 570 base pairs
 (B) TYPE: nucleic acid

EP 0 866 129 A2

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1061RP

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GATCTGCTTT TGTAAGTATT CATCAGCTAA ATACCGTAAA GCTGGTTTGA ACGGAGGTCC	60
TGCTTTGTGC TCATATATTA TAGAAGTATC AATGACGAGG GGATGCCGCA TTITCAAGAC	120
15 GTTCAAGTCG GCTGCAATG AATGGCGGAT AAGCACATCT GTTGCGCTTA TCATCCGCAA	180
GAGATCCTGT TGGACGTCTT GCAAAGTGT GGTCACCCCG ACCAACTTCT CCTCTGTAAT	240
ACCGCTGTAC TTGCTCAAGT AGTCCACAAT GGGCTCATCT GGCTTGACAA ACTTGTGATA	300
20 AACTAAGTTA CAATCAAAAT CGACGACGCT CACACGGGTC AACACGTATC CGT'TTTTAGA	360
AAGGCACATC TCACAGTCGA TGGCAAACGT GTGAGAACCG TCGTGTGGA AACTGACAGT	420
GTCACCCAC CCACTGCACT TCTCCTTATT CTGATACTTT AGCAACAAAG CCTTTTGGGT	480
25 ACTCCTCGA TAAGCCAGGT GTGTTTAGAT GGATGGGGTA CTCATTATGC AATAAGTCAA	540
CAACGGGCAT AGCAAATCAA GCAAGTGATT	570

(2) INFORMATION FOR SEQ ID NO:160:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1062RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GATCTCGGTG ACGTGGCGCT GGTATGGCTT CATCCAGTCG CCGTTCAACA AGAAGTTTCT	60
GTTAACGTCG AAGTTACAGC TGGTGAAGGA ATCAACCTCT GGGCCACGG CCTTGATCAC	120
45 CTCTGGTGTG TTCAAATACT CCTCACTGTA CTTCATGTCA TCGTAGCAGA GCTGGCCCTC	180
ACACTCCTTG CGAACGTCGT AGACGTTCTT ACCAGTTCTC TGGAAACGGG TCAACTGGTT	240
GCCATTACAG TACAGAGAGG CTGGAACACA CGACCACAG TTCTGCAGGG TGTAGCATGT	300
50 GCGGATCAAA CGCAAGCACC GTGGCAAGGT CTGGTTCATT GCGGAGCATT GCTCTGGGCC	360
AAGAATGGCG GGTTCGCGGC CACCACGCA GGCCATACGC TCGTAGTAGG GGTACTGTGT	420
CAATGGGTCT GTCAACCGGT TOCCAATTAG CACAGAGCTC AACTTAAACG AGCGCTCTC	480

55

GCCTGGGTGC GACAAGATCT CGGCAGCAAT AGCAGGAATG TG

522

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 633 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1062UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GATCCTGGTT GTATCATAGA GAATGAACAT ATTGATAAAA AAATGCTACT GTGTACAGTA	60
ATGTCTGAAC ACCAACATGC TCTTTTCTTG TATTAAATGA TGGGATAACG AAGTCTTGGA	120
AGAATCCTGG GCGGAAATAG TAGACATGTT TAGAGAGATT TTTGTAATGG CTAGAGTCGG	180
TTTTGATGCC CGAAAAAGAA GTGCCAACAT TTAATTTTGA AGGTTTATCA GGTAGGTCAG	240
GGAATATACT ATCCTCGTAT AAACCTTGA TTGTACTTGC AAGGAGCTCC AAGTCGTCTG	300
AGTTAGGCGA TGGTTCATCT TTAGTGTCAG CATGACGAG GACCTCACAT GTGATTCCTG	360
AGTCAATTGC ATCTATGACC TCTCCATTCA CAATCAAGCC CATGGGTCCA AACTCCTTGA	420
GAGCCGCTTT GATAAGCTCA GTACGCAGCT CGACCGAAGT ATCCAACGTA AGTGACTCCT	480
TTATTTTGGAA TTGCAGATAT TGGGCGCGCA CTGCATGTAT AGATCCCCCA TGAATAAAGG	540
AGAATTGCTG CACAGTAGTA AACGCAAATC CCGGTAAAT AGTTGGTTGG CTCTTAGGA	600
AGTCAGTGAA CCGATTATTT GGTCTCTGAT CCT	633

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1063RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GATGACTTGG ACCGTCACCC GGTACTGGTC GTACTTGTGC ATGAACTGGT CCTGTAGTTC	60
CCCCAGTTGC TAGATGAGCA CGCCAGTTT GTGGTCACG TCGACACAT CGTCGTCGTT	120
GTCCATGCCC CACATGACA GCTGCCGCGC AGGGCGCGC CGCTCATTGG CCACCACTTC	180
CAGGCGACGT AGCACCCCTT TTTCCGTCTT CAGGAACGAA GACAGCTTCC GTGCCAACTC	240

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GGGGCCAAAG TTTCOCGCTG CATTCTTGCG GAACGAGGAA GCAATCCCGG CACGCCCAAA 300
 GAACTTGGAA CGTGTGGAAG AGGGTGGGGG AGGGGGTGAC TGGAGGTCTG ACGCAGTAGG 360
 CGCCTTCTGG TTCTCCTAAAG AGTATGTCTT GTGCATATTC TCGTGCTTAG ACTGGTCTGG 420
 CAGTCGGTAT TTGTAGGTCC GATAAGATTC TCAGACGACA GCAAGTAAAG TACAACGGTG 480
 GTCGGTGCCC CTCCAACGTC TTTT 505

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1063UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GATCTTAATA GCAATAGTCG ACTACAGGAA ACACAAGCTT TCATAATGTC GAAATCTTTA 60
 TCATGGGATA CACTAGACTA TACTCTACAA CCATGGATTC GTACTGCTGT TGATGCCATG 120
 GGTATGAGA CCATGACACC TGTACAGGCA TCGACGATCC CGCTATTTGC CAGAAACAAA 180
 GATGTGGTTG TAGAATCTGT GACCGGTTTC GGAAGACCG TGGCATTGT CATACCTGTA 240
 TTGAGAGAG TGATACAGGA TGATGCCAAT AGTTCAAAGC TCAAAAAGG CCACTTCCAC 300
 ACCATAATAA TCTCCCTAC GCGGAGCTT GCATCACAGA TACAGGGCGT GATTGAAGCG 360
 TTTCTGACAT ACTATCCAGA TGGAGAATAT CCTATAAAT CACAGTTGCT TATCGGTAGC 420
 AATACCAGTA GTGTCAGAGA TGATGTTGCA GCGTTTTTGG AACATAGACC GCAAATTTTA 480
 GTTGGTACGC CTGGAAGGCT ATTAGACTTT CTTAAGATGC CAAACATCAA GACGTCTTCA 540
 TGTGGCGCAG CTATTCTTGA TGAGGCCGAC AAGTATTGGA TATGAATTTG AGAAGGATGT 600
 CCAGACAATA CTGGAGATGC TACCAAGCCA A 631

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG0164I1

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

	GCAGGAANTG GGTAGCCAAG AACCCGGCAA GACCTTCCCG AGCTACAACC GCGTCATCTC	60
5	GCAGGTGTTT GGCATCTGCG TCAGCATGGC CGGCTGTATC GGGTACGGCT GGGGAATTCA	120
	ATTTCACTAT CACATCGCTA TCGTGCTATT CTTTTCTTTC CTAATGGCGT TGGGTATGAC	180
	CTGGTGCTCT AACTCCACCA TGACCTTCCT TACGGAGTCC AACCCAAAAA GAGCTGCCGG	240
10	TACCATTGCC GTAAGCAACA GCTTCCGCAA TATCGCTGCC GCCATCAGCT CCGCCATTAT	300
	TTTCAAACTA TGCAACGCCA TGGCGGTGG ATGGTGINTT ACAGGCTTGG GTCTAATCGA	360
	CTTGCTATCC ATGTTGAGCG TCTATTACTT GATCCGTAAT GGGGCGGAGA TTACAAGGAT	420
15	AGCTGCTGAG CTATGATATC ATAACACATC CGCATTTTTA CGGATTTAGA TAACCAAAAC	480
	AGCATANTTA GCATGTTTAG AATCTATCAG AAGAACCTCC CTGTTCCTT TAATGATTAA	540
	TTTGAACAGT CATTGATTCC GTCTTTGAC CAAGAAGITA GCACGTGATA TCCGCTGACG	600
20	CCGAAACGGC GTGCCTTGTC TTTTAC	626

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG106412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

	AAAAATCATT TTTATCACCA CTCAAGATGC AGTCTGATTG AAGTGTAAG CTGCAGTAGA	60
	AGAGACAAGT AAGCCATCAT GAAGGTATGT TATAGGTGCT AAGTTCCCGA TACNAGCACA	120
40	GTGGGCATGC TAGGGCTGCA GAGACAGGGC ATGGGCGTGT TACGATAGCC GGAGACTCCG	180
	ATTGGCGGGC TAGCGGGAGG TTAGCGGGC GTTGAAACGA TAATGGGTGC CAGGACGGCG	240
	GCCACGGCGG CACTGATGCT TGTATTGTTT GGCATGAATC TGATACTAAC ATTCTGTAG	300
45	TTGAACATTT CTTACCCAGT TAATGGTACG CNAAGACCA TTGAGGTGCA TGACGAACAC	360
	CGTGTCGGTG TCTTCTACGA CAAGAGAATT GGCC	394

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 559 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1064RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

5	TAGTGGATCC AGCATCCCGT CTCGACCACT CCTGAGTTCC GCGGGCTCTA TCCTAGACCG	60
10	CCAAAGCCCA GCTTGAAGAC GTACTGGGAG ATCGTGAAG AACCAAACCT CACTATATGT	120
	TCCTGAGCA CAGCGCTAAT GTTCGCCACC TACTATGGGT TCAGCGTCAC GTTCGCCAC	180
	TACTTGAAC TTGACTATGG CTTCAGTAAC CTTCGGATCG GCGCGTGCTA TGCTGTCCA	240
15	GCGGTGGCC TAATGATGG CTCCCTCTTG GCGGTGACA TTTCGACCG CTTCGGCAGG	300
	AAGTGGGTAG CCAAGAACC CGGNAAGACC TTCCCGAGCT ACAACCGCCT CATCTGCAG	360
	GTGTTTGGCA TCTGGGTCAG CATGCCCGC TGTATCGGT ACGGCTGGG AATCAATTT	420
20	CACTATCACA TCGTATCGC GCTATCTTT TCTTTCTAA TGGGTTGGG TATGACCTGG	480
	TGCTCTAACT CCAACATGAC CTTCCTTACG GAGTCCAACC CAAAAGAGC TGCCGGTACC	540
	ATTGCGTAAG CAACAGCTT	559

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 611 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1064UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

40	GATCTGTCT CGCCCGCTTA TGGGCCCTGC CTGGGGCAG AGGGAGATCG TCCTGGTGG	60
	CCTAGGCTAG GCACGGCCCT AGGCGGAGCT TGTCTGCGG AGGCGGGCC GCGTGAGCC	120
	CGCTGGCAG GCGGCGAGC CGTGAGAGG TAGGGGCGG CCTAATGCT CTAAGCAGC	180
	GACCGGCGAG CGGACCTGCA CGTTAGTAAA AAATCATTTT TATCACTACT CAAGATGCAG	240
45	TCTGATTGAA GTGTAAAGCT GCAGTAGAAG AGACAAGTAA GGCATCATGA AGGTATTTTA	300
	TAGGTGCTAA GTTCCGATA CAAAGCACAG GTGGGCATTC TAGGGCTGCA GAGACAGGC	360
	ATGGGGTTT TACGGATAGC CGGAGACTC CCATTTGGC GGGCTTAGCG GGAGGGTTAG	420
50	CGCGGNGTTT GGAAACGAAT AATGGGNTGC CAGACGCGG GCCACGGNG GACTGATGCT	480
	TGTTTTTGT TGGGAATNAA TCTTATACT AACCAATCCN GINGGNGGA CAATCTTAC	540
	CCNGTTAAT NGGTACGCAA AAGACCATGN AGGTGGGNTG ANGACAACN NNTCCNNNT	600
55	TTCTTNCAN A	611

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 615 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1065RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GATCTGTAGT TTCGCAGTCC CTGATGCGGT CCGCCAGAGC AGGCAGCGCG GGCCAGGGTC 60
 TCGCAAGGC AGGCGTTGTG TCACCGGGA GCCACTCTCT GGCAGGCAG TTCCACGCT 120
 CCTGAACGAG CGCGGCATG ATGGGGCCCA GAATCTGCG ATAGGCATCC AGAATGTGGA 180
 ACAGGGTGGT CTTTATGGCC AGACGCTCT TATTATGTGG GGGTTCCATG TAAAGCGTGT 240
 CCTTCGAAGC ATCAAAGTAG AGGGACAGGT CGTTGCTCAT GTGTACAGA ACAAGACTG 300
 ATGACATGG AGTAGGTCTG GGATTCGCA CAGACCTGA CACTTGGGG GCAAAATTCT 360
 TTGCTTTGTC GAGGGNTTTT CCCNTCANTC CCCNGGCAGG TGGGGGCAGN CTTCCCCNGG 420
 GCAAAAAGG CTNITCCCCA CCNAGATNAA CCCCTGGGA ANCCCGAAGG TGNCANNAAT 480
 TNAGNGGAAG TNNCCTNACC NCTCCACCNA ATCGGAAAAA TTGGGGANNA ANGCCCCANC 540
 CCAACNCCA AANTTTTCTT GGAATAAAAA AGGGGNGCC CCCCCGNG GANTINANTTT 600
 TTTCCCCCCC NATCC 615

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 604 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1065UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GATCTCTTCC CTTCGATCAT CCCTCAGTTG GGTCTGAGT CCATCGATGC GTTGACGCAG 60
 TTGGCCACAC AGTTGCAGAA CGCACAGGCT GCAGCTCCAG CAACCGAGG CCATGAGGCA 120
 GGCGAGAAGA AGGACAACGA CATCCAGAG TTGATGAGG GCCAGTCTTT CGACGGGGAT 180
 GTTGAATAAG TGGCTGTGC GAGGACTGTG TTCTGCGGC CCATCTCAGA ATTTGTCTAT 240

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TTCTGCAGGG AATATACATA TATTGAGTGC ACATATGGAT ATTAATGTATA TATATGTACA 300
TAACTATAC CGCCCCCGTC TTAGTGGGAC CACATAAACC TACGGGTGG CGCCCTATA 360
5 TCGTTTTACA ATAAACGGCG CGNCTTGGG GGNVINCTTC GANAATCTCN TTGGGGGGCC 420
CNCNNCNCNT TANNAGGTNC TTCNCCGGG TNGGAAGTNA AAAAGCNNNN GTTCNGTTGN 480
NAGNGTCCCC GGGGAAANC CNCCCCGNG GNGGATTTTC NCCCAAACCG NAGAAACNN 540
10 CNTTGCNCCA AGTTGCCCGT GGGAGAAAAA AANCCNATGN NGAAGNAAAA TTGCCCCCTG 600
CCCN 604

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 653 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1066RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GATCCTGAGG CCTCACTAAG CCATTCAATC GGTACTAGCG ACGGGCGGTG TGTACAAAGG 60
GCAGGGAGCT AATCAACGCA AGCTGATGAC TTGGGCTTAC TAGGAATTCC TCGTTGAAGA 120
30 GCAATAATTG CAATGCTCTA TCCCAGCAC GACGGAGTTT CACAAGATTA CCCAGACCTC 180
TGGCCAAGG TTATACTCGC TGGCTCCGTC AGTGTAGCGC GGTGCGGCC CAGAACGCT 240
AAGGGCATCA CAGACCTGTT ATTGCCTCAA ACTTCCATCG GCTTGAAACC GATAGTCCCT 300
35 CTAAGAAGTG CGCAACCAGC AAATGCTAGC AGCACTATTT AGTAGGTAA GGCTCGTTC 360
GTTATCGCAA TTAAGCAGAC AAATCACTCC ACCAACTAAG AACGGCCATG CACCACCACC 420
CACAAATCA AGAAAGAGCT CTCAATCTGT CAATCCTTAT TGCTCTGGA CCGGTGAGT 480
TTCCCCGTGT TGAGTCAAAT TAAGCCGAG GCTCCACTCC TGGTGGTGCC CTTCGGTCAA 540
TTCTTTTAAG TTTGAGCTT GCGAACATAC TCCCCCAGA ACCCAAAGAC TTTGATTTCT 600
45 CGTAAGGTGC CGAGTGGGTC ATAAGAAAAC ACCACCCGAT CCTAATCGG CAT 653

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 669 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1066UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

	GATCTGGAGG ACCTATATAT ACCATTTCGC TGCACCTTTC TTTTGTGCC TGATGTTTTA	60
5	TAAGTAGACG ATCTCTGATT ATTATGCGA GGTGCTTAAA GTCCCATGCG AGCACACTGT	120
	TTGCAATGAT GGCCATCGCC CACCAGACCA GTCAGAAGTA GATATCTGAA TTGCATGTGA	180
10	GCCATACTAG GGTGACCTGT GTTGGCGGCC AGCTTGCCAG AGGAGGAAAA AAAAAAGATT	240
	GCAGCACCTG AGTTTCGGT ATGGTCACCC ACTACACTAC TCGGTCAGGC TCTTACCAGC	300
	TTAACTACAG TTGATCGGAC GGGAAACGGT GCTTTCCTGGT AGATATGGCC GCAACCGAAA	360
15	TATATAGCCT AGAGCAGACA TGATATCAGA TGGTGGATGC ACGTGAGGGC GTAGACATGT	420
	AATAACGATA TCGAGTACAT TTGGTGCCAG ATGGCTGGGG CTATGGCGCA GATGTGTGGT	480
	AATTGGCACA TCGGGGTAAG TCACGGGGTA AGAAGAGTTT GTGGGCATTG GAGTGCCATT	540
20	CCGTACCGAA TGTACGCTAG TGATCTGAAA AGTGATATGC TATGTGAAGT GCAAAGTATG	600
	GGAAGTCTGG CTGGGGTTAR GAAGAAGATG TCRACCTCAA GSCAACGGAA CGTCCGARCA	660
	ATGCTTTGA	669

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 652 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1067RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

	GATCCCTTAA CTTCGTTCT TGAATTAATGA AAACGTCCTT GGCAAATGCT TTCGCAGTAG	60
40	TTAGTCTTCA ATAAATCCAA GAATTTCAAC TCTGACAATT GAATACTGAT GCGCCGACC	120
	GTCCCTATTA ATCATTAACGA TGGTCCTAGA AACCAACAAA ATAGAACCAA ACGTCCTATT	180
45	CCATTATTCC ATGCTAATAT ATTGAGCTT GCGCCTGCTT TGAACACTCT AATTTTTC	240
	AAGTAAAGT CCTGGTTGCG CTAGAGTACA AGTACCCTAG GTTAGCCAGA AGGAAAGGTT	300
	CGGTTGGATC CCGTACACGA AGAAAATCGG ACGGGCCAAC CAAACCCAAA GTTCAACTAC	360
50	GAGCTTTTTA ACTGCAACAA CTTTAATATA CGCTATTGGA GCTGGAATTG CCGCGGCTGC	420
	TGGCACCAGA CTGCCCCCTC AATGTGTCCT CGTTAAGGTA TTTACATTGT ACTCATTC	480
	ATTACAAGAC CCGTATGGGC CCGTATCGT TATTTATGT CACTACCTCC CTGAATTAGG	540
55	ATTGGGTAAT TTGCGCGCCT GCTGCCTTCC TTGGATGTGG TAGCCGTTTC TCAGGCTCCC	600

TCTCCGGAAT CGAACCTTAT TCCCCGTTAC CGGTGAAAC CATGGTAGGC CA

652

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1067UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GATCGGGTAG TGAGGGCCTT GGTGAGACGC GGCAAGTGTG CTTGTGGTCT GTCCGCGGG	60
GCTTGCTCCT GGGACGGAC TGCTTGCGTG CTCTGTGTA GACGGCCTTG GTAGACCATC	120
TCTGGTCGTC GCTTGCTACA ATTAACGATC AACTTAGAAC TGGTACGGAC AAGGGGAATC	180
TGACTGTCTA ATTAAAACAT AGCATGCGA TGGTCAGAAA GTGATGTTGA CGCAATGTGA	240
TTTCTGCCCA GTGCTCTGAA TGTCAAAGTG AAGAAATCA ACCAAGCGCG GGTAAACGGC	300
GGGAGTAACT ATGACTCTCT TAAGGTAGCC AAATGCCTCG TCATCTAAT AGTGACGGCG	360
ATGAATGGAT TAACGAGATT CCCACTGTCC CTATCTACTA TCTAGCGAAA CCACAGCCAA	420
GGGAACGGGC TTGGCAGAAT CAGCGGGGAA AGAAGACCTG TTGAGCTTGA CTCTAGTTTG	480
ACATTGTGAA GAGACATAGA AGGTGTAGAA TAAGTGGGAG CTTGGCGGCC AGTGAAATAC	540
CACTACCTTT ATAGTTTCTT TACTTATTCA ATTAAGCGGA GCTGGAATTC ATTTTCACC	600
TTCTAGCATT TAAAGTCCTA TACGGGCTGA TCGGGTTGA ARACATTGTC AGGTGGGGAG	660
TTTGGCTGG	669

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1068RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GATCCACCNC TNNCCATTG AATCGGTACN ACTCGACGGG CGNNMTGNN AANCGGNCCG	60
GACCTAATCA ACGANAGCTG ATGACTAGAC GCTTACTAGG AATNCGTCCT TCAAGANCAA	120

TGATTGCTC TGINTCTATC CCGAGTCATT ACNGNCTANC AGACATGATC CTCCATGATC 180
 TGTCGGTGCT GTGTGGTATN CCGCAGGACN CCGNCNCTGT ACCGGGGGTG CGGCCAGAA 240
 5 NNICTPANGGG CCTOCCAGAC NTGTTATNGC CTCTAACTTN CATCGGNTCN ANACCGANAN 300
 TCCTNCTAAG ANGTGGGCNA CCAGCANNTG CNNGCNGNC TATTTACTAG GTTAAGGTCT 360
 CGTTGGTTAT CNCCNITANT CAGACAAATC ACTCCANCN CTAANAACGG CNNTGCCCCN 420
 10 NCNNOCNGAA NNINNGAAA CANCTCTCAT CTGTCAATCC TTATCGTGTG TGGACCGCT 480
 GAGTTTCCCG TGTGAATCT AANTAAACCG CAGGCTCNAC TCCTNNTGGT GCCTTCGGTC 540
 NATTCCTTTA AGTTTCAACC CTGGACATA NTCCCCAGA ACTCANAGAC TMTGAT 596

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 641 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1068UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

30 GATCTGGAGG ACCTATATAT ACCATTTCG TGCACTTTC TTTTGTGCC TGATGTITTA 60
 TAAGTAGACG ATCTCTGATT ATTATGGGA GGTGTTTAA GTCCCATGG AGCACTGT 120
 TTGCAATGAT GGCCATGGC CACCAGACCA GTCAGAAGTA GATATCTGAA TGCATGTGA 180
 35 GCCATACTAG GGTGACCTGT GTTGGGGCC AGCTTCAGG AGGAGGAAA AAAAAAGATT 240
 GCAGCACCTG AGTTTGGGT ATGGTCACC ACTACACTAC TGGTCAGGC TCTTACCAGC 300
 TTAACCTACG TTGATGGAC GGGAAACGG GCTTCTGGT AGATATGGC GCAACOGAA 360
 40 TATATAGCCT AGAGCAGACA TGATATCAGA TGGTGGATC ACGTGAGGC GTAGACATGT 420
 AATAACGATA TCGAGTACAT TTGGTGCCAG ATGGCTGGG CTATGGGCA GATGTGTGGT 480
 AGTTGGCACA TCGGGTAAG TCACGGGTA RGAAGARGTT TGTGGCATT GGAGTGCCAT 540
 45 TCGTACCGA ATGTACGTA GTGATCTGAA AAGTGATATG CTATGTGAAG TGCAAAGTAT 600
 GGAAGTCTG GCTGGGGTA AGAAGARGAT GCACTGCAA G 641

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 654 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1069RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GATGACCCC GGTCCCGCTC GCATCAGCGA GCTGCCCGTG CCGATCAGCA GCCCGGTCCC 60
 TAGCGACCCG CCGATGGCTA TCATCGACAC ATGACGTGCC TGCAGGTCCCT TCTTGAGCCG 120
 GATGCCCTCG TGCTTGCCAT CGTAGTTCCA GTCTACGGAC TGGGCTCCCT GGTCTGTGCT 180
 GCTGTGGGTA TGCCGCAGAC CGCGGCCCTC ACCAGCGGCG GCCAGCTTGG GGCTTTTCAA 240
 CTGCTCCAGC GTGGACGGCT CTGATGCGTG TGGGAAGTTC TCTTCGGCCA TAAGTGGGGA 300
 GCTGTATCTT ATGCTACTCA AGCTCCCGCC GTATAGCCTT GCTATATATA CTTACGCTGC 360
 GACGCCCTAT TCCGGACACA GCTATATATT GGCCCGCGGT CTGGGCGGCT GCTTGGGGAG 420
 CCGACTGACC CCACCGTGAT AGTGCCGTG CACTTCTGCT GGGCCGCGCT AGCCCGTTCA 480
 GCGTCGACT GTGACATGGG GCTGCGGAG CGCGATTAAAT CACCGACTG GGCTGCATGC 540
 CGCACTAAAC CTCCCTCGC GGCGCAGGCG GCCCTTATCG CCTCCGTGAT GACGTACGTA 600
 TGTTTATCAA AGATCCGGAG AMCTGTTCCA GGCTCTACG TTGCGATAAG AGGC 654

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1069UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GATCTTTCTG CCCTTATCAG GGATGGCACC ACCGGTCTTC ACCTCGTTTG ACTGTAGCC 60
 ACAGTGCTCG CAGACCGTGG ACATGATGAT GACCTCTTTG AAGTGTGGGA TGTGACCGG 120
 CTTCATATGC GTGTACATG GGTGAACACA TGATGGGCAC GTGGCAGTGA AGGCTGCAC 180
 CTGTTGTGG AAGTCTCGA TATCCGTAGC GTCAGATAAG AGACCGGCT GTGCGCTTG 240
 CGATTGTGTT CGCTCGCGCT GCGACAGCTC CGCGCGCTTC TCTGAAGGC GTTGCTCCAA 300
 TTGGTCGCGC GTAATGATGC CCACCTGGAC GTTTTGCTCA TCTGAACGCA GGTACTCGGT 360
 TTTGGACCAT TTTGGCGCAG CTTGCGCTGG CTTGTATTCG ATCCAGGAAT TGCCAGCAGG 420
 GTCGTCCAGC GTAAAAGTCA GCGGTAGAGT GCGCGCTCG CACGACAGCG CAGCGCGGAC 480
 CTTGGCAATG AACTGGGCAA TCTGATCGTA CAGGTTCTCG TCCACTTCCT TCCGCGCGCG 540
 CTGGTCGGCG TCCAAGTCTT CGATCATCTC GGTCAGCAGG CCTCCACAG TCGTCAGCTG 600

GCCGCGCTTG GGAAGAATCT CCAGGTCCAA TTCAACGAAG CGGGAAGCOG CAGTTTGGC 660
 CTTGATGACT GCGTGTCAAA ATCGGCGCTC TCCTCAACCT TCAGCTGA 708

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1070RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GATCCCGTAC ACGAAGAAAA TCGGACGGGC CAACCAAAACC CAAAGTTCAA CTACGAGCTT 60
 TTTAAGTACA ACAACTTTAA TATACGCTAT TGGAGCTGGA ATTACCGCGG CTGCTGGCAC 120
 CAGACTTGCC CTCGAATTGT TCCTCGTTAA GGTATTTACA TTGTACTCAT TCCAATTACA 180
 AGWCCCGTAT GGGCCCTGTA TCGTTATTTA TTGTACTTAC CTCCTGAAT TAGGWTGGG 240
 TAATTTGCGC GCGTGTGCGC TTCCTTGGAT GGGGTAGCGG TTTCTCAGGC TCCCTCTCCG 300
 GAATCGAACC CTTATTCCCC GTTACCGGTT GAAACCATGG TAGGCCACTA TCCTACCATC 360
 GAAAGTTGAT AGGCAGAAAA TTTGAATGAA CCATCGCCAG CACAAGGCCA TGCGATTGGA 420
 AAAGTTATTA TGAATCATCA AAGAGTCCGA AGACATTGAT TTTTATCTA ATAAATACAT 480
 CTCTTCCAAA AGGTGAGAT TTTAAGCATG TATTAGCTCT AGAATTACCA CAGATATCCA 540
 TGTAGTAAAG GAACTATCAA ATAAACGATA ACTGATTTAA TGAGCCATTC GCAGTTTCAC 600
 TGTATAAATT GCTTATACCT AGACATGCAT GCGTTAATCT TTGAGACAAG CATATGACTA 660
 CTGGCAGGAT CAACCAGATA ACTATCTTAA AGAACAACCC GAA 703

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1070UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GATCCTTTAG TTCTCGGAG TTTGAGGCTA GAGGTGCCAG AAAAGTTACC ACAGGGATAA 60

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CTGGCTTGTC GCAGTCAAGC GTTCATAGCG ACATTGCTTT TTGATTCTTC GATGTGGCT 120
 CTTCCTATCA TACCGAAGCA GAATTCGGTA AGCGTTGGAT TGTTCAACCA CTAATAGGGA 180
 5 ACGTGAGCTG GGTTTAGACC GTCGTGAGAC AGGTTAGTTT TACCTACTG ATGAATGTTA 240
 TCGCAATAGT AATTGAACTT AGTACGAGAG GAACAGTTCA TTCGGATAAT TGGTTTTTGC 300
 GGCTGTCCGA CCGGGCATTG CCGCGAAGCT ACCATCCGCT GGATTATGGC TGAACGCTC 360
 10 TAAGTCAGAA TOCATGCTAG AACGCGATGA TTCTTTTTCT CGCACATTAT AGATGGATAC 420
 GAATAAGGTG CTTTTAGCAT CGCTGAACCA TAGCAGGCCG GCAACTGGTG TTCANACGGA 480
 AAGGTCTGGG CCGTGCCGG CGGATTGCAA TGTCATACTG CCGGAGAGTA AATCATTTGT 540
 15 ACACGACTTA RATGTACAAC AGGTATTTGT AAGCAGTARA GTAGCCTTGT TGTTACGATC 600
 TGCTGAGATT AAGCCTTGGT TGCTGATTT GTTTCTATT TGAAGTCTG CAGGACCAGG 660
 CTTTGAAATA RAGTT 675

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 498 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1071RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GATCTGNGGG GGAAACNCAG CATTACCGT TGTGCAAAAA GATTTGACTG GTAACATCAC 60
 CAAGCTTCGC AACAGACAAT TGTOGCACCC CCGTGAGTCT GCAACCCGTC AGGAGCTTGT 120
 GATTGCAGAG CGTGACAGG GCAGCAAGAC TGCTTCGGAA GGGCTGCTGT GGCTCACCAG 180
 40 AGGCTTGCAA TTCACCGCGC AAGCTCTTAG AGAAACGCTA GACCATCCAG AGCTCGAATT 240
 GTCTAAGACA TTCACAGATG CGTATTGGAA GACGTTGACG AAGCACCATG GTATGCTTGT 300
 ACGTCCGGTT TTCAAAGCTG GCCATGAAAG CTGCCCCCTA CAGGAAGGAC TTTTTTGACG 360
 45 AAAGTAGGCA GCGACCAAGA GAAGGTGAC ACGCAACTTT AAGCAGTGGC TGGCTGCACT 420
 TGAAAAGATC GTAGAGATTG TGCTTCAAAT CCTTGGGGG AAACGTGCAA AGGATTTATG 480
 AGTATTATTA TAGAAGCC 498

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 625 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1071UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

10	GATCGACAGC CTCGAAGAAG TAGCCTCCAC AGCTTCAAAC ACAGCGCACA GGTCTGCATA	60
	CATCAAGCTG GTGCTTGCTG CAGGCTTAAC CGGAGAACTT TGTGGCGGTG GCACGGCGCT	120
	GGCAGACTGT GGCAGCACCC CCCCCGGGCG GGGCTTATCT GCAAGCTCGG GGAGGATGTT	180
15	CTTCACCTCG GGTCTCTGTT CATGGGCTGC CGGTGCGGCT AGGCACTCGG GAGACTCTAC	240
	CTTCGATTTC TTGACCTCTG CTGTTGACGT CGCTOCATCT TGAGGCTCTT TCAGCGCAGC	300
	GAAGAATCGG ACCAATGTGG CCTGCTTCTT TGGAGTAGAC ATTGGGCTGA AGTAAAACCC	360
20	TACTGACCTG CCAAATAGCT CCACCTTGGT CTGGGACAG GAGCTTCNA AGANTGACAT	420
	TNNNTGTNGN NAAGGCCNNN NNNNNCAAA GACGAANCTN NTATCAAGGN CCTNNNTNCC	480
	CCAGNCNNA NAAGNAANAA NNNNATNNN GGNATNNNN AAATTANGGT TNNNNNATNN	540
25	NCTTNGNAAA TTNNNNNGNN TTNNNATTC CANNNGGNT TNNNTTNCC NNCNCTNN	600
	GGVTTTTTNN NANNNNNAAN NNCC	625

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1072RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

40	GAGCAACTAT TATTAGGCGC CCCCCACCC AGTCTGCAGC ATTGAAAGC CTTCCTAGCC	60
	TTTGTGGGAT GTCCCAAGGT ACAATTTTCT CGCAGNTGAA AATACGAAAG AAGCGCCAAG	120
45	AAGTGGGCTT CTTTGAATCC AACGCCGACG CCAATGATGT CGAGCGGGC GAACATTTTA	180
	TAACAGAGCT CGATAAGGC GATAAGCGC TGGGCTGTT TTCTTGATC GGCTTGATAT	240
	GCAATAGAAT GCTGGGACA GGTATCTTTG TGGTCCCGC GAAGATCTTC CAGTCCGACT	300
50	GGCTCAGTAT ACTTTGGGCT AGGGTTATGG GTACTAGGAG CTTTAATTGC TCTAGCAGGT	360
	CTTTATGTTT ACATGGAATT TGGTAACTGC AATACCGCGC AACGGTGGCG AGAAGAACTA	420
	CCTTGAGTGC ATCTCCAATG AAACCGAACT TCTTCACTTA CAGTCAAGTG TACTCAGCAT	480
55	ATGATCATCT T	491

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 726 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1072UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GATCGCAGC TTCGGCAAGC GCGCTTCTC CTCGIGTAC TCCTCGTGGT CGTGTACTC	60
CGGCACCATC GACGCTCCG GCTCCTCTC ATCCGCGTC GGTCTTCTT CCTGTCCAC	120
CGTCTCCGGC AGAAGAGAGT CGGCTTCCG CCGGCTCTG TGTGTGTGC GCTCCAGCAG	180
AGGCCCCGA AGCGGCTGCT CGTCCGGGAG CGGCCCCGAG TACGGGTACT TCACCGGACC	240
CATCTCCCGC TCAATCCGCG GGATCAACAC CTCGCGCAG TACCGGTCCA TGATCTGGC	300
ATAGTGGTAA GATTACCTAA TTCATACGTG TAGATCATCC CATGCTTACC ATGTTGAACC	360
GTCACCATGT AAATTTCCAA TAATCTCTA GTCTCTCATT TGPAGANATT AGNANCTTTC	420
CTTTATATTA ATNCTTTTAC TNAATAATTN ATNNANNITT TNNITTGANC ANTTCTCCAT	480
ATTGTATTAA ANINATATAT AATATTATTN TCTACTAATC TAACAAATTA NNVCTINTAT	540
TATATATTTA NNNANCATAT NATNATATTA AATTATTIAT AATNATNCTN TCCTCTTNTA	600
ATNTTTAAAT NNNANNVITT TIVNCNLANN CTAATNNATT TTINGATATT TINTTINNTA	660
NNNNNTAAA AAATATNNNN TTTATCNANT ATCTTCCATT TATNAATCNV NTTTTATCA	720
AACCCC	726

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 641 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1073RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GATCAATTAA TAAATGGITT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA	60
CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT	120

5
 10
 15

ATTGAGTTTA TATTAAATTC ACCAOCCTCTT ATTCATTCAT TTAATACTOC TCTAATTCAA 180
 TCTTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAATTG 240
 GTAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATTAT 300
 ATCATTAAATA TAATAACTCT TTAATTAGAG TGGTACCACA AGAATGCTGA AAGCATTAGG 360
 GGTGTGTACC TTAGCTCTCT AATTAAAGTT ATAAATTAT CTTAACATAA AAAAATAATT 420
 AATTAAATAA ATAAATAATT AATTAAATTT AAAATGTTTA AAAAAAGAAA TAAATAATAT 480
 GTTATATTTA AATAGATCAA AATTTCAACA ATTTCATTTC CATTAGTAC TACCATCACC 540
 ATGACCAATT GTTACATCAT TTAGTTTATT AGGTTTACTA TTAACCTTAG CTTTTACTAT 600
 ACATGGTATT ATTGGTAATA TTTATCCTTT ATTATTATCT T 641

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- 20
 25
- (A) LENGTH: 662 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 30
 35
 40
 45
 50
- (A) ORGANISM: PAG1073UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

30
 35
 40
 45
 50

GATCTTAATT TAAATTTTA ATTAACATTT TATAATTTAG AATATATATA TCTAGAGATA 60
 TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120
 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTC TGGCATCTTA 180
 ATTTTATTA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240
 ATAAATAAGA AATTACTTAT AGAATATTTA TTAANTAGTA TTTAATTTAA TTTTAATATT 300
 AAATATACCA TTTTATTATA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA 360
 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420
 TTTTATAATA TTTATTTTAA TTAGTCTAGT AATATTTCTA TTTAATAGTC TACCCTTTAA 480
 TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC 540
 TAATAATTTA TTATCTAAAG TATATAAATT AATTAAATCN TTTTATTATA TTATTTAAAT 600
 TATTATTAAT TAGTAAATTA TATTTATTTA TTTTATTAAAC ATAATTTTMT GNATAATAAT 660
 AT 662

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- 55
- (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1074RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

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10  GATCTAAATA TATATAATTT AATTTATAAA GATTAATATA AACTTTTTTA TTATAATATT      60
    TAAGTATTAA ATTATTTAAA CTATTATTAT CATTATTTAA TAAATTAATT ATTTGATTAT      120
15  TAATACTTAT TATATAATTA TTATATAATT TACTTAATTC ATCATTATTA ATATTTATAT      180
    AATTATAAAA ATAATATTTA ATATGAATAC TATTTAGTCT ATGTTCAAAT TTAAATTAG      240
    TTATTAAAAT ATTATTAGAT ATTATTATTT TCTTTAATAA ATTATTAAAT AGATTATCAA      300
20  TAATTAATAT ATTATTTATT AATTGTTTAT TAAAATAATA TATTTTATTA TTATAAAGAT      360
    TTAATTTATT TAAATATTGT AAATTATTAT TTTTATTATA ATATCTATTT TTATAAATAT      420
    TATGTTGATT TATATTATTT AACTTTTTAT AAGAATTATT ATTAAAATTA ATTTTAACTT      480
25  TAACTTCTTA TTATTAATTT TTATATTATT TAATAAATTA TATTCATTTT ATTTATTTAT      540
    TTATTTAATT AAATTAATTA TTAAATTAAT ATTTTATCAT TATTTAATTA ATTAATAAAA      600
    TATTATAAAG AATGT                                          615
  
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(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 663 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1074UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

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45  GATCTTGATA CTAGAGCTTA TTTTACTTCA GCTACTATAA TTATCTTAT TCCTACTAGT      60
    ATTAAAGTAT TTAGTTGATT ACTAACTATT TATGGTGGTT CATTAAGATT ACTAACACCA      120
    ATATTATATC TATTATCATT TTTATTTTFA TTTACTGTAG GTGGTTTAAC TGGTGTAGTA      180
    TTAGCTAATC TATCATTAGA TGTAGCATTG CATGATACTT ATTATGTAGT ACTACATTTT      240
50  CATTATGTAT TAAGTTTAGG TGCTGTATTC TCTATGTTTG CTGGTTATTA TTATTGAAGT      300
    CCTCTTGTTT TAGGTTTAAA TTATAATGAA AAATTATCAC AAATCAATT CTGATTAAAT      360
    TTCTTAGGTC TTAATATTAT TTTCTTCCCT ATGCATTTCT TAGGTATTAA TGGTATACCA      420
55  AGAAGAATTC CTGATTATCC TGATCTATTC CTAGGTGAA ATTTAGTATC TTCATTTGGT      480
  
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TCTATAATAA CTATTATATC ATTAATGTTA TTCCTTTATA TTATTTATGA TCAATTAATA 540
 AATGGTTTAA CTAATAAAGT TAATAATAAA TCTATTAAAT ATATAAACT ACCTGATTTT 600
 ATTGAATCAA ATAATATTTT CTTAATGAAT ACTACTAAAT CATCATCTAT TGAGTTTATA 660
 TTA 663

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 639 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PAG1075RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GATCTATCTA ATTACAGTAA AGCTGCAAAG GGTCTTTTCG TCTTCTACA AATACTTAGC 60
 ATCTTCACTA AGATTTC AAT TTCACTTAGA TTAAAGGAGA GACAGTTGTT GTATCATTAC 120
 GTCATTCATG CAGGACCATA ATTAGTGGAC AATGAATTTT GCTACATTAT AACCCTCATA 180
 ATAAGGCTGC TATTTAATAA AATTTATTAT TATTATCTTT ATTAAATAT TAATTTTAT 240
 ATTTTATCAT GGAGCAGAGT TCACACTTTA TACTTTAACT TACGTTTCTG CAAAGTGTG 300
 TGTTTTTAGT AAACAGTTGT ACAACTTTGT TCTTATTATT AATTATTATT TTAATTAATA 360
 TCTCTTTATT GACTAACGTC AGAGCTATTT TTGCCGAGTT CCTTTCCTTT AATTATCTAA 420
 TTCACCTTCA TATACTCTAC TAACATACTT GAGTGGTCT ACATTACGGT ATTTTATACA 480
 TAAATATTTC TTGAACCTAA TAAATTTATA AAGACATTAT TTAAGTTAAT TTATATATTA 540
 GATTATTTCT ATCATATTAT ATTTTTAAT ATATTACTTA AGAACCGCTT TTATTGTTAA 600
 ACCTTATGCT TTAGGTGATA AGGATTATAC CTTATTTTC 639

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 663 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PAG1075UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

EP 0 866 129 A2

GATCCAGTTA CTTAGTAGAA TGATAAAATT AATAAATATT ATTTATTAAT ATTTGGTTAA 60
 CAATAAAATT CAATAATTTA TTAAATAAT GATTAAATAA TCTCAATATA AAATTATTAA 120
 5 TATAATGAGA TATATATTTT TAAAAAGAAT ATATAATTAA ATAATCCCAA CCAAAATTTG 180
 TGCCAGCAGC TCGGGTAAGA CAANGGGGGT TAGCGTTAAT CGTAATGGCT TANAGGGTTC 240
 GTAGAATGAT TATTTAAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA 300
 10 GTAAAGATGA AATAATAATT ATATGAATAA GACTTATAAA GTGAAAATTT AAATTATATA 360
 TTAATTGACA TTGAGGAAAG AAGGCTAAAG TAGCAAATCG GATTGATAC CCGAGTAGTT 420
 TTAGCAGTAA ACAATGAATA CCTATTTATT TTTTATTAAT TAAAGAATAA ATTAAATGAA 480
 15 AATTAAAGTA TTCCGCTGA TGACTACGTT AGCAATAATA AAAATCAAAA CAATAGACGG 540
 TTACAGACTT AAGCAGTGGG ACATGTTATT TAATTCOGAT AATCCTCCGA TAAATCTTAC 600
 CATTTTTTGA ATATTTAATT ATAATAATTT ATAATTAATT ACAGGOGTTA CATAGTTGTC 660
 20 TTC 663

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 650 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1076RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GATCTTAAAA TAAGATAGAA TGGTAATAAA TATCATTCAG GTACAATAGA TGCTGGTGTT 60
 ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT 120
 40 ACAATAATG AAAAGAAAAT TATAAATACA AATACTGTTA CTAAATCTTT AAAAATAAAA 180
 TAACCATGCA TTGGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA 240
 TGTACATGTA ATAGCATTAA ATGCATAATT ACTATGCTG CAATAATAAA TGGTACTAAA 300
 45 TAATGAAATA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TOCTCATAAT 360
 CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA 420
 GCACCTCAAT GTGACATTTG TCCATATACT AAACAATAAC CTAAGAAAGC TGCTGCTATA 480
 50 GTTAAATAA AGATAATAAC ACCAACTGTT CATACAATAA CTCTAGGTGA TTTATAAGAA 540
 CCATAATATA AACCTTTACC AATATGAATA TACATACCAA TAAAGAAGAA TGAAGCACCA 600
 TTAAGATGCA TATATCTAAT TAATCAACCT AGTTGTTCAT CTCTCATAAT 650

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 663 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1076UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GATCTAGAAT TATTAAGTCA ACTATTAAC T AATACTATA ATAATAATGG TTTATCATTA	60
AAATCATTAAGATAATTAT TAATAAATTA CCATTTAATA ATGATATAAT ATTATCAAAA	120
AATTATGTTA ATAAAATAAA TAAATATAAT TTTACTAATTA ATAATAATTT AAATAATAAT	180
AAAAAGATT TAATTAATTT ATATACITTA GATAATAAAT TATTAGATTT AAGTATTCTT	240
ATAATATAT TATTAGGTAA ATATTTACTA GGTAGTAATA TCCAATTARR GGGTAGACTA	300
TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAAGGTAC ATTTAATAAT	360
TATATATATC AATGAAGTAA ATTAAATAAT TTATATAAAT TAAATTATAT ATCACTTAAT	420
ATTAATAAAC TTAATAATCT ATTTATTAAT AAAATGGTA TATTTAATAT TAAATTAATA	480
TTAAATACTA TTTAATAAAT ATTCTATAAG TAATTTCTTA TTTATTTTAT AACATTTTAA	540
AATGTTTTAT GTTAAATAGA TAATAATCAA TTAAATAATA AAAATTAAGA TGCCACAAAT	600
AATCCATTTT CCTTTATGAA TCAATTAACT TATGGTTTNC TATTTATTTT ACTAATTTTA	660
TCT	663

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 642 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1077RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GATCCAGTTA CTAGTAGAA TGATAAAATT AATAAATATT ATTTATTAAT ATTIGGTTAA	60
CAATAAAATT CAATAATTTA TTAAATAAT GATTAAATAA TCICAAATATA AAATTATTAA	120
TATAATGAGA TATATATTTT TAAAAAGAAT ATATAATTAA ATAATCCCAA CCAAAATTTG	180
TGCCAGCAGC TGCGGTAAGA CAAAGGGGGT TAGCGTTAAT CGTAATGGCT TAAAGGGTTC	240
GTAGAATGAT TATTTAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA	300

EP 0 866 129 A2

GTAAAGATGA AATAATAATT ATATGAATAA GACTTATAAA GTGAAAATTT AAATTATATA 360
 5 TTAATTGACA TTGAGGAACG AAGGCTAAAG TAGCAAATCG GATTGATAC CCGAGTAGTT 420
 TTAGCAGTAA ACAATGAATA OCTATTTATT TTTTATTAAT TAAAGAATAA ATTAAATGAA 480
 AATTAAAGTA TTCCGCCTGA TGA CTACGTT AGCAATAATA AAAATCAAAA CAATAGACGG 540
 10 TTACAGACTT AAGCAGTGGG ACATGTTATT TAATTCGATA ATCTCGATA AATCTTACCA 600
 TTTTITGAAT ATTAAATTAT AATAATTAT AATTAATTAC AG 642

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 658 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1077UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GATCCGIGTA TTTTITATTT ACATTATTIA ATTAAAAATA ATGATTTAAA TAAATATTTT 60
 30 TTATAAAAAA TAATTAGTGC ATTGTTACAT GTTCATTAAA GAATGATTAT TATCAAAACC 120
 ATCAACTAAT TGTTATATAT TTATTAAATA TTAATTTTAC TTAATTAAGA ATTAGGAACT 180
 TTATCTATTA GTCTGGGCTG TTCCCTTTT GATTATTAAAC CTTATCGCTA ATAATCTGAA 240
 35 ATATTTTAATT TTAGATTAAAT AATATATTCT GAGATTTAAT ATTTTAAATA AAATAAATAA 300
 TTATTCCTTA AATAATATTA ATAACTATAC CATATATATC TAATATTAA ATAATCATAC 360
 TAACATATGT TTCGTAGAAA ACCAGCTATT TGCAAATCAG ATTTGACTTT CTCTACTTAC 420
 40 CATTATTCAT CAGATAATAT TGCTACATTA ACCTGTTCAA TCGTTTTTAT ATTTTATTAT 480
 ATTTTAAATA TAATAAATAT ATATTTTAAAT CATTGATAA TAGTAAGATC ATCTGCTTTC 540
 GGGTTAATTA ATATTAACTA AATTAAATTT ATTTTAAATTA ATTTTAACAT TGTTAAATAT 600
 45 TTATATTATT TTTAATATCA TTTTITATTT TAATATTATG CTAATATTAA TTAATTGC 658

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 445 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1078I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

	GATCTAGTTC GTTAACTTCC GCAAAACACC TGTCAGGCGC TTCAACAAAC GTCTGGATCA	60
5	GATCCAAGAT GGCCAGTTCT GACTCCTGGT CGTCGACAAT GAAAGTAAAA TAGAGTGTTC	120
	CATAGTTCTT GTAGATTATT TGGATATCTT CGTTAATGGT TTCACTACCA CTCGATAGTA	180
	GCGAGGGCGG CGTAATTAAG AATGAAGACT GAATTGAAGT GTTGGGCTGG CTGATCAGCT	240
10	CGTAAACCTG CTCCTAGTAGT AGCTTCTGCT TGGGAGATC GACAGGAGTA TAGTACTTTA	300
	CAAGCCTAGG TTGGCACTTC TGTTAACCTT CATGTGTTAG TAGGATAATT TAAGTACTGC	360
	GGCTGGCGGG TGGCAAAGGG GTTCACCCAT ATCAGGACGG CGNCGNNTCA TCNCGTCC	420
15	CCACCACGGN TACNCGCCNC NOCCA	445

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 443 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1078I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

	GATCTAATAT TCAATTGGCA AACTCTTGAG AGTGTCTTGG AGGAAATTAT TCAAGGGGGT	60
	ATGGTAATTG AAACGAACGT GAAGAAAATT GTGGAGACG TCGACGAGCT CAATAGAACT	120
35	TCTAACCAGG AAGCCAGGTT TGGGAATGGA CTAGGAAACG CTTTTCAGGC CATCACCATG	180
	GGTGGCTTTT CAAATTGGGG TGGCGGCGAG TGAATATTAG CACACACTGT CTTGAAACCC	240
	CATAATAAAT GAAATAAATA CTCCTTGCTA GTGTCTAAGT ACGAAACAAC GCCAAGGCTT	300
40	TTGGATCATC TATGTACGCA TTCAGTTCGG CAGCACTCAC CATGGGCACC AACTCTTCTT	360
	ACTTGCTATT TCCTGTGICT TCATTGCGC TTCGGCTGCC TGATGTCTC AAAGCTCCTC	420
	CCTAATCCTC TGTAATTCTC CTG	443

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 451 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1078RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

5	GATCAGGATG GCGATGAGAT ACTACCTTGA AGCAGCAGCC TTGACCTCAG CTAACCTCCGC	60
	AAATTCCTTT CATTTTTCGA AAGCAGATTA TAATTGCTTC TAAGCCATTC AATTGCTTTA	120
	CTTTTCCGTT AATCAATGCT CTATTTTACC ATCATTCGAA GTAAGAGTAT GTCGATATGT	180
10	CTGACCTAAG CTACAGATTA TCTAATCACA TAGTTATGTA CGAACCAATA AGATTATCGA	240
	ATTTGCTTGA AAAACTCAGG CGAACGGCAC AGCGTTGCTT GCGCCTATTA GATGCTTTGG	300
	CCATAGCATA TCACGAAGTG ACCTCACAGT TTTTAAGTAA CCGGAATAGT CTGTAGATAT	360
15	GGTATTGTGA AAAGTTTATT NGCTGGTTTC ACCCCCTGGG AATCTNGGNG CTGCTCTGGG	420
	TTCTTAGGTG GGAATCCGG NCCCCCNNT C	451

(2) INFORMATION FOR SEQ ID NO:197:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1078UP

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

	GATCTCCTTC CTTCCTGGTG TCTTGCCAAG CCCTTATTTC TTGACCAAAG TATTCTTCAC	60
35	CGTTGCCCTG TACTCTGTTC TCATAAATTT CCGCGGTAGG ACACTCTCG GCTTTCTCTT	120
	GGGATCTAT GAGGGCTTTG CAATCATCTT CACCGCCGCT AAAGTTTTC CACCATTTT	180
	GATGAGCAG CTACTTCAGT AAGCCCCGT ATTAGGATTG TTAAAAGAAG TAGGATOGAT	240
40	ACCTTCAAT TCCAGATGAT CGTTGCGGTG GGCTATTAAT TTGTTAGCCA CCTAATACTG	300
	AAATTTACAT ATTATTGCAC TAGTTAATTA ATATTTATGA TGCAATGGGA ATCTATATCG	360
	GTCTCCGTT CCATCTTCTC GTAATTAGAT CACGTCGGAT ATNGTNGCCC CGTACCGAGG	420
45	AGGGACCOGA TTGGGNTTAT CTTTATGGTC CCGAGAANTN ATAGAGNGCC NNAANATAGA	480

(2) INFORMATION FOR SEQ ID NO:198:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 703 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1079RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GATCGCTCAT TATTTTGGT CGGAGCCTGG GCGCTCTCT GCTTCTTCTC AAATACTTTC	60
AAATTTTGGT CTATATAGGT CTGCAGCTCT TCGTCTCTCG AACATTCCGC CTGTGAAGC	120
TGGTTGAAAT ACTGCAGGGC CTCTGCACTC ATGCGATTCA CCATTGAATT GCGCTCTTGT	180
ATCTCTTGCT GGAAGTGTTC TTGTTTGGCA ATGGGTTTTT GCGCAGTTG AGCTTGCAA	240
CTGGTTGTAT CAGACTCGTC CACTTCATCT TCCAGTCCA GTGGATCCAT CCTGCAGCT	300
AGTCTAGGTG GAGTGGTCTA TGTACAGTGC TGCTGTGGT GTTAGCGCGC TCACCTTCTG	360
CGACTGTTC AAGATGTGGG TTTCAGCAA GAAAAGAGAC AACCGAAGT ATAAGTACAG	420
CACGCGAGCC TAATTTTGTG AGCTTGCGGA TTTAGCTCAG TTGGGAGAGC GCCAGACTGA	480
AGAGAACTT CCGTCAATCG TAATCTGGAA GTCTGTGTT CGATCCACAG AATTCCGATA	540
TTTTTTGCTC ACGTACCCA CCGGTANGA ACTGGCATTG CCTACCTAAT GGCCAGCAGT	600
GGAAAGCGCT CTTGTGATAT ATATATATCA AGTAACACAT CTATGTAACC TTTTGACACA	660
GTCCCAAGGT GAATCTTGCC TCGGATCTGC CTCATCTGAR TCC	703

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 673 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1079UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GATCAGCGAG CTAGGTACCC GGACGAACAT GCGTTGCGC AGCTTCCCAT ACTTCAGCGA	60
CCGTGTGTGT AGCGCAGAGC TTCGTCCTG GAATAGCGAC TGCACTCTG CGTTCAGCAG	120
ATCGCCCTCT TTCAGAAAGC TGCGCATCTG CAGCTCATCG CTCTCAGACT TCCGCCGAG	180
CACGCGCCCG GGCAGTTTCA CAGAAGCCAG CATGAGCACT GCGTCTGCT TCCGCCAAT	240
ATCCACCTTC CATCGTTTGT TCGCGACCTC CACGATCTG CCGACAATGT GGTGCGCCGT	300
CTCTGGCGTG TACCGCCCGC GCCAAGGAAT CACGACAGG AGTCGGTTCA CCTGGAAC	360
GGTGGCGCC ACGGACGAGT ACGTTTGTGTT CTCCAGGAAG TATGTCCGT GGCTCGCAT	420
CCACACAGGA TCATCTGTAA TCAGCTCTCC TGGCGTCATA ATCAGGACG AATCCGCTCC	480
TTCCATCTCC ACGTCCAAAT CAAACTCTTC TTCTCATCG TCCAGGTACT GGCTCGGATG	540

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GAAGTGAAC CCACGCCGCT TGGGATCGT TATTACCTCG CTCATTACTG CTGAGACGAC 600
ACGTTTCARA ACTTCAGAGG CTGCTAGGC CAGGCGAAAC AGTGTGARG ATACGCTTTG 660
5 TACTTCTTG AAG 673

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
15 (A) ORGANISM: PAG1080UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

20 GATCCGGCCA CGCATGTATT CCACTATGTA CGCTATATCG CGGCCTCGCC TCCGTGCGGG 60
GCACCGCCTT ACACCTCAAA GCGCAGCCT TTCATGCAGC CCTTGTACTT TTGCACCACT 120
25 TCCTGGCACT TGACCGCATC CAGCGCGTTG AACAGCAGAC AGCTGTCTCT CGCTTCCTTC 180
TCGGGCTTGC ACACACAGCA TGGCTTTTGC TTGTGGTAC TACTACCTTG TGAAACACCT 240
GGCACAGAAG AGGATTCAGG CATGATTAAT GCTACAGTTC TTGGAGATCT TCCAACACCG 300
30 CCGCTCCTT GGGGTTTTTC TCACTTTATT TTTGCTTCAA CCGCAGAAAA TTGTGTGCGA 360
ATTACAATAT ACAGAGGCGC AGTAACCCCT TTAGTGGCTT TTTGGCTTCT TGGGCTGGAA 420
ANTINGACCC CCCAACNVNC C 441

35 (2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 644 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
45 (A) ORGANISM: PAG1081RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

50 GATCTTTGCG AGTGACTAGT GCATGCGGCT ATTTAAAAAG TATCGAGTTA CCCTTGGAAG 60
TTTCAGCATT TATAGTACTG ACGGAGCGGC TACAAAGCCA AGGCTTTGAA GGTACTAGGA 120
GACATATTCA GCGCATAAA TCACCGCAAG CTGGATTGAG CGATGTTTTG GGTGTGTTTT 180
55 ACAGGAGCCA GCGCGGTGGC ATGCGTTTTT GCGTATGGGA TGGTGGACCG ATATCTCTCC 240

TTCAAGCTGC ACAGGCATAC GCACCCGTTT GTGTGGTAA CACTTTTCGC AAATATGACA 300
 CTGTTGCTCT CGATCACATA CCTGCTTCCA CTOGATGTGT TTTACTCAA CCAGACAAGC 360
 5 GGGCGGGAAG ACGAGCGGCC AGAGCTGCCG AACCTCGCGT TGTTCGGGC GGTGATCTAC 420
 TGGGCGGAGT TTGTGATATG CTGGTTGGTG TTCCCGGTGC TGATTTOGTA CGTGGATCTC 480
 AAGTACTTGT ATCCGCGCGA GCCACAGGAG CCGGGCGGCG GCAGCGTGCT TCGGCGACTG 540
 10 CGANGCGCCG TTATATGCAA TCTCAAGTTC TATGGTCTTT GTCTACTGGG GGTGATCTGC 600
 NGGCTGGTAT ATCTCAAGAC GACGACOGAT CGCGGGCGTC AGAC 644

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1081UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GATCCAAGAC GAGCTGCGCC AGGGGAGAAA ACCCCCCAC ATATGTCCAG CGATACGCTC 60
 30 AGCATGGAAA ACCCAACCGT GGACTTGCGC TCGTAGTGTG GCTTGGGCTG TCGATATAC 120
 TTCAGCACAG ACATGATGAT TTTTATAAAG TACAGCACAT GGCAGTAGAA CAGTGTGAC 180
 TGATTGTTC ACOCTGTTTG CGTAATGCTA ACCACATATT GCACTGTGCC AATGCAAAAA 240
 35 AGCCCGATGA ACAACTGCAT CATCTTCGG TGGCTGTGC TCATCCTATT CGCCGGCTCT 300
 CCGGTGAAGC CCCATAGTCT GTGCCCCAT AGCACTGGG ACGCCAGCAG TCCGTTAAGA 360
 AGCCAGCTAT GCATGGCATA CCAGTAGTCC GACCACCTA CCGACGGCT CACCGGCTG 420
 40 GACGTGTGCG CTTCATTCTG CCAGAGCAAG TCTGCACAAC CAGCGAGAGT ACTAGCGCTG 480
 TATACCGGAT GCAATTAAAC ACCAAGTAGC CTTTGGACAA TGCTCTTGG CTCTGCGCT 540
 TCCAGTTGAT CCATAGTGGC GGATACATCG ACACCGACCA ACATGTGCG TACAAGTATC 600
 45 CGAGCAACTG TCTCTTCTC ATTCCAGCT CGTTCCAAGT GCTTCTACGC CGGTCTTCTG 660
 GGTTCAGAT 669

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1082RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

	GATCCACGAG CAAACTAATTA TTAGGGGCCC CCCACCCAG TCTGCAGCAT TCGAAAGCCT	60
10	TCCTAGCCTT TGTCGATGT OCCAAGGTAC AATTTTCTCG CAGCTGAAAA TACGAAAGAA	120
	GCGCCAAGAA GTGGCCTTCT TTGAATCCAA CGCCGACGCC AATGATGTG AGGCGGGCGA	180
	ACATTTTATA ACAGAGCTCG ATAAGGGCGA TAAGCGGCTC GGCTGTGTTT CTTGATOGG	240
15	CTTGATATGC AATANAATGC TCGGACAGG TATCTTTGTC GTTCCCGCGA ANATCTTOCA	300
	GTTGACTGGC TCAGTATACT TTGCGCTAGG GTTATGGGTA CTAGGAGCTT TAATGTCTCT	360
	AGCAGGTCTT TATGTTTACA TGGAATTTGG AACTGCAATA CCGCGAAG GTGGCGAGAA	420
20	GAACTACCTT GAGTTCATCT TCAAGAAACC GAAATCTTC ATTAAGTCAA TGTACTCAGC	480
	ATATGTCATC TTTTTAGGCT GGGCCGAGG TAACTCTGTG ATGGCAGCTG CAATGTTCCT	540
	TGATGCTGGA AAGTGAAG CAACACGTTG GCGTTGAAG CCGTCTTGA GTTGCGGTCA	600
25	TTTTCTTCTG CTTCCTTGTC AACTCTCTCA GTGTCAAAGC TGGGTGTGTA CTTC	654

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 680 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1082UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

40	GATCCGCAGC TTCCGCAAGC GCGCTTCTC CTCGGTGAC TCCTCGTGGT CGTCGTACTC	60
	CGGCACCATC GACGCTCCG GCTCTCTC ATCCGCGTC GCGTCTTCT CCTCGTCCAC	120
	CGTCTCCGC AGCAGCGAGT CGTCCCTGC CCGCTCTCG TCGTCTGC GCTCCAGCAG	180
45	TGCGCCCGGA AGCGCTGCT CGTCCGGAG CGGCCGAGG TACGGTACT TCACCGGCC	240
	CATCTCCGC TCAATCCGC GGATCACCAC CTCCGCAGC TACCGTCCA TGATCTGCGC	300
	ATAGTGGTAG ATTTCGACT CCTTCGTGTT GTACATCCG GCGTCCAGC TGATCCGCAC	360
50	CAAGTGGTTC ACGAACTCCT GGGCCGCTT GTAGTGGTGT AGCTTCTTTT TCACCGTGC	420
	GAGGCTGAGC GCGTCTTGA TGATCCGTA GTAGTGGGA TAATCTTCC TCAGCGCAA	480
	AGTGTAGAAA ATCGCAAAA TCTCAATACC ATTTTCTCTC TTAAAGTCAA ACACGCCATC	540
55	CAACAAACT TTGAGCTGGT CCGTAGCAA CATCGTTAGC CCTCGCCACC TGAAAGCTG	600

AAGACTTTGG TAGTGTACTA TGTGTTCCGA AACAAATCC CACGGTCCGT TTCTGCCCGT 660
 TCACAGCCTT GCTTCAAGTT 680

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 613 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1083RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GATCATCAAT TTCTTTTGG CTGTTTCTT ATTTACAGCC TCTATTTCTG AGCGAACATG 60
 CGACGCCACA GCAGTCTTAA TGAGCTCATC TGTTAGTTGG GTTGCAACCG CGTTACGCAG 120
 TTCATTCCCT TCTATTGCTT TGGAGCCAGA ATCTCTAGCT TCATCTTGAG CGCTAGCTTC 180
 AGTTTGGGCT CCCAGTTTAA AAGCTGTTG GTTAAATGA AAAGTATTTT CCTCTTTTAG 240
 CTGGGAATTG CCAGCAAATG GTTTCTGTG CGATGACTCA AACGGTACAT CTTTTTTAGT 300
 TTTTGTTCCT TCTAAAATAT GCGGTGAGGT TGTAGAGCCG AACTAGACA TAAATGGTGC 360
 CGTAAACTGT TTOGTGGACT GCAGATCAGA CTGTGCTGT GCGTTGAACT GCATGCTAGA 420
 TTTCACTTCA CTTCACGCG GGGATTGGGT AGTGGGTTGG GTAGTCTTAT AATCTCCACT 480
 ATCGAAGTTG AAAGTTTLAG ATATATCCTG GTGTCTCCG TGCAAGGAAG ACCCCTGCTC 540
 AATGATGCTT TCCGAATATG TGGGTAGATT TGAATCATTG CTCCTAGNA GCAGCATCAT 600
 CCTCCGAAAG AGA 613

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 656 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1083UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GATCCTGAGC GGTGCGGACG AGGAGGAGCG CGAGGAGGAG CCGGAGGCGG TTGTGGGGGA 60
 AACCGTGAGC CGCAGCGCGA CCGCGGCGAC GAAGGGGCGC TTTGCGGATG AGGAGGCGGA 120

GAAGGCGGAA GAGGCGGCGA CGGCGCGCTC GGAAGACGAG GAGGCGCCCA AGAAGGCGCG 180
 GAAGTAGCGT AGATAGAAGG ATATAACTGT AAGTAGCAT GCAAGACGAA TCTGAGGCGG 240
 GGGGACGCGC GCTGGCGCGG CGCGCGGTA GCTGGCGAGG GCAGAAAAA TCGCGTCTGA 300
 CAATCTCTGC GTCATCATCC CGGCCAGAGG ACAAGATGCG TGGCAAGAAG ATTGCGGGTG 360
 TGCTAGGCGC GACGGGCTCC GTGGGGCAGC GGTATTATCT GCTGTGGCG GACCACTCTG 420
 ACTTTGAGCT GAAGGTGCTT GGGGCATCGC CGCGATCCG TGGCAAGCGG TATGCGGACG 480
 CGGTGAATTG GAAGCAGACC GAGCTGATGC CGCGTTTGC CGAAGACATC GTGGTGAGCG 540
 AGTGCAAGGC TGAAGCATTT TCGCGCTGCG ACGTTGTGTT CTCTGGGCTC GATGCGGACT 600
 ACGCAGGCCC CATCCAAGCG GGAATTTGCC GACGCGGAC TGGCTGTGTG CTGAA 656

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 453 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1200RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GATCGCTCAT TATTTTGGT CGGAGCTGG GCGCTCTCT GCTTCTCTC AAATACCTTC 60
 AAATTTTGGT CTATATAGGT CTGCAGCTCT TCCTTCTTC AACATTCCGC CTGTGAAGC 120
 TGTTGAAAT ACTGCAGGGC CTCTGCACTC ATGCGATTCA CCATTGAATT GCGCTCTTGT 180
 ATCTCTTGCT GGAAGTGTTC TTGTTTGGG ATGGCGTTT GCGCGAGTTC AGCTTGCAA 240
 CTGGTGTAT CAGACTGGTC CACTTCATCT TCACGTCOA GTGGATCCAT CCTGCGAGT 300
 AGTCTAGGTG GAGTGGTCTA TGTACAGTGC TGCTGTGGT GTTAGCGCGC TCACCTTCTG 360
 CGACTGTTCA AAGATGTGCG TTTCAGCAA GAAAGAGAC AACCGAAGT ATAAGTACAG 420
 CACGCGAGCC TAATTTTGTG AGCTTGCGGA TTT 453

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 590 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1200UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

5 GATCAGCGAG CTAGGTACCC GGACGAACAT GCGTTGSGC AGCTTCCCAT ACTTCAGCGA 60
 CCGTGTGTGT AGCGCAGAGC TTCGGTCTTG GAATAGCGAC TGCACCTCTG CGTTCAGCAG 120
 ATCGCCCTCT TTCAGAAAGC TGGCATCTG CAGCTCATCG CTCTCAGACT TCGCCGCGAG 180
 CACGCCGCGG GGCAGGTTCA CAGAACCAG CATGAGCACT GYGTGCTGCT TTCCGYCAAT 240
 10 ATCCACCTTC CATCGYTTGT TGGGACCTC CACGATCCTG CCGACAATGT GGTGCGCCGT 300
 CTCTGGCGTG TACCGCCCGC GCCAAGGAAT CACCGACAGG AGTCGGTTCA CCTTGGAAAC 360
 GGTGYCCGCC ACCCAAGAGT ACGTTTGTGT CTCAGGAAG TATGTGCGGT GGCTCGCAT 420
 15 CCACACAGGA TCATCTGTAA TCAGCTCTCC TGGGTCATA ATCACCGAG AATCCGCTCC 480
 TTCCATCTCC ACGTCCAAAT CAAACTCTTC TTCTCATCG TCCAGGTAAT GGCTCCGATG 540
 GAACTGAAAC CCACGCGCT TGGGGATCGT TTTTACCTCG CTCATTACTG 590

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1201RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

35 GATCTTCGAG ATGAACCCAA TATGGAACAC GGGCTTGGC AGCTGATGT GCGGGAAGTG 60
 GCGCGGCGAG TCGTTCATGC CCGGCCACA CGTCTGACAC TTGAAGTTCC GGTGATGGA 120
 GCGCAGCCGG GGTGCTTCA GCGCTCCAC CTTTGGCGC ATCTGGTCT CTCCATCGT 180
 40 CTCTGGAAC TCAATCTTGG CCACGAAAT GCGCGCACC TCCTGGGCG AGAACAGCCC 240
 AACTGCAAC TCCTTGATGG TCGCAGAGG CCGCTCGAA TACGGAAGT CCACCATCGC 300
 TGTGTCGTAC TACCGCTCCC GGAGATACAC CGTTTGCAA GTGTGTGT GTACCTGACG 360
 45 CCCAGCCGCC ACTCGCAATC CTCGTTTACG CCGACCGCTT TGTTTGGCTC CCTTGGCCGA 420
 ACAACGAAGC TCTGTATAT GTGCGGCTC GAGACCTAA GCTGCTCT GTGAACACA 480
 CGCTCAGCC CAGAACTCG TGTCTTTACC TTGAGCTCT GGAATTGGT CCGCCAAAC 540
 50 CNGCTTATTG CTGGGGGAA CNOCTATGCT CCGTGINATC TCAGCTGGAA TNCACCANAA 600
 ACNGACCCCC CACCTACCCC NCAACTCTGG TTATTTGATT TTGCGGGGAA TAAACNCANT 660
 GTTNCATC CTTCACCCC CAACTGTGT NTCNCTGTT CNGTNCNTN TTACTIONA 720
 55 CCTCCNACN CCAATTTTTT TTNCCGTTG CCT 754

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 643 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1201UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GATCCTCCGA	TTAGCCTCGT	CTTAAACTC	AACCAAGCTG	CTCTGAAACA	AACAACAGT	60
ACCACTTCTG	TGTTGTTTCT	CTGCGCTTGT	TGACCGTCCC	GCAACTACTA	TGTCGTTACG	120
TGTTTTTTTT	CGGAAACTT	GCCACCGTCT	CAGAATCAGA	GGCTGTGAGA	TTCCTCTGTC	180
GAATATCGCT	CTGGACGTTT	GCTTACGTGC	GCCCCGCCAG	TGCTCTTAAC	CGGCGCGTA	240
GCCCCCGGCC	CTGGCCGGTA	CCAACAAGCA	TGGCAGGAGA	CACAGAGTAC	TACAAGCAGG	300
CGGTGGAGGA	GTAAGCGGCG	CTCAAGCAGG	ACACCGACCC	GGAGGAGTGG	GACAGGCGGA	360
TGCGCAGAC	GGGCTGCTAA	GTCGAGAATA	TGGCGCTGCA	GCTGTGCCAC	GCGGAGACCG	420
GGGACTGGCG	GGCGTGGCG	GCGGACATGG	CGCGTTCAA	GGCGTGTGG	GCGGCGCAGG	480
CAACCGCGAG	CGCGTGAAGC	ACCGTGGACG	GTGAGCTGG	GGCTGTAAAT	AGGTGTATCT	540
GGAGCGGTGT	CAGTTGACA	CTGGACAGT	TACGAANCAT	TNTCNGGGIN	GCCNCCGGA	600
ATGCCANCC	CCNATCTNAN	NACCCAAACN	GGGATATGAT	NIN		643

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 735 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1202RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GATCGAAAC	GCTGCCACG	AAAGCTTGAC	ACTGAAGGGA	TTTGAGTATT	CTCTTGCAIT	60
TTCCAAGGCG	AATACCAGCT	TGTCACAGC	TGCGATCCA	ACCTTCCCCT	CCTTCAGGCG	120
CTGCTTGAC	CTGTGCTTA	TCTGCAGCTG	AGGTAGCAGC	TCTGTGATCA	GCAAGACGAC	180
GCCAGCGCA	GAGGTAAAC	CTTTCAGAAA	GCCCTTTGAG	ATTGCATTGT	CGATGAAACC	240

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GAGCCTGAAG ATGCCCATGG CGAACACCAG GACCCCTGAT ATGCATCOGA TAACCGCAAC 300
 GGTCAATCAAC GGTTCAGCG ACTTGTGCGC CCATGCATCG CAGCTCTGGC CCACCACAAG 360
 5 GAGCGCAACC GTCTGCGGCC CTACAACCAT CGTCGGGACG CTGCGGAAGA CTGCATATAT 420
 CAGTGGGGGG ATCAACAGTG CGTACAGCCC TGGCTATGGT GACACATGTG CCATAGTGGT 480
 CAGCGAAATG GCCAGCGGTA TCTGGAATGA CGTCAGCGTC AGCCCGAGCA GCATGTCTTT 540
 10 CGCATTTTCC CAGAATACTC TGSCAGCCAG CGTATAATGG GCCGTAGTAA GACNCATAAA 600
 ATTNTTTTCC TNCCTACCGT TGTCNNTTTA TNGNCTGTAC CCNTACGAC TTGTCAAAAG 660
 CAGNINCCCC CCGCCCGGAG ACTTCCANCC CNVCCCTACT CCCAATTTGG ACCANGACCC 720
 15 GGTTCCTGGT GCTTN 735

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1202UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GATGCGCGCC GCGCCCCAGG ACTACGTGGA CTCTCTCTCG CTCACACAG TACTGGACGA 60
 CCGCGAGCAG CCGGAAGCGG ACTGCGTGA GCACAGCTAC ACGCCCGATC CGCTGCAGCT 120
 35 CGCCGTCTAC GCGCAGCGCC AATGAGAGCT CATCGCTCCC GCGCAGTGGC ATTTTCTTGC 180
 CGGCGCGCCG CAGCGCTCCG CCTGGCGGTC ACCGAAGGCC CAGCGATGAC AGCCAGCGTC 240
 CAGGATATCG TGGTGCCAC CGCCGGGAC AGCGCGGCG GCGCGACGG GCGCCCCAAC 300
 40 CAGGCGGTCA CCTTCCCGT CGCGCTGAC AGCGGACCG GCGAGGTGCT CGTGCGCAAG 360
 GGCACCGGCA AGACCCCGT GCGCAAGGCG CAGACAGAAG AGCAGTACTG CGAGCAGCTG 420
 CAGCAGTACT TCGAGCGTGA CGCGGTTCC GAGTGACGG ACGAGGCTG GCTGACCGC 480
 GCGCGCGCCG CGGCGCGGC GCGCACCAAG CAGGAGCGCC AGCGCTCGC CCGCGTCTA 540
 45 CCAACGCTC TACTTCTCG CGCGCGTGG CGAANCGCC GCNNTGCCC GCGACTGCTG 600
 TATACGTTCC CNGVTCNGG CNGCTNCNA TNGCGCGG AANTNCTNA NCTNNNNCT 660
 50 NNNTNNNN GACCCNNNN CCTTAATTT TTNNTTNNN NNNTTNTCTT TCCCCCTCC 720
 NCTGTTACCC TCNCTNCNT CNGGTTNNT CNGTTGGTG NGCTNCTTC CNVNTC 777

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1203RP

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GATCAAACAG CTGCAGTTGT TGAAAAGGTT GCTTGAATCC AAACCAAGGA AGGACGTATT	60
TTCTGTTTCTA GGCTTGATA ACTAATCTCT TCTCCACTCT AGCTGGGGAT AACACCTGCA	120
15 GGACGTGAAC TAACAAGTTG ACTACTATAC AGCAAAATAA CTGGAACAAG TTATACAGAA	180
TTTTGTAAAT ATATTATAGC AGCCCTATTA CTATAATTCC ATCATTGTGT AACGCTTTAG	240
CCTTCGTTCT CAGACTCGTC GTCATTTTCT TCATGATAGT TGATATTTTT GCGTTGCCCT	300
20 GAGCTTTTCC TTAGTGGGOC TGCAATGAGG CTCTACTCT TTTGGCTGTA GTCACTGCA	360
GAGCTTGGTG TATCTTCGTC CTGCTTCCC TCATCGACAA CTTTGCGCTT CTTCTTAGTT	420
TTAGATGAGG CTGATGATGG CCGTTGGGCT TCTTGAATTC TCTTCTCTG CCTTGGGGA	480
25 TGTGAATTG GCGGATTAG AGAAGCGGA TACTTTGGCC CTTATATTTA CTGTCAAGTT	540
TTCAACATGC TGGTCTGATA TATAGCTCAT GAAAGCGTTT CTTTGCGCTT CTTCCCATAT	600
TGGGGAATGG CTGATAAAGT TCAGAAGGCA GATTAGCTCC CAGGTAGACT GGTAGATTCC	660
30 ACCCCCGTTG GTTTTAGCTC AAANATNATC AATTGGCAAC CNGCTAGANA TAATNINIGA	720
ACATATGCTC CGTGTGGGAT CCGTTGGGAT CTTCCC	756

(2) INFORMATION FOR SEQ ID NO:214:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 781 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1203UP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GATCATTTGC TGCTGCTCG GGGAGACCAT CTGGAATGC GACACTGTGT CGATGTCTGT	60
50 GCTCGGGAAG ATCTTCAACA AGTTTCTGAC ACACGATTTT GGCCCGCTGC GCTCCCTGCA	120
GGCTCCGCG CGGACCCCG CCTTTGATTT TTCTCTGAG ATCTGCCAGT CGTACAGTAA	180
CCGACTCGGG CGGCAATTCA CGAAGTTCTA CTCCGAGATC CTGTACGGGA TTACGAACCC	240
55 TGGCTCGGCC GGCTCAGGCG AGACCGGGG CCTGCAGTCG AACTTGAAGT CGGAGTTCAA	300

GACTCTTCTG AAACTGCATA AACTTACGGC CAACATATGG GAGCATGTGC CGGAAGTGGT 360
 GGGCTCCGTC GTCCGATTTC TGCATCAGGA GTTATGCTCA GACAATGTGC CGCTCCGAAT 420
 5 TGGGGCTACG CGACTTGTAG GTGATTGTGT AGCCGCACCC TCCGCTGCCA ACTTCGTAC 480
 GATGCATACG GACACATATA ATGCTTGGAT GTCGAAGATA GCGGACATAG ACGCCACGGT 540
 GAGGCGCGAA TGGGTGAAAG CCATACCTAA GATACTGGAT AACAGTCTGA TTTGGCAACA 600
 10 GATATCTGCA AAGGCTCAAC AAGACACTAA TGGATACCGA CGATGTGGTT AGACTATGCA 660
 GCTTAGAAGC GCCTGAAAGA ACTACAGTCC CCACGATTCT GGGANATCTC AAAATTCCAC 720
 TTNTCCNAA TTGTTGGGCC TACCCAAANA AAACNAANCT TAGGAACTTT TCATTTGTAC 780
 15 C 781

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 765 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1204RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GATCCGCTTG GCTAGGTCCT CAGCCGGCAT GTGTCACGG TATAGGGCCT CGGAGCCAAC 60
 TAGGAAGCCG CGCACCGTGT CGACTTGAT CCATGGCAAG TAGGTCTTGA GGCATCCTT 120
 35 CTCCATCGAA AAGTAGCGT CGTCGTCTGG CCAGACACCG ACCCATAGCT TGAAGCCAGC 180
 ACGGTCCGCA GCAGGACCA AGAACTGCAA CGTGTTCAG TCAGAGGTAG AGTAGACTTT 240
 GACCGTGTCC GTGTAGGGC GCAAGGCTC GAAGTCGTG AGGTAGTCTT GAGTGTACTT 300
 40 GCAGGTACCG TGTGCTTCT TCACACCTAG GTTGAAGGCC AAATCGCCA TAGCGTGTAC 360
 AGACGAGGCA CCAAGCAGAG CTGCGGAAAC AGTGGCAGAG AAACGCATAG CTAACGAATT 420
 GATGGTGAGT TAGTCTGGCT AAAGTGGCTT GACTGGAGA AACGACAGAG AGGACAAAT 480
 45 ATATGTTAAT ACCAGGTCAG CGCCATCTGC CGAGGAAAA AGAAATGTGC CGCGTGTTC 540
 CGGCACCTTC CTTAATTTAG AAGCAATTAT TATCACGTGA ATATCACGTG AAACACGTTA 600
 AGCCTACAGA GAGCTATTGA CGGTGGCTCG GAACACGTTA GCACTGAGTT ATGTACTAAG 660
 50 GTGGCCACGC ACCATGCAGC TGTCTCGAT GCAATATAAC CCCCAGGCC CCGGCAGTCA 720
 ACCGCCATCA AAAGTCTGNN CCGGAGNNC CCTCAATGT CCNTG 765

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

EP 0 866 129 A2

(A) LENGTH: 776 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1024UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GATCAGGAAG CAATAGGTAC TCAATTGOGG AAGATTCAGA GACAGCAAAG GTCAAGTGCA	60
GTTCAGCAAC ATOGAATCCA CACAAGTTAT GTCGTACAGA GGCCATAACT ACAACGCAAT	120
GGCACCCGGG GGGCAGACGT TCTCCAACAG TOCATATACG AGCAATATGG GGTCCACGGG	180
GGCTCGGGGG CGCAGCTCAG AGCTGTTCCA GAAGTTGAG CGATTTGCGA AGCGCATAGA	240
GGACGTGACG GACCAACCGC TGGTGCAGCG GTTCGTGCGG TACACACCGC TGATTGCGCG	300
GTTTPTTATT GTGGCCAGT TCTACGAAGA CTGATCCCG APTCTGTGCG AATGGCCGGA	360
GCAGGTGTG TTTCTATCCT ACTACCGCG CTACCCCGA GPTTTCGTAG TGCTGTTTTT	420
GATGGTGGTC GCGGTGCTGA TGATGGTGGG GGCCACGATG ATCCTGCTGC GCAAGCAGCA	480
GCTGTATGCG ACTGCGATCC TATGCGGTG TATCATCTCC CAGGATTGTGT GTACGGGCTG	540
TTCTCCGGCA CTCTTGTGTG TTGCGGAAT TTCAGCGTAA TCGGCGGTG CTGATTACTT	600
CCGTGACTCC ATCCGTGCAG AAGCGCATCA CATTCGGCAT GCTGCCGGAG CTAACAGCAG	660
GAAGGGCAC CAAGGCTACA TCTGCTTGC GCGCGCATAT CATAGTCTTA GTTTGTGACT	720
TTACCTCCGC AAAGTGGTGA CGVTCTCTCN OCTGCGNAC GGTCCTCCCC TCGGIN	776

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1205RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GATCGCACTT CAACCCATT C AAGAAGACG ACGGCAGTCC GGAGGACGAG AACCGTCACG	60
TGGGCGACAT GGCAACGTG CTGCGGACG CAAACGGCGT GCGGTAGGA TGGCGAAGG	120
ACCTCTAAT CAAGATTTTT GTTCTACGT CGATTCTGGG CCGTACGGTC GTTGTCACG	180
CCGCAAGGA CGACTTAGGC CGCGCGGCA ACGAGGAGTC GCTAAAGACG GGCAATGCGG	240

GCCCCAGACC TGCTTGCGGC GTGATTGGCA TTGCCAACTG AGCTGGCTGC TGCCGGGTGC 300
 CGGAAGCTCT GGAAGGTTGC CAACTAGAAG CTCTGATGAC TATGTTAGCA GAATAAACGT 360
 5 TTTATGGTTC GCTGTGTTGG CGCTGTATGT TACAATTGCA GCAATTAGAA GTCTGCTCTC 420
 GCGCCCGACG GCACGCTCGG CAGCGAGTAG CTTGGTAGGA TGTTTGCGGC CGCCAGCAAC 480
 AAGCCGAGGA AGGGCTCGGA AGGGTCTAG CACCTTGGAC ATGTTACTCT GGTGGTACT 540
 10 GGTGGGAC GTTAGTAGGG TTGGTCGACG AGCTCGAGAA TCTCGCACCG GTGCCGTCTC 600
 GTCTCTGCC CCAATTACG CCAGCNCOCG ATTTCTGCNC ACTTTGGTTG ATCCCTACN 660
 ATGAAATNTT CCCCCAAAG AGCTGCGGT TATTTCTNAN ATGACATCGG TTCCCCGAA 720
 15 AAGTGTCTAA ACATCCCTGT CCCCCN 747

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PAG1205UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GATCTTCAGG TTCCGCGACA TGATTATCAG CGAGATGGGG TGGCTGGCC GCGCCCCCGG 60
 CTCCTGCACA CGCTCGTGA ACTGCTCCCG CTCGGCAGG TCTCGGCA GCACCGCAGA 120
 35 GATCATCTTG TCCAGCAGGA TGTCATGAA GTGCTCTGC TCTGTACTT GAGACACCGC 180
 GCGCAACTTG GCGCGCGCT GCTCTCGGT ATCTCTCTG TCCGACATAC CGCGCCATT 240
 GTGGCTGGTC TCTCTCTGC AGAAGCTGTC CGCGCTGCTC TCCAGCTGCT GCGCAACGC 300
 40 GAACTCGTCG AAGTCGTGT CGATTGTTT GCGCTGCTG TCTTTGCCCG TCCGCGCGG 360
 CTCCATGTC GGTGCAACA GTGAGCAGC GATGTTGGTC ACCAGCTCCC GGTTCGTGAC 420
 GCAGGCGCGC GCTTTTCAT CGCTGCCAC CTTCTCTCT GCTCATGA TCGGTTCATA 480
 45 CTTGCGCGC AGGAATTCCC CCAGCAGGA AGCGCGCTC TTGCTGCCAA TTGCAACGCT 540
 CTCAGCGCC TTGGTCTATC GTCTCTCTC ATCGGTCTC CGCCCCACG TCATATAGAT 600
 TCGGCTCGC GGTAGCACAC TGGGAAGGC TGCTTTGGT ATATGCCGT AGAAGCAGTC 660
 50 TCGGCGTCA GTTAGTCTT TGTGATGAT GAGTGTCA CGATGACTG GATATAGAAC 720
 AGTCATCTAT CGATTGAGAA CATAGCTATA TAGAAATGAT TTAGTGAAT ATATCGA 777

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 751 base pairs

EP 0 866 129 A2

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1206RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GATCGCGTCC	GTCGTCGTGG	GCTCCTCGTC	CTCGTTGAAC	TCCGTCCACA	GCTTGAACGG	60
CCGCGCGGAC	AGGTCCACCT	TGCGCAACGT	CTCGGTCACC	ACCTCGGFTC	CGAACTTCAC	120
GGACTGCGCC	TTTCATCCGT	CCATGAGGTC	GCTGCCCCGT	AGCCCGTCCG	GGAACCCCGG	180
GAAGTTCTCA	ATCTCCGTGG	TTGTGTCAG	TTGCCCCGCT	GCAGCCACTC	CGTTGCGGAA	240
CATGCCCTCG	TACAGCGTGG	GCTTGATCTC	CGCGCGCGCT	AGGTAAATGG	CCGCAGTGTG	300
TGCGGCAGGG	CCGGAGCCAA	TGATCGTAAC	TTTGTGATGC	ACCATTCGTG	TCTGCAAAGC	360
TTGTCCCAAC	CGGTATCTTG	TTGCTGCTGC	TAGCATCAAC	TGTGCACCGC	TAAGTTTCGC	420
TGCGGCTTGC	TGGTTTATA	CCTCTGGGCT	TCACCATCGG	TGAACCTTGA	TGCGCGTTAC	480
TATTTCCGAC	GCTTATGTCC	GCACCTGACA	AAATCGGCTT	CGCGGGTGGG	CGACTGCGGT	540
CAGTGGGGGG	TGCAGTACAA	GATACGCACC	GCGGGCCTNT	NGNNNTCNC	GGCCCTCTCN	600
GNCGCCCGCC	GNCCCTTCNC	AGGATCMTN	CCTCANCTAN	AACNNGGCC	GGNNGNNTCT	660
TTTTTTTGTN	CNGCNAACGA	AGGCAATNNA	ATNTTTNNIN	GGNCNTNNGT	TNGAANTGTC	720
CNNCNGTGGG	CATCGCNGCT	TATNAACACN	C			751

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 778 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1206UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GATCGGCTGC	TGTTGCACCA	CCTGCTGCAG	GTAGGTTGCT	ACTCCACGCG	CGAGATATGG	60
GTCCTGGTCA	ACATCCTACA	GCTGACCTGC	TTTAAAGAGA	CAACCAAGGA	CAAGTACGAC	120
CGCCGCATCA	TCAGTTGGCG	CGGAACGGTT	TGACCGGCC	TGTTCTGCAGA	TAAGACCTTC	180
GCTCAGGAGT	TTAACTCCAA	ATGTTCTAAC	TTTACGACCT	GGTGGCACCT	CATGGCCCCG	240
CTAGACCACG	CTGTTTTTCAT	GTGGTGTCTA	GACATTATCG	TGGCCGAGAA	CTCACAACCC	300

TTCAAAAGCA ACCCATCAT CCGGATAAG CTCAACGGCA AGGACTGGGA CTACTACCGT 360
 GATCTACAG TTGTGTTCAN CTATAGGATT ATCTGGCCCC TGACTCTTAC AGTGCTTCTC 420
 5 AGCTATCATT TTGGCTTCAA TAATCTCTAC GACCTCTCTT TTGTGACCC AGCCTTCCAG 480
 ATAATAGGGC CCGAACAAGC GACTTGGGGG ACGTGCATGC AACCTTTATC AAGAAATGGC 540
 ATCACAACTA TAAAAAGTTC TAGTTGCTCG ACTTGTAAATC TCATCTCTAA ACATAATATT 600
 10 CTTTTATATG CTGTATTAC TTANCTCAA CATGATNACN TATGCCTGGA AGATTTCNC 660
 GNTGGCCGIN AGAACNGATT TGGTCAACT TMTATAAAC TGACCCGTC GCCCCCTCCG 720
 TAACCCGANA TTCTCTGAIN CMTGATCTTA TGANGATGCC GGCNCATTNN CANTATTC 778

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 756 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PAG1207RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GATCTGTTC AAAAATTGGA AACGCTTACC ACCTCACCAA CACACCAGGA CTTTATTTTG 60
 TAGAAACAGG CGATCGGCTT GAACAACAGT CACTAGAAAC GGTGCACCAA GGCAGCTTGG 120
 CAACGAGGAG GCACCTAGG GCTCAATGCG TTGATAGTAA AGCATGTACA CGAGCTTTGT 180
 35 CTCCGAGAGA AGGAACGAGC TCTTGCACTC CGACACGTAC GAGTCTGAGA TACACCACCA 240
 CGGGTGGTA GTGGTGGAC GTAAAGCCTT CAGTTTGGCG GACGCGCCTT GGGGACGGGG 300
 GAGTACCTTC GTGGCAGCG AAGATACGCC CGATGAGCTC GCAGAGCTGG CTCCGAGCT 360
 40 GTCTGCTCG GCTGACGGT CGGGCTTGA GACGGTCTT TCGTTAGTA GTGACTGTG 420
 ATGGAAGCTC CCCAGTAACG GTCTTGAGCA AGCGGCCATC GCGCCAGGCG GAAGGCTTCC 480
 AGCTGGCGTA GGGCACAGGC ATTGAGGGG CTGGCTGCGG GACGGCTCC GACGAGATCA 540
 45 CATCTGAGCG AATGATATCT CGCCGTCCTT TGGTCTTCC TAAGTCAGTT TGTGGCGAA 600
 CATGCGTTAT GCGCTGAGAA TGGTGGCAT GTGCTTGATT CATGCGCCAA CAGCTTATAG 660
 CGAATGCCAA ACCCCCACCA TTGTNTTCCC CACACTGCT CMTGAGACAC CCCCCCGGA 720
 50 AANINAATGC GGTNTTNTTG TTAACCCCN TMAAAA 756

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 771 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1207UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GATCTAATGA GCGATAAGTC ACCGGTTATA GAAAGTTGCG CGAATCCTAC AACTGACTCC	60
AACTCGCCAC AGGAGATATC TCTATTAGAA AAGAATATCA AGGATGTCAT GCGTTCACCTA	120
AAGGGCGTTG ACACGCACTC ATGTGAACAG ATCATTAACG AAATTCTTGT GGTTGATTAC	180
GATGTTGAT GGAAGATAT AGCTGGTCTT ACAATAGCAA AGAAGTGTTC GAAGGAAACA	240
GTGTTTACC CATTTTTGCG GCCAGACCTT TTTGCGGGTC TCCGGGAACC TATCTCCGGG	300
ATGTTGTTAT TTGGACCTOC AGGAACAGGT AAAACGATGA TTGCCAGGGC CGTTGCGACT	360
GAATCGAATT CAACTTTCTT TTGCATCAGT GCTTCCCTT TGTATCGAA ATACTTGGGT	420
GAGTCGAAA AACTTGTCAA GGCTTATTT TACCTAGCCA AACGGCTTC CCCCTCAATT	480
ATATTCATTG ACGAAATCGA CTCTCTACTA ACTACCGTTC AGATAATGAG AACGAATCAT	540
CCAGAAGATT AGACGAGCTC TTGGTCCAAT GTCCTCCTA ACGAGCGCCA CGGCTAGGAA	600
CAGAGAGGCG AAGAGGCCAG ACGGTACTG TCTTGGCGC AACCACTTAC CGTGGGCAAN	660
AANGANGCTG CNATAAACTT TTTACGGGT CTATNATCCC TTGCCGGAAT ACAACNAAAT	720
GTCTTTGAA AACTTNTGGC CTCCAAAAAG AATTTCGAAC TNATTNNNN T	771

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 740 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1208RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GATCAATTAA TAAATGSTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA	60
CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT	120
ATTGAGTTTA TATTAAATTC ACCACCTCTT ATTCATTCAT TTAATACTCC TCTAATTCAA	180
TCTTAAATA TTCTTAATT TTAATTATA TAATAAAGT TAGTGGATAT AGTTTAATTG	240
GTAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAA ACTGAATATC TACATATTAT	300

ATCATTAAATA TAATAACTCT TTAATTAGAG TTGGTACCAC AAGAATGCTG AAAGCAITTAG 360
GGGTGTGTAC CTTAGCTCTC CTAATTAAAG TTTATAAAAT TATCCTTAAC TAATAAAAAT 420
5 AATTAATTAA ATAAATAAAT AATTAATTAA ATTTAAAATG TTTTAAAAA AGAATAAAT 480
AATATGTTTA TATTTAAATA GATTCAAATT TCCAACAATT CCCATTCATT TAGTACTACC 540
ATCACCATGA ACAATTGTTA CATCATTAGT TTATAGTTTA CTACTACTAG CTACTAACA 600
10 TGGTATATGG TATAATANCC CTAATAAACC TTATANANIT TTTACCNAAC TTAGATTAAA 660
AAAAGGGCGA NCNCTTTTGG NGGACCCCTA CCCNTAAAAG GNGTAATGGT TCCCCAATTG 720
GTGGCCGAAA TAANTTGGCC 740

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 782 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1208UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GATCTTAATT TAAATTTTA ATTAACTATT TATAATTITAG AAATATATAA TCTAGAGATA 60
30 TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120
AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA 180
ATTTTTATTA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240
35 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTTAATATT 300
AAATATACCA TTITTATTA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA 360
ATTTAATTTA TATAAATTAT TTAATTTACT TCCCCTGATA TATATAATTA TTAATGTTT 420
40 CTTTCATAAT ATTTATTTT ATTAGICTAG TAATATTTCT ATTTAATAGT CTACCCCTTT 480
AATGGATAT TACTACCTAC TAAATATTTA CCTAATAAT ATATTATTAA GAATACTTAA 540
TCCTAATAAT TTATTATCT AGTTTATATA AATTAATTAA TCCTTTTAT TATTATTAA 600
45 ATTATTATTA ATTAGTAATT ATATTATTA TTTTATTAAC ATAATTTTG ATAATATATA 660
TCCATATAAT GGTATTTATT ATATACCNIN ATGAATTAAT GANAACCCCTA TATATGANAT 720
TAGTTATAGT GACTTAATCC CNATCTCAAT ATATATAATT ATTATAGAN ANTACTTTT 780
50 TC 782

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 base pairs

EP 0 866 129 A2

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1209RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GATCAGCCTA TGTAGCAACT GATCGGCGCT GGTCCGTGTC AAACGCCGAA AACACCCAC	60
CAGATTACGC AGACACTOCC ATATTTTGAC CGACTGGAAC TTTGIGTACA CAAAGCTATT	120
CAGCTTGTC A CTGGCCACCG TCAGCGGCAT GTTGTTCAGC CGAGTCGCTA GCGCGCACT	180
GCTGTTGCC TCGCCAGCG ATGGCTCCTT AAGATCCTGC GTTCGCATAT ATTGCGCAA	240
CTTCGATAGG TCTCGACTGA GCGAATTACC GACATGGTCC AGTAATAACA ACACCCAGG	300
GCAGCCCCC CAGCTGTAAT TCACCGTTTT GACCAGCAGA AAGTGCAATT GTAAAAGAAT	360
GTACCACTAA TGCCAGTAAA ATGTGGAAAA GACCTGGTCG TTCTGAAGAT ACGAAATCAT	420
CACCTGAAGA TTCTTCAGTC TTCTCCGTCC CGAACATCTT GGAAAAATCT GCNGTGTGTC	480
GCTTCTCTTC CACTCGAACC GCAGGGCTTC CAAGGACACT CCTTGCAATT GAA	533

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 534 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1209UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GGAGGATCGT CGAACTTGAT TATTTCTTTC TGGTACGACG ACAGCTCGTC CGGTTTCGC	60
TTTAACGCCA CCAGCACCCAC GTACTTGTTC GACCGCAGCC CGACTGTGCG GCTCCCCGTC	120
TTGATGGCCT CTAGCGCGTA CTCACCTGG AACAGTCTCC CAGTCGGGGA AAAAGTCACA	180
GTATCACCGT CGTAGTTATT TCTGAACATC ACTAACTCAC AGNGCCCCAA TTGNTCGTGC	240
ACACCGCCCT CTTTACTGGT GCTAGTTAAC TGGACAGGAG CTGTGTTTGC CACCCGGCGC	300
CGGGAAGTAG CTCTGGTATT GTCATTTGAT ACGGAGATTT GATATTCTGT GAAAGGTATA	360
TAGATGATTC CGTCTCCGCG ATTGATTTGA GGCTCGGTGC CATACTGGAG TCGTCCGANG	420
TGTCGNATCT TCTACATAAC CGTTGNAGGN CAGGGGAGAG GTTTGNNNGC GCAGTTGTGC	480
CGAGTACCA TATTAGGCGA TGTGCGGTGA AGAGSTATCT ACTGTGGTG TTAT	534

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1210RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GATCTAAATT TATCAGCCCA TGGACGGATG GATTTCAGGC AGCGTGTGCG CGCAGCACGG	60
GGCAGCCAG ACTGCGAGGT GGCAATAAT TCACATAGCA ACGTCATTA TAAACATCCC	120
AAGTCATTAA ACTTACTAAA TATTGTTGCG TAACCAAAAG CACCGTGTAT CATCATCTTC	180
ATAGTCTTAG CTGAACCTAC TGTCGCACCA GCGCTTACT ACGTATTGTA TCTCCCTTIT	240
ACAATGCTTG CCCACTGCCA GTTTTCGCCA CGGCGTTAG CATGAAGTCT TTGCGGCTT	300
TGTACCACGG CTTGACGCT GACTCTACG GGAACACGA GGTAGACGG AGTGCACCCG	360
GGACCGAGTC ATCTCGCTC GCGTGTGCC AGAGACAATT TGAGGTCCA CGGAGCATCC	420
ACGCCATGC AATCTGCCC GTAAAGTTT GCACANTTCA TCCACACTT GGGGGTTTNT	480
TATCACNCCA NCGTATCTG GTACGNAAAA NTTTTCCNIN TTTGTGAGG AAATCAGGTT	540
CCCAATA	547

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1210UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GATCGAGAAG ATGCGGGGCC GCAACGAGGC CGCCACGCC GAGCGGGCG GCNACGAGCT	60
CCTGACGCC GCGGAGCGCT ACGCGCTGGA GCAGGGGCAG GGCTTCTTGG CGCTGTCTGT	120
CCCTGTGCN GAGCGGGCNC GGGCCCTGGC CGTGCCCTGC AACGAGCTTC CGATGAATA	180
CTGCATCACC AAGACTGACT TCGACCGGCT CGCTAGCCAC GGCATCCCGG TCGAGGAGGT	240
CCACGAGGAC AGCAAGGACT GGTACTTCCA GTGCCCTGT GGAGTAGAGG AGGTTAGCCC	300

GGGCCTAGAG AGCCCCGGGC TGCAGCAGGC CCTGGTCTGC TGGACCAAT GCCTCGGGT 360
 GGCAGCAGCT GGGACTGCCA GCACCCCGCA GCGATTGAGC TTGCTGGCCN GCGGGCAAGA 420
 CTCTCACTA TTTTGCCCTC CNTGCCCCCT TGGCCTGCC CAAGCGCCCG CGCCCTCAG 480
 GCGGNGNCG GCGCNAAC CCTACCAGA ACCAAANNA CNAAGCCNCC GCGGCCNTC 540
 GGTGAAGCGA ACCCTTTTIN NCTCTGTCT TCCNCCCTG AAAGACCTAN TTCTCTTCA 600

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1211RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GATCTCTCC AGTAATGGCG TCAGAGCACA CTGGTAGCG ACCCTGCCA GGTAGCTCAT 60
 CGGCAAAAG ATAGCAGCG TATGTACCA CCAGCGAGC GGGTGATAAG GAACTGGTA 120
 CGGCAGCAGC CATAGCTCTG GTGGCGCTGG GTTCAGGCC TCCACTTGT ATAAATTGAG 180
 CACGAAAGC CACACTTTAC CCCAGTAGG CGAGCCAATA GCACCCCCA TCGCAGCAG 240
 GGTCTTCGC GCGCGCTGCA TCACGATGTG TTGCGCTCC ATCCCTAAGA GCGCAGCAG 300
 AACGTAGTTC AGCGGGTGC CCATCGACAG TCGACTTGT CTCCGAATGC AATCCCACC 360
 CGCGTCGAC AGGTGTGCG TGTTACCAC GTTAGCGCAC TAGCTCCGC CGCTGAGGCT 420
 CAGGAATACC ACCCGGCCA CATGCATGC CACCACATAC CCATATCATN ACATNGGCC 480
 CCTGTTACA ACAGGAAANT GCCNAACCT CCTCTGCAG ANGGCCCAA CCGCCCCCG 539

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1211UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GATCTACATC ATGGGAGGCT AGGAAGAGCA AGGCACCGC TGCATTTGTA GACTACAGC 60

EP 0 866 129 A2

TATAATATGC AAATGGCCAA TACCTTTGCC CCGGATCCAA AGAAGGGCAC TGTCAGCAT 120
 ATGGTTATCG AGACGAGCTT CAACCACTTG GCTCTAGGCA TGGTCAGCCA GATATTTCCG 180
 5 CACTAAACAA CGTCTAGAAA ATGACTTGAC CTATGACGIG CCGGGCTTGA CTCATCTTAC 240
 TATCCTCAGG CCGGGCCCTC TTCTTGCGGA GCATGGCTCT AAACCCGTAA TAAGCCCTAC 300
 CAACCCGTAT ACAGGAAACA TGCTTACGG CTGTTACACT TATAAGAAGA ATGTTATGCG 360
 10 CACGCAATTT AATTGGCTTG CGCCAGTTTA AGAAGTTGG CCAACACTAA GTCACCCGAA 420
 CTATCCGCGA AGGCTACCTA TCATTTACCC TGGAACTGGA TTGTTTGGCT ACTCANTCCC 480
 CAGCNIGAAA ATTGCCCCNA ATTGCGGCTC CAGAAAGCT ATCCAAAGGA ACTACTCGAC 540
 15 CAAATCTAAT TTCCCTATA ATGTGAATTA CACTGTNAAT TCAGAANTGA ACN 593

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1212RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GAGATCTOCC AGTACGCTTT CAAGCTGGGC TTGCGGGTC TAGGATAGAG CCGCGCGAAC 60
 TCAGGACTGG TCGAGACGGG ATGCTGGATC CGAAGCTCT TCATAAGCAA CAACCGCGGT 120
 TGCCGCGTGT AGTCATCGAA CGTCCCTCA GCGAATCTG CGAGTCTCCA CTTGACATCA 180
 35 CCATTGCCCA CGATGCACCG AAGCGTTTCT GGAAGGAACA CGCAAACTAG CAAGAAGCCG 240
 ATGCCGGCCA TGATGCTAGT GAAACCAAAC AACCATCTCC AACGGTCATT ATCGAATAGG 300
 ATCAAGCCAG CAATAATGGG CGCCCAAAT CCGGCCACN TTTAGGGCCC CAACATNAAT 360
 40 TACGCAATG CTTGCCGGG GTTTTTCGGN GGTGTGATT TCNCTTACCG TACGGGCCCC 420
 TGAGAAAACG AGAACTCGA GGAAATGCTG CCCCCCTNTT AAAAAAATAC NCCCATCGNG 480
 45 CAGCNIGAAA GCANVTACNC TTGACTATAA ATCANCCCC GANAANNTTA NACTCG 536

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 586 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1212UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

5 GATCAGCAGT GTCTTCGGG ACGTCAACGG CTTGACGGTC TTGCGTACCG TGGCCAGCGT 60
 CCGCACGCCA TGAAATGCGT GCACTGCGTG CCGCAGTCCA CAGTTGCGCA GCGATGCCAG 120
 ACACGAAAAC ATCCTCGTTA ATGCAGCTTG GGTCCTTCGG TCGTCACTGT GCGTCTCGAT 180
 10 TAAGCCCAGG TTATCAGTAA CATCAAAATT TTACATAACT GCCACGTGAT ATACACGTGA 240
 TAAAGATCTA CAGCCATGCC CCTTGATTGT GTAAAAAGC AACTTTTGAA AAATTTTCTA 300
 CGTTTCCATC CGATGAGATG AGCTTAGCGT AGTGGAGTC CAATATCAGT GCACTAAGTT 360
 15 TATCCAGTGA TACTTGTTCT CGAGCTTTCA GCAACAGCAT CAGTTTACAA ATGCGACCAG 420
 CAGTTATCCC TGAAAGAAA TCCTACGGTC CGAACTCCCA TGATAGTTTG ATACGGCCCT 480
 TACAGACGCC AGCGAAAATC CCACATCTCC NGGNGGCTTC AAATNNNCTT CCGNGGTTCT 540
 20 AAAGCTTAGG GGNATTCOCA TGCANGGGTT TATNAAATTT GANAAT 586

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1213RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

35 GATCTTTTTT AGAGAGTTCA GTGTGCGGAC CAACACGGTC GGAGGCCCTT CAGCTACTTC 60
 CAGAAGGTCG TAAAGAGTCT CCAGTAGCCC CAGGGTGGC TCGTGGTCAT AACAGTCCAT 120
 40 CTGAGGTAGC GTGTTAATAA CCGCTTTTCAG CATGCTCGTA GAGGACTTCT TTAGTAGGGC 180
 AGAACTTATA AACTTAAATG TCTCGTCTAT GCATTCAGGG GTACGAAGAG CTGCCAGTGT 240
 CCGAATGTCA TCAGCCGATC TGCTCGTTTT ACTTTGCTCA GAATCGCGCC ATAGTTTAAC 300
 45 TNCNGTCCC AAATTAACCC GGTTTCCCGG GACCTTTTIN AACAAAAAGG AAAAAAATT 360
 CCGTTTCCCC CCNCTNCCC NNNNTGGGCN AAAAAATTTT TNCNCGGCN AAAATTTANC 420
 CCCCCNCTT AAGNCCCATT AAAAAAAN NNNNNNTTTT TTTTTTTTNT NGNGCCCN 480
 50 NAAAAANNIN CCCNNTTTN NAAAAANGG NGGNTTNNG NNNNANANN NANNN 535

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1213UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GATCGCCAC	TTCACGA	ACT	CCAGCTCCG	AGGCCGAA	AC	GTGTCGCA	GTC	CCGCTC	60
GGCGAGCGC	CCCACGTT	CA	CATACACG	TA	GAAGCGCCG	CCCTCCGCG	CTGCCTG	CTC	120
CCCCGGTAC	CGCCGCCCA	GCGCGT	GAGT	CACCCGCT	TAC	ACCTGGT	ACC	CCAGCCCCG	180
CAACCGCAG	TTCATCTCG	TTACGT	ATGT	CCCCAGCT	CT	CCCCCGT	CGC	CCAGCGC	240
GCCCCGAC	TGTGCCAG	CA	CTTGCTCG	TG	CACCGCCCC	CGCGCCGCA	GGATGCA	CTG	300
CAGCAGCAG	CGCCGCTAT	CGTCGCG	GT	CGTCTCG	TG	ATTGCTCT	CC	TGCGCCCCG	360
ATGCACGCA	ATCCGCTCT	C	GAATGCC	TTT	GGCTGCCCC	GGCTTGCG	GT	CTGGGGT	420
GATTGCCAG	AATGCTGAA	C	AACTGACA	CATTTTG	CCA	AAAGAAA	CGC	CAATGTCT	480
CGAACGAAT	TGCGCTCT	C	GTTGAAC	TAA	CCGCGCGCC	CAGTTGGG	TG	AAGCCGCTG	540
TGTTCCACC	TATCCGGT	AG	GGTTCAG	CT	TCCTGTG	NTT	CCACTAN	TGG	600
CTT									603

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1214RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GATCGTTCAC	GTCAGCCA	AT	TCTGTGTC	GT	AGCCACTAC	ATTGTAG	AGC	TTATAGATTA	60
AACCTCGAAT	GCAATCATT	G	GGTAAAGCA	CAGCTTCT	GT	AGTCTGC	CTA	TAGCAGAACT	120
TTTCATCTTC	AAGGTATGT	CTTGAAG	CG	GCTTTAAG	GGA	ACCTTCAT	C	GAAGTACTGG	180
GTCTTTCTAC	CCCTCCGGG	GAGCAGG	ATG	TTAGCCGG	GAG	CTTCTGA	ATC	AAACTCTTGC	240
ACTTCAAACT	CTTGTCGTG	G	ACCGAACG	CA	ACTTTAG	CTG	CGCTTCAG	G	300
TTACTGCCAG	AACTTGTGG	G	CGTGATGT	G	AGGAATTT	TTC	TCCCATCT	G	360
TTCCATATCN	ATTGACACT	G	CACGCCCC	CA	CATTCAAT	T	TCCANAN	CCC	420

NANATGTTAA TTTTTCNGGT TTAAAGGACT TATCNCCT NTCAATTTT CTNAATNAA 480
CTOCATTTGT CCNNAACNAA CAATINAATT CCCCCTGTCC TTCCNA 527

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1214UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GATCAAGACC TGACGGCTTC CTAAAATGCG TAAGTTTGT ACATAAATTG CGGCAAGAAT 60
TACCCAAATC ACCTGCTGTG GAGATACGAG GCAAGCTGAG CCGGTGGATG TGCCCATTC 120
ACACCGATTA CTCTTTGGTG TGTGGCTGTC ATGGTACTGC TCGCTACCGC CGTGTTCACG 180
GCTTGTCTA ACGGGAAGCG ATGCCGGTAA AGCCAAATCA TGTAACACCC AGCGATAAGT 240
CCACGAGCAG ATGCTGAGAG GCTCGACGAG AAGCACTG CATGGGTGAT GCTACAGATG 300
CCTATGCGTG TGACAGGTG AAGCAACTGT GTTCTGCTTC AAGTAATAGC CAAACTTGGC 360
CGGTAGAGA ATGACACTGC GGTGTCTGTG CATATGTTGG CACTATGCAA GGTACAGAT 420
TGCAAGCTG CCGAATGTT GCGCCAAATT CGAACAACCA GCCAGCTATT GGTATGGAAT 480
TATATACAAC TTGGTGGGG AGGAATTCG GTGAAAACG GCGCACCAGG NAACTTTACT 540
GGAACGGGAA NOGGGNAATT TCCCCCNC CCGGGTTT TGAACCGGC CCNTTG 597

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1215RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GATCAGAGCA AAGTGATTCA AAGCGATTTT GGACGACCG TAAGCTGCCA GCGCAGGATG 60
GCCATCTGA CTGAGCCCCG AGGTTACGCG AATGAAAGCG CCTGCGACT TACGTAGCAG 120
TGGAAGCGCC TTGCTGGCCA GATTACGAC GCTAAACAGA TTAATCTCGA ATAGGOGTCT 180
CCATTCTTG ATGTCCGCT CCGGATGCG TTGTTGGTAC GAGACACCG CGTTCGCTAC 240

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GACAGCGTCT AGCCGCCCAT ACTCCGAGGA CACCTTATCG ATCAGGCGCT GCACCACACG 300
 CTGTCAGTG ACGTCTCCGA CAACATAGTC GAAATTCTTG CCATGTCTCG CCTTCAGCTC 360
 5 CTGCAATTTG GTTTCGCCCC GTGCAACCCC TACTACAACC ACGTCGGGGG TTGAGCACAA 420
 TCTGTCAACG GTTGCCGCGC CAATGCCACG CGATGCACCT GTCACAATTA TAACCTTCAT 480
 TCTTGCTTGG TACTTTTATCT TCAATGGGCC ACGAACGCTC CCGCTGTAG TTTATATATG 540
 10 ACTTCAGGGG CTGTTGGCAC AGCTCACTAG CACACTACCC TTCACATGTC ACACCAGTTC 600
 GAGAATGAAT GGCACAGTTC CATTGTGAAT CATGATTATC AATACAATAT GTGTGTGAAT 660
 TATTGATTTG TAATATGCAT AATATAGATG GTTATGATTT GTAATACAGT AAATATACGG 720
 15 TAAATATAAA GTATTTTAAG GAATATTTAT AATT 754

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1215UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GATGCCCCGG GGCTACGTC ACTGCAGATT GGCGCAAGCC AGGAACAAGA CGGACACTAA 60
 GTCAATCTGT TTATGTAGAT TGGGTGGCGA GCAGCGCAG CGGCGCGGCT GATCTAGCGG 120
 35 TACCGCACCA ACGGCGGGAC GCATGCGGGC CCGGCGGCT AAACCAAGAC CGTCGTGCCC 180
 GGTGCCAATG GACCGCGGGG TCATCCACCC CGCTCAGCCG GAATGTAGAC CAAAAAAGA 240
 GTGTGGTTC AGCTCTCAA TTGGGCTGGT CTCAAGGGGT CGCGGCCCCG CAATGGCCTA 300
 40 TATAAACGGA CAGCGGAGAC AGTCGTGCA CTGTGAGGA CAGGCACACC GATGGTGAGG 360
 GTTATCATTG TGACAGGCGC GTGCGCGGC ATCGGTGAGG CAACCGTTGA AAAGTTGTGC 420
 ACAGCCCCCG ACGTTGTGGT GGTGGAGTT GCGCGGCGG AAAAGACTTG AAGGTGCTGA 480
 45 AAGAGAGATA TGCCAGTAAA TTCGACTACG TTGCTGGAGA CGTCACCGAT GAAAGCGTGG 540
 TGCAGGCGGT GCTCGACAAG GTGTCTCGG ATTATGGCG GCTAGACGCC ATCATAGCGA 600
 ACGCAGCGT CTCGCGCTTC GAACGCATCG CCGAGGCAGA CATCCAGCAG TGGAAAGCGA 660
 50 CGTTTGAGAT CAATTGTTTA GCGGGTAAG CCTGGTGAGC AAGGCGCTCC GATGCTAANG 720
 AATCCCAGGG TTACGGTGAN TGTGGTTACC TCNNGANTCA ACNAGGTAGN TANCCG 776

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

EP 0 866 129 A2

(A) LENGTH: 546 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1216RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GATCAAGTCT TTTATCACTA CAAATGAGCA GCGCTTAAAT TTCCAGAATC GTTTACAGCT	60
GCGTACGCTT GCAAGCAAAT TTGGCCTTTT TGAGCTAGCG GAGGAACAGT TCGCTCAGCG	120
CAAGCGCCTC ATGCGGCTTA CAGAGCGCGG CGAGCTTTAC ATGTATTACA AATCTCTCAG	180
CGGTTCTTAT TCCTTAGOCA AAATGCCGAC CTGCTTAATA GATACTCTGC GTGCTTTTAA	240
TAACGAGCCG CACTCGTCCC TCCGTAACAC ACTACTGGCT GCGCTCTATC CGAACACATA	300
TCCACTGGCT CCGCCGCAAT AATGCAGAAG AAGAGGTCCA TAGATGAGCT GAACCCAGCCA	360
GCGCCANCAG AATGTACTCC CACTTATGCG AACTCCNANA NTGGAAGGCC CTGCATACAT	420
TTCCGGTCCC ACCNACTTCT GCGTTCTTTG GCTTACCACT CTTGTGAACC GAATNGTGCG	480
GCATGCCTTG CCCAAAAACC CCTGGAAATC CATAAATACC TNCGGGGGT TANCTGCGCT	540
CCCCCG	546

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 593 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1216UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GATCTGTGAA TATATGCTTG GGGTCGATTG GTTTGCCAGT GCTATAGAGA GCGGTCAACG	60
GCGTACGCAC GGCAACTCTT CGAGTGTGCA GCGCAAGTAG CCGATCATA TACAGGTGAT	120
GGATGGCTCC TGTATACCTT CCCCACTGC AAGCCCTGA GTTGCTCAGG TGTACTGCG	180
GCAGATGGTC ACATCGCTTC GGAGTATATA GTCTGCGCTT TGAGCCACTT AAAAGGGGCT	240
CGCCGGCTAG CCGGCGCGG TGGTCAAGTG ATTGCCATCT GCGCGAAGC GAAACGTAAC	300
AGGCCGTGTG AACGTGGTGC TCATCCGTCA GCAGGCCGGT CTCCCAATGT ACTTCGCATA	360
TGTTATTTTA CGTTTATGTT ACCTATGAG GGTGCTCAG GGTATGCCC GCGGTGCTGC	420

CCTGCCACGG AACCCGCAGC CTGCAANCT CCCTAATTGC CCATGGTGAA TTGAACTCNC 480
 AAGCTTATAT CTCCTTGCCCT GATCCCCCAT NATGCATTG AAGTTCNCCA NAGGACAAGA 540
 5 AACANACNCA AAAAACNAAA TGGTTAAGTA AAATIGATTT GGTGTTCOCN CCT 593

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1217UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GATCTCGTTT CTGGGGATT TTTATTGGGTT GGAAGAGGAC CTTGGGCTA CACCACTGAA 60
 GGTGTGCGAG TTCTCCAGTT GAGGCTATT GAAGTGATA TCTGATGATA GAGCGCTCAA 120
 ATGTTCTGAT CCTGACATCG AATAGAGCGC ATTTTCTGT ATGTAGCGC CTGGGTCTC 180
 25 GCGTGGGATA TCTTTGATGT TTGGAGTGGT GTTGTGCATC ATGTACACCA TATTTGATGT 240
 AATCGGTTGA ATACCATGAG GAAGTGGACT CATTGATTG GCTGGTGGCT GCGGATGTGT 300
 TACCATTGCG GTAGAGGTTA GAAATTTGGT GAGTTTGCCA AAGGAAGAGC TGGCTGGCTA 360
 30 GCAGAATGAT GGACTGGCGT TCAAGCGCCA TGTTCNTCC TTTGAGGTT AAAAATTAGG 420
 AAGGGGACAA GGACTCCCCCT GAATCCTACT ANCCCTTCT AAAACTTGGC AATATTGGTC 480
 CCTGAACAG ATGNCNCCNC CACATCCCCC TATTAAATTT TTTAACAACC ATATTGTGG 540
 35 ANACCTNGAA NTTGAACTTG CCNGCNAANN GATTCCOCTN CCTCCCCAGA TN 592

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1218RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GATCTTTGTG GGCACGACG ACCACCGAG TACCGCCCGT GCCTTGGACG TACCACTGAA 60
 AAATGTTCTG CATGAATCCC ACCTTGATAA TACCATGGA CCACTGGAAG TTCTGCGACC 120
 55 ACCGAGCAGC GATGGGTGGC ACACGAGCCA CTCCATCAT AGAGTGATC GCCAAATTTT 180

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GGAAGTACGA GAAAAGAGAG ATCGAGTTGG AAGCGATGTG CCGGGCAGTG GTTGAGTGGC 240
 5 CGATCACAGA CACAAACCCG GAAGTCCAGG ACACCCACAC CAGCTATCGC GCGGAATCGG 300
 CCACGAATGC ATACTTCGTC TGCACCGTCT TCGCGTCCG ACAGCACCCG CCTGCAACA 360
 CAGGCCCAAT GGATGCTCCG TACTGGTGT TCAGCTTTCC GCNAAGGCT TTACACCATC 420
 10 CGTGCTTCCC AGTTCOCNGG AAAATATACC CCGCTTGGT ATCTTCCNT GAAAAATCAC 480
 CGCCGAAATT TCCAGTTGA ANCTCTTTG ATTCCCCCCC CMTGCCCTCC CCAGNINCGG 540
 GANATTCACA ACNAATNC 558

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 604 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1218UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GATCCACAGT TTCCGCACTG AACTTACTAT CCTCAGCAA CCGCAGGTCA TCGTCAAGCG 60
 30 TTGTGACATC AGGCTTCACC CCGTAGCTCA TAATGCTGG GACGGATGCC TTGGTAGAGT 120
 AACAAACAAA AAGGCATGTT GGATCAGCTG CATAAGCTAG TAAAAAGAG CAGACGCGCG
 CTGAGCCACT AAAGGCAACG ACCCGCCAAT ATATGATAAA TAGAGAATAT AGAATGTTGC 240
 35 CACTAGGCCA AGATGACCTG CATTGAGATC CAGGACAAA GTGCCAGGAA TTAAGGGATC 300
 TTCAACATTC CTGATCATAT GAGAAGAGCA ATACAGGGTT AAAACGGCGG CGTTTAAAT 360
 TTACAGACT CAATCAAATG TTTCACAATA CCTGGTTTGG ACAAGTCCGA GACATCCCCC 420
 40 TAACTGATCT GCTTCCCCCA GCCAAGGATT TTGGCCATA TACGGGCCAT ATTTTGCTTG 480
 ACGATTCTTT TGCAATCTCT CCCGAACCAC AAANACCTTA GGGGCACNAA CGGCCCAATT 540
 CCGNANNGAA AAAAAAATA GGTGCTTTGN ATNNCCGNA CCCCCCCCCC CCTTNTTTC 600
 45 CCNG 604

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 550 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1219RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

5 GATCCTGATA TTGTACCGGC TCATAAATAC TTTGGATATC TTCGGACAAT GTATCGTACC 60
 CGATACCTTT CAGCACATGG ATCAGTATAT CATGCTTCTT CCTAAATGCA GCAACAGTAT 120
 10 TGAGGACTTC CTTCAGACTG TCCGTCTGAG TATCTATCTT CATAAAGATG AACTTTTCGG 180
 ACCTCTTCTT CATCAGCTCT CTGATGAGTG ACGTTGAATT CTTTAAATAG CGCTTCCAC 240
 TGGTTTGATA ATCTTGATAC AGTGGTCCAT AGTCTCCCT GGAAAGAAAT GAAGTCGGAA 300
 15 GAAATCAGTT TTGGCAGCAC TCTCTCAGTT TCTGATTCAA CTCCGTTAG ATATTTCTTC 360
 CCACAAATGT TTACGGCCCT ACAGTTGGTT TCTTTTGANA CCTTCACTTC CNTCCNAAGC 420
 CATGAAAATG ANTCATCNC CCCCCCCCCA CTTTGTGANA NTTCOCATTC GCAAATTNCA 480
 20 CAGTTGAATT CCCCCANCCG GGTGTTCCOC GCGTCCCCC NAAAAANAC NGAGGGGGGT 540
 TTTAAAAAAN 550

(2) INFORMATION FOR SEQ ID NO:245:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 598 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1219UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GATCGGGGCG CTGCGGCGCG CGTCGGAGTG GCGCCACGTG GCGCGGCCCT TTTGGCCAAA 60
 40 TCCAGGGGT GGGGGGTTT CGAGCTGCTT GACCTTCCGC GGCATGTCAA AGTGCGGGT 120
 TAGTTTGGTC CTGTAGGCGA ACTGTAGCGG CGATGCGACC GTCTGCGCA CGGTGGGGAG 180
 CAGGCCCTCG GCCAGCAGCT GGGGAGCAAA GAACTTGAAC GCATTTGACA CGGTTCGCTG 240
 45 TTTGAGCTGC AGCTGCTGGT CATACGTCAG GAACTGATAC TGGCAACCGG AGCACTTCCC 300
 GAAGTACTTG CAGTTGATGA GGTGCTCGTG GCGCATTTCA GCAGAGGTCT GCACTCCAG 360
 CAGAGACGCT TGGCGTAGT GCGGTGTGTC TTGTGCACTT GGATGGTGAC CAGTGGGCC 420
 50 TGGCCAGCCC AAATTGGCAC CCAGCACTAC TGTTTCTTTG TTGCTATCC TCCGGGGCTG 480
 TCCAACAANA CCCATCCCTC CCCATCCACT TTACNTCCAC ACATCACTTT CATCAGCNCC 540
 GGTGTGTTCT CTGCTGCATC GCCCCCGAA TTINTCAGA ATGATTACTC CTCNCNG 598

(2) INFORMATION FOR SEQ ID NO:246:

EP 0 866 129 A2

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 747 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1220RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GATGGCGCAG TTGTGCGCCT CAGCCAGCCG CTTTITGGGC ACGGGGGGA GCGTGTCCAT	60
GTACCCGTCG GGCACGCCCC CGTCGCCCTC GCGATCAGC TGCAAGTGCT GCTGTAGCTC	120
CTCGGCATC AGTCTACGA TCACATTAG TAGCGGGTG CTGTGGCAT CTGCCTCCTG	180
GAACATGTCA GCCAGCTGCC TGGGAAGTTC GGACCGTGC CCTGGTGGT CTGTGAGAGT	240
TAGTATTCTT GGCCGAGTC GGTGCACAT TGGCATCACT TACTATTGTC GCTGGGCATT	300
CACCTCCCTG GATCACTGGT GCTCCCGTG GCGTAAGGG GCAACAGACA GGCTTTTTTT	360
ATTTTCCTCT ATAATACGCT GCTCTATGTA GCGTATACTA TACAAGTCTT AACTAAGGTG	420
AAGTGAGAAG TCATTATTTA GCTGCGTTTC GGCCGGTCAT GCAGCCGGCT ACCATATTAG	480
CATGCCGCTG GCCTTGACGG CTTTGGAGCT GGGGAATTG TTGATGCCCC AGGACCTTAT	540
GGAGTTC AAC CTCACGGAGA GGTITCCGAG ATCGAAAATG TCACTTTCCG CAAATTGCGA	600
CACACCGTAA TACTCGGCAA ACGAGTTCTC GACACCGCTG AGCTGGTGGT CGACGTGCTC	660
GACATAGGAC AGAAGAGGCT TCGTTGGGC TGGCGGGCGC GCGCGCGCAA CCGGAAGNGC	720
CCCCCANAG CTGGCGCCNG GCGGCC	747

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1220UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GATCCAGAAT ACTGTCGCA CCACTTCTTG AACCGCGGT ACAGCGCGG GTCCGTGCGG	60
TCCAGCGCGG CCTGTGCGC CGGTGGAAC AGCGCGCGT CCTCTGTGA CAGGTAGCTT	120
GGGTGAGGT CCGAGCCGCC GCGAACCAC CAGTCTGGG GCTTGCCCGC CGGTCCAC	180
GTCTCAAAGT AGCGTAGTT GAGGTGCACG GTCCGCGGT GGGGTTTAC GGGGTGCATC	240

ACCAGAGAAA TGCCGCAGGC GAAGAAGGCG ACGCCGGCCG CCGGCTGCCC GGTCACGGGG 300
 TCCGTGGGGA GGTGCAGGTT TTTGTGCTCG GCCCGCATGG CACTGACGGC TGCCGGGCGAC 360
 5 AGCTCGCCGT GGA CTACCGA GACGTTAAG CCGGCTTTT CGAACGTGGT GCCGTGCTGC 420
 AGCAGCGACG ACGTGCCGCG GCCACCTCC TTGGCTCCC AGGAGTGGC CTTGAACTTG 480
 ACCGTGTGCA TCGCTCGAA CCGGCTGTG ATCTCGGCT GCTTGCGCG CACGAGCTCT 540
 10 TCCATGCGCT CGCGCATGTG GGGGGTGTGG GCGGATGCCA TTGCTGGGGC GCCGCAAGAG 600
 GCGAAATNAN CNGTGCGCCC GCGGCTTAT ATAAAAGCGT GGCACGGGTG TTTTGCCAC 660
 GNCACCANGG GCTGCNAAAG TCCGCGCCAA NANANCCAGG GTCCCGGCCA NAACACNTCG 720
 15 GCGGGCGGCC NAACGCCGCG NCNCACAATC ACNCCGACAA TCGCGCNCNG GGATTCC 777

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1221RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GATCTCTGCT GTTTGGGCTT GCAAGCATCT TCCTCGCTAA CTCGTTGGC GTTTACGTTT 60
 GAGGTTCGGG GGACGTATGC TANACCGAGG GCATTGCGGG GTTGAGGGGA AGAGGTTGAG 120
 35 ATTATGAATG ATATATACTG TTATACCGGC TCGGGTGGC TGTGCGGTC ATCACGAGG 180
 ACTTACAAGT TCAAAGGTC TTCATGATA TTTACCAACT TGTAATAACG CTCTGTGAG 240
 TCTGAGTTGG AGGAGCGGG CTGGTGGCCA TACTCCATCA ACGTGTTTAC CATTGCGGT 300
 40 GTATAGCTGA TCAGGTTTTC GAGGGATGAC TCGCTCTCT OCTTTAGGAA CATCAAAATG 360
 GTGGTGTTC ACAANCNGGA AAACCTATCC TGTTAGTNN GAAGGGTTGA GAACACCGCT 420
 AATCCCTTAG GCACTOCACC ATGGTTTAT CCGTACCCA TTACCCAAAT TTCCCCAAG 480
 45 TGCCCTTNA CTTTGNCGAA CCCCCGNAA ATNCCGTTT TTAAAACCN AAAAANG 537

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1221UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

5 GATGACCOCT ATCAACGCOCT TGCAGGCTGC TATGGAGGGC TATCAGGTCA CCACTATGGA 60
 CCACTGCGCC AGCTACGGCC AGGTTTTTGT CACCACCACC GGCTGCAGAN ACATCATCAA 120
 10 GAAGGAGCAC TTCTTGGCCA TGCTGAGGA CGCATTTGTG TGCAACATCG GCCACTTCGA 180
 CATCGAGATC GAAGTGGCCT GGCTAAAGGC CAACGGCGTC GAGCGGTCA ACATTAAGCC 240
 ACAAGTCGAC CGCTACTTGC TTCTCTCCG CAGACAGTC ATCTGCTTG CCGATGGTTA 300
 15 GACTAGTCAA CCTAAGCTGT GCCACTGGCC ACTCTCGGT TTGTCATGTC TTGCTCTTTC 360
 TCCAACCACT CTTTGGCACA GATGGTCTCN TTCAAGGGCA ATNAAAAGGC CTTCAAANAA 420
 ATTNNTTNNT TTCCAAAAA ACGGCNTCA AANCGGNTT CATTTCTNNC CNAAAATTGN 480
 20 AAAGGCGCNC CCATTTCCCC CTAATTTGG GTTTTNTTTT AAAACATTCC CCCCCCCCCA 540
 TTTCGGGTT CCCAAAAGGG TTTTNGGGG NCCCTTAAAT NITA 584

(2) INFORMATION FOR SEQ ID NO:250:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 535 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1222RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

GATCGAATAA TAAAAGTGGC TAATACTTGG TAATAATATA ATAGAAAGGG AAATAGAAGA 60
 GAAGTCAAAT GGGAAATAGT CAACGGGTA CTAGGTGAGT GTTCAGTTGC ATGGAATGCT 120
 40 AGTCAGAGAG GTTTATCAAA AACGGCAGTC GTCTGATGAT AGCAGTATCA CGAAGTGCTC 180
 ATGCGCCCTG CATACAATGG CAGGCTCAGC GCAGGATCAA ATGATAGCA GCGGGGTAC 240
 CCGGAACGG ACTCAGTGGG TGGAGTGGCC CCGGTGGTAC TTGAGGCGGT TGAGGTCTTT 300
 45 GTAAAGTTTG CCACAGACCT CGCACGGTA AGGCTTGTCC TTCTGGAAC CATGCCGTC 360
 TGGATAGGGC TGGTTGGACT CCGGTCCAT GATGCTAAAA GTGCCGTCT GGGTTTTCAT 420
 GAAGCTTTTG ATTCTGGTGG CCGTGGTTT ATGGTACTTG AGTCCCGTTT GATCCTGGTT 480
 50 AGTCTTATCG CAGCCCATGA GGGACNNTG AAGGCTTNTC CCCNCTTGT CCNEN 535

(2) INFORMATION FOR SEQ ID NO:251:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 581 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1222UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GATCTGGCTC AGACCGTCAC CCACGTTGTC TGCAAGGGCC TCCGCGCTT TANCTGGCTG	60
CCACGGCTTG GAGCAGCTA GCTGCAAGCC AAACCGGGC AGCTCGAGC AGTGGCGCTT	120
GGCAGCGCC CACTCGAGT TGGTGGCTG GATCAGGGC ACAGCGAGC CCATCTCACT	180
GTAGTCAAG TCGGGGCCA ATTGGGCGAT CAGGCGCGG AACGGCAGT TCCGACGGT	240
GGTCAGCGA GAAACGATCT TCTGTGATG CAGGTCCAGC GGCTTCTTCT CCTGTGCAA	300
GTAGCGTGC TGTGATACT GGGGTACAG CTGGCGCTG CCGCGCGCT TGTGCTCAA	360
TTGCTCCTCC CGCTGCTGA CCTGGGCAC CTCTGGACC GCGCTCCG GCGCGCGCG	420
GCCCCGTGA TCTGTGCGC GGAATCTCT CTGGATGGG TCAAAATTCC ACNATTTCTC	480
CCTGCNCGG AAGGGCCCAA NTTTTCCCA ATNANCCCA ATGAACCAIT GVINCCCCCN	540
TGGTTNCAA ACNAATTTTG CCCCCCGG AGATTNCCC A	581

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 544 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1223RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

GATCGGTTTT CACCTCAATT CGTTTCTGGT CGCGAGTTG GTGATGCTGC TGATGCTGAA	60
GCTGTAATTG CTGTTTCTGC TGAGCAAACT GCTGCTGCTG TTTCATCCAG GGATTCTCCG	120
GAGGAGCTGA GTCCGGTTTG CGCGTCTCT GCTTGTGGT CAACAAGTTG TTATATAGCT	180
GGTTCATACC TTGGGAGGTC AGGAAGTAC TGACATTGCG GTCGCCCTGC GGGTGGTCTA	240
GCAACCGAG CATGGCTCT CTCTCCTGTA GAGTTTCTTT TGCGGCATC TCAAACTTCC	300
TAGATTCCAT TATCAGCGCT TCTTCTCAG CAATCTCAGC CGCCGACCTC GAAAGCAGCC	360
TCCGTCAAAT ACTTCTTCG CTGTATTTC CTGGTCTTG GAATAGCTA GGATGGTAGT	420
AGCGGTTTC CCGGTCTTT CGCCTGAAA TTATTTTGG CATACNGGT TAAAAATCTC	480

CCCGTANTTC CTCCAACGGT CCTNNANNCG NCNTAAANAN ACNGGTCNGT AAATNATAGC 540
 MNCC 544

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1223UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GATCGCGCGC TTGAACATGG ACGTGGACAC GGCGAAGTGG CGCTGGAGCG CGCGCACCGC 60
 TGCGTCTCGG AGCTCTGTGT GTGCCATGGT GCGCTCTGTC TTGAGCTGGC GCACAACCGC 120
 GGCGGATATG GCGTGGACCC TACTGGCGGC GAGGACATCT GGTAGCGCGG CCGCCTGCTC 180
 GGACTTGACC ACGACAGTGG CGACGCGGAC CTGGGTGGTC GGCGCCGTGA ACGCCGTGTT 240
 GACTGCAAAG TGGTCCGAGG GCGCGATGGT GCGGGGAGGG AGGGGTTTTG GTGAGGATGC 300
 GTGTGCGCGG CCGGACGGCG AGCGAGATGA GCTGGCGCTG CAGCTCGGCA TCTGGATTGC 360
 GGTACGGTCC TGAATCTGCT CGGTGGTCAG TTCTGCGTAG TCTCCGAAA AACAGGAAAA 420
 ATGGTGGCG GCATNGTICA ACATCCTTGG CCCCCGCGT TAAAAATGGC CGAACTGGNN 480
 GCGATTTC CCGAGAACCC ATTTTGTAT CCCCCCTCCT TCTGCVNCC GATTTTTTTG 540
 CAAAANTNAA AACCCCCCT AAGAAGANN CGGGGNGCC CCNCGCGGN TTTTTTTTTC 600
 CNCCCCCA 608

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1224RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

GATCAGTAAC AACCATAGCA GCGCACCTA CGAAAGCATT CGATACATT TTAATAAATT 60
 CGACAGCAGG TAGTAGTCTT CTTCCGATT GCTTTACAGG CTCGCTAAAG ATGTGTTCGT 120

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AGCTCTTCCA AAGAGAAATT TGTGTAACCT CAGAGTCAGC AGCGGACTCA AAACAGCACC 180
TCAACCAAGC GGTGACCGC ATAGGTTTCAT TCAAGCCCAA TAGTTTTTGG AATAGATCAG 240
5 GGGGAAGAGT TGAACATGC GTAGGGGGTC TCGTTTTTAC TCGOCTAACT AGTTTTATCT 300
CTACTTTTGA AAGATAGTGC TAGTCGGGAA GCTCAACATT GTAAGTCAAC AAGCTAGGCA 360
AAACTGTAGT CAAGATTGAG TTCGGCTCAG GGTMTTGACA ACAGAGTAGT TATTCTCTCA 420
10 CTCCCCAGGC AAGATGTAAT GGTATAGAAA ATCCAGTTGA AGCCATAACC AGCTCGTTGT 480
CACAGTCCAC CAGAAGATAG GANACATCAG GTTGAAGAAT TCCTCATCTA GGTATCTGTC 540
TGCCCTTTCCT GTTCTGCTTT GGACCAACCC ACAACCCNAA AACCAACGCN AAATCAAANA 600
15 CCNGGTTTCCT TCCTTGNTCC CCCCNATGA AANAGGTTTT GAAANGGTTN TCCCTCTGTC 660
CGGGCCAANT AAAAAAAGG CCCNCAGGT CNACNATATT ANCANCCCC NAAAAAGGCC 720
TTCTGNTCTA A 731

(2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1224UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GATCGGGTGC GGCACATGCC TCATCGGGCA GGTGGGGTGG CGGAGGCATA AACCCACCCC 60
TGGTGTGTGC AGTGAATAGG TATGGGTACA GCCTTGGGCG CCACGAATGT GCGGAGACGT 120
TTCAGCTGCC AGAGGGACCC GACCGCACCG GTGGACTGTT GGCTTGGTTG GACGCTCCAG 180
40 GGTTACGAGC CGGCGCCCTG CGGAGCACAT GATGTCGAGC TGTGCATTGG TCCAGGTGCG 240
CACTAACCAT GCCAAGGGCA TCCGGCCAAG GCGGATGGGG CTGGACGGCG CCAGGGCGGG 300
ACGACTATCA CTAAGAAATC ATCGATTAAA ATATAAACTA CATAAAGTAA AGGCGGACT 360
45 GAGTGCACCTC TCAGCGCACT AGCAGCGAGT AGCGGTAGTT GAACCACTTG CNTGGATCC 420
GTGGCACGAA GCGGAAGTAA CCGGAATCC GATAGTTTCA AACGAAGAAC CGAAAAAGCC 480
TTAAATGGC TTCACNCTA GTTCCCCCAA CNGGTCTCC TGTTTGGAAT TAGGGTGGGC 540
50 GGAAACCCAA ACTGCCCCANT TGTINTCCAA TTCCCCGGNG GCCCCAATTT NAATTTCCAA 600
ACCNATCNEN ATCTGGGCTG NATCCCCCCC NTGCCCCCCC TCAATGGCCC CGAACCTTTT 660
NTGCCCCCCC CCCAAGGGCC CTGNGNATT TTTTCCCG CCGNCCGNT TNTCTAAAA 720
55 NAAAGCNGCA TTTTCAATT CCCNGGAAC NCTTTTGT TT 762

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1225RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GATCCTTTTC TTCTCTCTTC CCTCCTCCGA GGATTCOCTT TTTGAGCTTG CCCACTGCGC 60
 CCAACCCACC GCCTATGACA CTAGTACCGG CGGACAGACC AGCGGATAAG CCCTTATTGG 120
 CAAATCGGC AACCTTTGTC TOCACCTTGG TAACAGAGAC AGTGTAOCTA GGAGAAAATT 180
 TGAAGITCAA GTAAAGAATA CCACCGTCTC CGCCGTTAGG ACCAGTTAGC TGGACTTCCA 240
 TTGGGGTTTC ACTGTCTGGG TOCACCTCAG CTAGAGOGAT GGTTCGGGTG CCAATGAGAT 300
 CGTCACTGTT TCCGGCATCC CAGTGCATGA CCTTGATGCG CAGGTAGTTG TTAATCCGGT 360
 TATTCAACTG CAGGGATGTG TTCTCGTTCC AAACAGGTTT AAGCGTCTTC TTCTGGGTTC 420
 TTGGTCTTGT ATATTACCTC ATCTGAATTG TCGAGGTAG AATTGTGACAT AAGGTCCGAC 480
 TTGCCGTTCC GGTGAGCAGG TAGAGCCTGA CTGCATTAG AACCTCCAGT GTTAGGTGCG 540
 AGTGTTGGTA TCAGTTTGCT TGTCGATCT CNAACCCAAA AAGGAACCAC AACCGTTANN 600
 TCCTTTTGNG ACCCAACCTT NNTTACAANN AGGTTTAAAT TACANTTTCN ATTNTTTGN 660
 TGGAANGAAC CCNAAGNGT CCNCTGTTT TACTGANCNT NNTCCNAAT 710

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1225UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GATCCTACTG GAACCAACCA CTCAGGAGCA GGTTAAAAAA CCAGCCAAAG TAAAGACAGA 60
 GACAAACGTA AGCATCCCAA AGCAGACCCC TACTCCAAAG TCTAAGTGG CTTCAGCTTC 120
 GTCTTCTAAA GTGCTACAC CCCTGTCAAA GCAGGAGCCC GAAGGCGCGT CTACCATTTT 180
 TGACGCTCCT TCTTCTTCTT CCTCCACTCC GGTGCTGGG CACTTGGATA TCTTTAGCAA 240

ATTTAGGAAA GCATOCAGTG ACTTTGACAA GOCCTTTGTG GOCGAGTCGA ATGAAGTTGC 300
 CGAGAAGCCG TCOGGAAGG CCAAACGGCA AACTACTCCC GCTGCCAGCA AATTAAAGCC 360
 5 CGCTGCAAAG AAAATAAAGA CGCCCGCCT CGATGAAAGC GAATCTGATT TTGACCTTGA 420
 CCTCAGCGAC TCCAGCCCG CCATCGCCCC TAGAAGTAGA GCCTOGGAG CTGTGCCAA 480
 AAAGCCAACC TACGTAGTTG ACCTTTCCGA TGACAGTTTT GTTGATGGAG ACGCCAGAG 540
 10 ATGTTGAGGA ACCGATACTG ACGAATCCTT CCAGCTCTGA CTAGCACTCT AGCTCGGCA 600
 TTGACAGTNC NCTACCTTAT GGAGGNTCC GAAATCCTT GAATACCCCC CGTTTTTTAC 660
 TAAACCCCC NCTTCTCTT TCACCCCCCA ACCCCAGGG GACGAATACT TTTTCTTTA 720
 15 CTTTCTATCA NGGGGTCTGT CCCCCTCTT 750

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1226RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

GATCGTCTC GCATGGGAGC ATCAGATGTC ATATGGGCGA AGCCTTTCCA TATGGGGCT 60
 ACGAAGATA CGAGTTCCG CTTGCTTGC GCTGTTGGG TCTGTGAGG TGCTGCTATT 120
 35 GCTGTCTCGT ACGCCACACA TGTGGCCTGG ATGGCATCT CCGGCAGCAC GGGAGGTCCC 180
 GGCTTCACCA GAGTCACAGG CCCCCTCTC ACCAGAGTTA CAGGCCCCGG CTTCACACA 240
 GCCACAGTCC CCAGCAGGT CTAAGACGCT ACTGCAAGAC TTAGTCTAG ATAGCAAAAA 300
 40 ACCGGAGGGG GCTCTACGC CACAGATGCA GTGCAAGGC TACTTTGAGG GCACATATCT 360
 CCGGAGCCT TCTGGGCAA ATAGGTGTT GCGCATGGCA GAGACTTTC TTACGGCTAC 420
 GCAATACACA GCGAGGCTGT TGGAGCGGTG GCGCATATTT GCTGATTGTT TCGTTATTCA 480
 45 GATTTCGGAT TTTCAAATAC NCTATCCAAA CAAAAAATC TGCCCAANTT CCATCAGCGA 540
 ANTTCCCTT TCNNGGCAA AAAAAAAN NGAGGANATT TTGCTNTCC CCNGAATTT 600
 NCCCGGAAA ATTTTAAAG NGGNTTTTT GNAAANGGC CCCACAAA NANAAAGG 660
 50 GCTTTTTTG GAAACGGC CTTTTCCTC GNGNGACA AATTNNNNN GGGGACGCC 720
 NGAATTTTC 729

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 742 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1226UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GATGCTTCA AATTTCAGC CGTTGATATT CAAAGAGTGG TCAAGTCCG AAAGATGGTC	60
CTTCTGTTCC TCTGTACGTT TGGAGGCGCG GCGTACCGG GCGTGGCG TTGTCGCCAC	120
GGTCCGGTGC TGTCCTATGG GGACATCTG GATGTTGTTG TGCAACGCAT TAGCAAATGA	180
GTTTTGTAG TGGTACTTAG GAAGTTTATA ATTAGGCTC AGTTCCTATAC TGCCGCTAAT	240
ACTTTGACCT GGAACAATCA TCGTTATGTG CTCACCTCTG GCGTGTCTC TAGCGTATTC	300
CCGCCGTGCT TCAGCATTTG GTTGTTCCTG GATCGTTGGG TATGGATCCT CCCACTTCTG	360
TAGCCAGTTG GTATCCAGCT TCTCACCTG CTGATGCGAT TCTGGACGCG GGGGTTTCAG	420
CAGGCGTTAG CAATGAAGTT GCGTTGCGG GTTCAAAAA AAANACCGN GGGGCGNTGG	480
TAANCCCGNC CCTTTAAGG CGCCCCATA TTCNCNATNA CCNNNACCGC NCCCCCATN	540
ACGCCCCCAA AANATNTTTG AAAAAATTG CNTACCTTTT TGNGGGAGCC CACNCNCTTA	600
NATACCCAT TTTTGAAAN AGCCNNTCT TTINTTTAAC NCCNCGGTC NONANTATGC	660
NGGGGCAAAA TTAAACCNCC CCCCNAAT GNAATCNMTT TCCCCTCNAA NACAAAAAAT	720
ATTTTNNITT NGGCGNGGA AT	742

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 744 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1227RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

GATGATGAA CAGACTGGAG AACAGAGAAA GGTGGTGCC CTCGAAGTC AACGGTTTTT	60
CCGCTCGAT TTTGATGAGA TATTACTCCG GGATACGATG CAGAGGAACG CAGCTATGGA	120
AGAGGAGGAC TACAGGGAGC TGGGAAAAG AGATATTGAG GTGGCGTTCC AGAACACCGG	180
CGTGACGCTG GATGACAGGC TCCAGTGTG GCGGCCATA TCGCTCTTCG GGAGGTATGT	240

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ACGGGATATC GACGGGATGT CGGAAGCGCT TCGGACGGG GACAGGCACA TCATGGTGT 300
 TGGCGCGACA AATGACGCCA TTACGGGAT GCGCAAGAAG CCGTGGGAGT ATCCACGGAA 360
 5 CATCGACAAG TTGGAGCAGG CAGGCGCGTC TCGGAGCGAA ATCCAAGAGC CCATCCAGGC 420
 GAATGTGAGA CGCTTTGTGC TAACCCACGT GGTTCGAC ATCGACCTCT CTAAGGTGGT 480
 TCGGGAAGAT TGCTCCAGCC GTGTTTGACA AGCGACTTCA TCCAAGAGC ATGCAGGGGA 540
 10 TATTCTTTTG CGCCAGGAT GGCAANGGT TTACAGTTC NCCCAANANN GGGCGGACCT 600
 TCGCGTINAG ANGTTACCC CCGCTCTAAC GGTTCATTTT GGTTCACN CCCCCTTGGN 660
 TCGGAATTNG AAAACCTCC NCGTGNCCN NCCCAATNAN TCNCTTGAAT CCCCCTTNG 720
 15 GAACNNNNN TTNCCCCAN CNCC 744

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 768 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1227UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GATCATTTGC CGGACCAAGA AATATTTTCA CTCTCGAAG AGCTGGCCAC TAAACTTCGT 60
 GTCTGGTTAG GTTCGGCTCC AGCTGATGTG CTAGATATCG AGGTGAGAGG TAAGCTTATT 120
 GAATACTGCA TGAATACTGC ACTTTATTGC GGTGGGAAA TAGAACATCC TACATGACG 180
 35 ACTTTGATGA CTGACCATGA TGAAGACGAA TCTGAAAGCT CTGATTGGA ATAGTCCAGG 240
 CAAGTTAATA CCAATGCTC GGTCTTAGCC TCAAGGGAGA TATCGGTAAC AGCTCTATCT 300
 ATGCTGCCAG CAGTACGAG TTTTACTAA ATTGCGCATA CAGTTCATGG TATTTGACAT 360
 40 AAGCTTAATG TTTCATTGCG AACACAAGC TTGCGGATGT GTAAAGTGG CCGCTCTCT 420
 GCATTCAAGA CAGCATACAT GAACCTTCAG TTTTATACGC CGATCATGTT GATTTCTAAT 480
 AGGGCTAGTC CATGGCCCT ACCTATAATA TACTACCATC CAGCCCNCG AACCGNAACN 540
 45 NNATTTTITA TTTTAATNAA ATTTTGGGG NATNCCACAC NNCCCTANC NNGGANTTC 600
 AATGTTTATT TAANINAAAA ANCAGTTTGA AGGGTATTCC NNNCCCCNC CCCACNGNT 660
 TCAAAACCAA ACNANACCGT GAAGCNGTN NCCCCCNCA AGGAGNGCC CCCCCTTCN 720
 50 AAAAACGGTN NCGTTTNCN CCTTGNCN ANATTCCCC CGCTGCC 768

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 738 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1228RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GATCCATTGG	GCCCAACGAT	GCTAATGAAG	TTCTTGCCCTC	CAAAACCCAC	ATTGTGCACA	60
CCCTTGTAAG	ACTTGAAGTT	CTTCACTCT	AAGCCAATCA	GCCTCCCCAT	CTTTTGTAGA	120
CACTGAAGCT	CAGTCTAACT	GCTCTCGATG	TTGTTAGTGC	GCTGTTAATA	TGTCCAAACA	180
AACGGGATCA	TGGTTGTGAA	GAACGCGCG	TTCCGATACA	GGTCAGCAC	GTAGCCGAGC	240
GGCCCCGCGG	GGCCGAAGAT	CACTGAGATC	GGCAGGAACA	GGGGGTCCA	CAACAGCACC	300
AGAAATACCA	AAATCGCCCG	AAACGTTATG	ATGTACAGGA	TCACCAGAGT	CACCGCCTGA	360
ACCCAGATCT	GGCCGTGGCC	CATCCCGACC	ACCATCGACT	GCCTGAATTA	GTATATTCCG	420
TCCCACTGCG	TGTTTCATAC	ATACCACCCC	AGGGCACACC	AGGGGGTAAC	AACCCCAAAG	480
GGTCCCTAG	GGAGCGCATG	CAAAATATCC	ACNCTCCGCA	TGGCATCTCC	CNNTTGGAAA	540
GGGNCNCCCC	NAAATTTGGG	CCNAAANCCC	TTAAAAGGNC	CCTGTGNCN	CAANNACTTC	600
NAATTTCCCG	NTTNGGCCCC	CCCCCCCCCTC	CAACGGGATT	TAAAACAGGN	GGGNGNGGGA	660
AAAACCNCG	AGGGGNTTTT	TTTNGCCCTT	TTCCGAAANA	ANCCNCCCC	CCNCGGAAAA	720
AAATATTTTT	TTTTNGGG					738

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 748 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1228UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GATCATGCCA	TTCTTACGCT	TTGCCACAT	GGACGCCCAA	ATGAATTTCT	GTGTATGCCA	60
GGATGCTGAC	GATGCAGCTG	AAGCAGGAGA	CGACAGCGAT	GTGACGCTG	GTTGTATGAC	120
GCCTACTATT	TCACCTGTGA	ATACTTGTTT	TTGGCCCTCT	GTAGACATAA	TCTTGTTAAG	180
GACAAAGCTC	CTGCTGTGCG	TGTGTATCAG	GTCAAGTAAA	GTAAGCGCCT	TAAATGCCAA	240
TTTGGAGATA	CCGAAGATTA	AGCATGCCAA	ATCGTTAGCC	GGCCTAAACT	GCCATGGGTG	300

EP 0 866 129 A2

ATGCTGGGAA CAGGTAAATA TGGCCTGAGG TGCTGTGTAC TTACCTGATA TAAAAGTATG 360
 CAGTATGCGG GGGCCTTCGT ACGTCTGCT GTAGTCTATC GGATCCTGGA TAGATGTTAG 420
 5 TTCATCGGTA AATGGTTGGA GATAATTTTC GTCTCGGAG GCTGTATAG TAGTTTCTTG 480
 TGTTTGAATA TTCATGAAAT GGTGCGGCTA GCTTTCAGCA GCTGCTTCTT TAGTCTTTC 540
 TCATACTGAC TTCTTCGCAG ATCTACNCCA CCGCCTTGGG GCTGACCCCA GCACACTTAT 600
 10 GATTTTANA AGGAATCCCC GTAATCCAAN GCGCTTNCNT ACCCTGTCCC AATNGTTNCA 660
 TCAAAANGTC ANNCCCTCNA TTTCCTCTTT TCTCNCCAAA ACNCCACNT TAATTGAANA 720
 NGNCCCTTTC ACCCGGAGAG GTGGCGNC 748

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 653 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PAG1229RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GATCGTAACA ACAAGGCTAC TCTACTGCTT ACAATACCT GTGTACATC TAAGTCGTGT 60
 ACAAATGATT TACTCTCGG CAGTATGACA TTGCAATCCG CCGGCACGG CCCAGACCTT 120
 TCGTCTGAA CACCAGTTGC CGGCTGCTA TGGTTCAGCG ATGCTAAAAG CACCTTATTC 180
 35 GTATCCATCT ATAATGTGCG AGAAAAAGAA TCATCGGTT CTAGCATGA TTCTGACTTA 240
 GAGGCGTICA GCCATAATCC AGCGGATGGT AGCTTCGGG CAATGCCCG TCGACAGCC 300
 GCAAAAACCA ATTATCCGAA TGAACGTTC CTCTGCTACT AAGTCAATT ACTATTGOGA 360
 40 TAACATTCAT CAGTAGGTA AACTAACCT GTCTACGAC GGCTAAACC CAGCTCAOCT 420
 TCCCTATTAG TGGGTGAACA ATCCAAGCT TACCGAATTC TGCTTCGGTA TGATAGAAGA 480
 GCGACATCG AAGAATCAA AAGCAATGTT CGCTATGAAC GCTTGACTGC CACAAGCCAG 540
 45 TTATCCCTGT GGTACTTTCT GCACCTCTAG CCTCCACTCC CGAGAACTAA GATTGATAG 600
 CACACTTTCA TGTTGTATC AACTGAATC AATCAGGACT TTACCTGTG TAC 653

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1229UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

	GATCAGATAC CGTCGTAGTC TTGGCCATAA ACTATGCCGA CTAGGGATCG GGTGGTGT	60
10	TCTTATGACC CACTCGGCAC CTTACGAGAA ATCAAAGTCT TTGGGTCTTG GGGGAGTAT	120
	GGTCGCAAGG CTGAAACTTA AAGGAATTGA CGGAAGGCCA CCACCAGGAG TGGAGCCTGC	180
	GGCTTAATTT GACTCAACAC GGGGAAACT CACCAGGTCC AGACACAATA AGGATTGACA	240
15	GATTGAGAGC TCTTTCTTGA TTTTGTGGGT GGTGGTGCAT GGCCGTCTCT AGTTGGTGGA	300
	GTGATTGTGC TGCTTAATTG CGATAACGAA CGAGACCTTA ACCTACTAAA TAGTGCTGCT	360
	AGCATTGCTT GGTTCGGCAC TTCTTAGAGG GACTATCGGT TTCAAGCCGA TGGAAGTTTG	420
20	AGGCAATAAC AGGTCTGTGA TGCCCTTAGA CGTCTCTGGC CGCAGCGCG CTACACTGAC	480
	GGAGCCAGCG AGTTATACCT TGGCCGAGAG TCTGGTATCT GTGAACTC	528

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 756 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1230RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

	GATCCCGGTA GCGCTCTGGC GGCATAATGT CTGCCGTATA GGTGGACTCT GGCTGTATTG	60
40	TCCGAGGGG AATGGCATGC TTCTTGTTAGA AATACAACCG ATCATAGGGC GAGCTCATAT	120
	CCACCGTACG TCGCTGGGAC ACGTACTTTT TGA CTGAGCC ATCATTCGG CTGTTCATTG	180
	CGACTCTAAT CTGATTGAGA ACCCTGACCT CTAGTGCTAT AGCGCAGGGC GTACCTGTCT	240
45	GATGATGCGC TTTTCAATGC TCGAGCGTGC GCAGTGTTAC ATCGATCGTC GCGGACGATG	300
	TTTAAGCAGG ATGCTGAGCT AATATGTATC GGTATAGGCT ATTGGCAGTA GACCTGGGTA	360
	TATACGCTTA GATATGGACA AGATGCTGCG CCTAGACATC CAGAACTTAA CCAGGCTCGG	420
50	GTAAAGCCA CCCAGATAAC ATTGGAACAT TAGAACAATT ACCACCGCGA ATGGAGGGGA	480
	ACCCAGTCGA AACCCACGG CATCCAATAG TTTCCCCCAA CNGCGAAANG GCAGAATGCA	540
	CCGCCCAATG CTGCCCAAC GCCCAGGCG ACCCTGACCC CATTGACCTN GAAGCCCTGG	600
55	GGCNAACTG CATTTTACCC CCCCCATTN GGAAAAANTG ACCGAATAAA ANNCCCCCN	660

AAAAANAAAN GGCCNCCCCC AATTACTTTT TNNCCNNGG CCCCNAACCC CNGGGCINNAA 720
 AAAANNANIG GGGGGGGGTT TCCGNNMTT AAAAGG 756

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1220UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GATCTTCCGC TCCACTTGGT TGGGCTGGCG CATGTCAAAG GTTAGTAAAA GCCCCGAATC 60
 GTGTACTGAC GCGAACTTGT TGGATCTTCC GGAAGAACAC AAGGACGTAT CCGCGCCCAA 120
 GGACGGGAAA TCATAGGTGG GCATCCACTT TACATCAOAG ACGGAATCTG AGCCTGAATT 180
 GAAATTCAGG TCGCTGCGGT TCACCTTGTA AGAGTGGGAC CGCAAGTCCC ACACCTTGAT 240
 GCAGCCGTCC TGGCCACCGC TGATAAGGAG ATGGCTCTGG CCCATGTTGA AGTCCACGCT 300
 GTTGATGGAA CCGAGTGTCT CCGACAGGCT CCGTGATCAG CCGGGAATCC TTTCGCCAGC 360
 CCGGGTTGAT ATCGTAGATG GAAACCGAGG TCGACGTCCC GCATATGGCG ATGTAATTCT 420
 TGTGGTGGTG GAACCCCGCC CTGTGAGTCC CGAAATCCGT GCTAATCTTG CGCATGTTT 480
 CCGGGCCCAT GCTGCTCGAA GAACTTCGTC CCGGCCCGCC AAGGNTCCCC NGTTGTTTNT 540
 GTTATTCCGT GCACCCCTGCT GCTCCCTGTA CCTCCGTCN AACTTGTTCA GCGCAAATGG 600
 TCTTCCCCCN CCCCNC AAC CATGCCCCCT ANCTTCTTTG ATTTTITTTCC AACCTTGCCA 660
 CCCCCGGTTG CTTGGAGGGG GGGTACCCCC CCAAAAACCC CNGCCCCCCC CAATTNTCCC 720
 ACGCCCNCCC GAATTGGTT TNCCTNNGG NCCCCNNGG GNCNNAAAA CCTCCCTAA 780
 AGNA 784

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1231RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

EP 0 866 129 A2

GATCATCTGC GTGAAGGGCG ACAGAAGCCT GGGATGGAA ACATTGGAAT TGATGCATTA 60
 ACGCAAACAC ATGGGTCATT TCCTCAAACCT CAACAGAAAG GGGACGAAGC TGCGCACACA 120
 5 GTGCTGCAA ATCTTTAGCC GAGTCTGAA AATTCAAAGT CCGTAGTTCT CGTATGTTGA 180
 AGCCAGATCC ATAAACTATC TTCTCACTCG CCGATGCAA AGTATCAAGG AATAGGCGAC 240
 AATCGGTAAT GATTGGCTCG AGCTACGGCA GATATTGGCG CACTTCTGAT ATCCGTGGGT 300
 10 TGTTCGATGC ATGATGCACA TGAATAAAG GAAGAAGCTT CGAAAGAGGT ACACGGCCCG 360
 GGTAGCCGTG TGATGAGAGC TGTTAGTTCC GCTTCAACAT CAGCAAGTTT CTCTATAGGG 420
 GACGAGGGT CGTCAACATC ATTTATTAGA CACTCCAGC ATTTGTTCTT GAAAAAAGT 480
 15 NGTGCATGNA CAATNGCNC CCCCCCTTTT GAAANGCCG AGAAAATTTT CCTNNAANAC 540
 NAATNCTING GTNNAANTGC TTNNAAANCC CCTTNAATTA AACCCCTNNN GGCNCAAAAA 600
 AATTNMTTAA ANCTTTTINA ACNCCCCGGG AAACANAAAC CCCCCCCCCA AAAAAAACA 660
 20 NGTTTINTCC NCCCCCCCCC CCCCCGANNT TTNNAAAACC TTNNAAAAT CCCCCCCCCC 720
 CNAAAAANCC CNCNAATTTT TTTTTTAANC C 751

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1231UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GATGTCAGC GTGCATGAC TTGGCATTC AAAGGGATGT GATCCCTGAG GGGAGGCTTG 60
 CAGCAGGCGC GCTCCTTGTT TCACATCATA GCTGTGAG GCGGACTGA TTCAGCTCTC 120
 40 AAGGCGAGCA CCTTCCAAC GCGCAATAGG GCGCCCTCC TGGGCTGTGC ACGGAATAC 180
 CTCAGACACT GCGTTAAGAT ATATGTATTT AAGAGGGCAC CAGCTGGCTA TCAATTGCC 240
 TCTCTGCTCT TGTTCCAACA CCAGGCAAGT ATCATGATGT CTGCTGCAGG AAAAATGTTT 300
 45 AAGAACAACG GCCAGAAGGA TGAGCGGAAG AATGCGGGCC AGAGAGAGGA GCGCCAGTAC 360
 AGGGTCGGCG ATGAGCAGGG CTGCGGCGC CAACAGCAGG CTGACTTGGG GCGCCAGTAC 420
 CCAGCAGGCG CCAAGCTGCG AGCAGTTGGA CGACACTTGG NGCTTCCNA CATTTGGGCC 480
 50 CCCCACCAAT TGGGNCOCNA GCAAAATNGG CCCCNCNCT TTNATTTTNG GGGCGAATGG 540
 GGCNPAACCT ATCCCCAANT TGNGGNAAC TCCCCCCCCA GNANGAGAAC NCATTTTTCG 600
 55 ATTGAAAAC NCACCTTNNN TTGNNPAAC CCCCCCCNA AAAGCCANGG GACTGTNTT 660

TTTNGAAAAC GNCCCCCTTT NIGTCNCNNN ANAAATTTT CTANAATTTG CGNGGATTCC 720
 TOCCTTGGGG CCATTCCNTT TTTACCCCTT TAACCCCCC CC 762

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 746 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1232RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GATCTTATTA ATGAATTTT CCCCACGAAG CTTGTGGAAT TTTGATTCTA TGCTTTGCAA 60
 GCACCTCAACT TGGGCTGTGG TCATGCGAAA CTAACACGCC GCGAAACAGA TACTGCCCAA 120
 GCGTTAGCAC TCGCTCTTTG CCGTGCTACA AACAAAGTGC GAGCATTAGC GTGTGACTTA 180
 TTTAGGGTGT GAATATACAA AAGTAAGGCG TACATGCGA TATCTCTCTT GTGTGCTCT 240
 CTCTTACCTA CATCTAGATG TATTACAGGA ACTTCCCCGC GAGATTCAAG GCCAAGGCCG 300
 TOCAGCCCGT AAAGTGCTGC ACCCGTTCAC CTTTCCATCG TTCTGGTTGT ATTGTTCGGT 360
 AACAAAAACC ACCTTTCCCC AAANTCNAAT AATTGNTTCA ACAGGTTGTT CCCCCATTG 420
 AAAGGGATAN NGTTTAAAC CCGGNCNAAA CAANNAANGG GNNGVTTTTT TTGGGCANAA 480
 ACCCCCCCCC NAATTNAACC GCGTGGGGCC CTNCNCAAAA TTNTTTTTTT CCCCCNVGG 540
 GGNCCCCNCC NAANAACCCC CGNGTINNA ATATATCCCN CTTTINOCAG AAGNGANTCC 600
 CCCNNAACCC GNGGATNT TTTTGTGNTT TAAAAANNCC CCCCCCCCCC CCNGGGAGGG 660
 NNTTCNCNC CCCANCATTT NNACCNAGN GAGTTTTTTT TCCCTCCCGG GGGAAAAAAC 720
 ANTGTINNTT TINNNCCNA AAAAAA 746

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1232UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

EP 0 866 129 A2

GATCAGTTTG CCGTAATTGA TACAAAAGGC AACTGGTGCG TGGGCGACGT TCGAGGAGT 60
 AAAAAGAAGT CCCGGCGACT GCGCTTGTTA AGGAAGTTTA GCGGGACTAT TTTTGACCCA 120
 5 GAGGAGTACT CCAATTGGAA TATGATAGAA TGGTCACATA TTCACACAAG ATTGCTTTGTG 180
 ATGAATAGGT CAACTTTTCAT GGAAATTGAC TTTGTAGACG GATGGCAGCA GGAAATTGTC 240
 CAAGCAAAGA CGTGGTCTAA CTTCGGCGAT TTAAACGCC TTTCOGATGA GAGCAGTGTG 300
 10 CTACTIONCT GCAAAGAGAT TATATTCTTA GACCACAAGC AGCAGGGAAC AAAGAGGGCG 360
 CTATCCTGGA AACACAATTG GGATAGCAAA GATTCATCTC TAAAGCTTGC TATACACATT 420
 TCTGGCAGCC ATATGAAACA ATATTTACAT GCATTCCTAT TTCCACCATG ACTCCCTGCA 480
 15 GTGCTTATGT GTCTTCTTC CCGGTCCGAA AACACTTTCC ATTTTTCAG CCATCCCCCC 540
 GCTGNTGTGT TTTTNCATT TACACNCCNG NTTTTACCGA AATTACCTCC CCGNIGINOC 600
 NAGAAACCGA GTTINANAGA ACCACACCCC CTTCATTTTC CCTANNVTG GCGGCCCCCC 660
 20 CCAGGGCGAG AGTTTGGGN CCCCCNTTTT NTGNACCATN TTNCCCCNOC CCNCNAGGGT 720
 TCCCCACNT AAAANCCCTG AAACCCCTTT TCCCCCCCAC ATTTTNGGTN GGGGATN 777

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 734 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1233RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GATCAGATG CTGTGGGCAT TGCTGCTGCT GCTGCTCTTG TGCCCCCAA GCGCGAAGT 60
 40 AGACAAGCTG CCAGCAAGCA CTGATTGGTA CAGGAGCTTT TTGTTACAGT TCTTAAGCAG 120
 GTTCGCGGTC GAGTCGCGT TGTTCAAAAC AGCGCCCGGC TGCAAGCTCG AGCTCGACTC 180
 CCCCCCGGC GACGAGCGCG TGGAATACAC CTCTGATGCC GGGTCGGCAT CCTCGCTCT 240
 45 CGCAGTCCCC CCGGAAGCAA AAAATTCTTC CACGGATGTA TTCCCGTGGT TGCCAGCTG 300
 CGCACCGGCG GTACCGCAG CGCTGTGAC ATTGGACGTG ATATTCTCCA TCAGCAGCTG 360
 CGAGCTGATG CCCCCCGGG CGCTGTCTT GCTCGCATCT GTAACTGCT CAGACCCGA 420
 50 GTTTGTGTTCT GTGTCACAG AACGAGAGCT TCAACCATGT GACGACGAG GCGGTTTTG 480
 CCTTCACCA CNAATTGGG CCTTCTGCT GGAACNCAA CCCCCGAAT TTCCCAACT 540
 NTGATTCCCN AANTGCCCCG CCNCCNTCC AAATTANAAT CCCCATTGN GNTTGAAATN 600
 55 GNCNAAATNA AACCCNTTT TCCCCNNVN CNNNNCCNG GCCNAANGA GCGNTGGGG 660

GNTTAAANNC CCCNACCCCC AAANTTATAC CCTTTTTTTTG NNCCCNCCCC CCNNCCCTNT 720
 TTTTTTNCCC NTCN 734

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 761 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1233UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GATCCAGCTT CCATATAAGC TGTGTGTTGC GGTGCGGACC TCTACAGAAG TGGTGATATA 60
 TGATACTGTT ACCACGAAAC CCATTGCACT GGTGGGAAAT TTGCATTACA CCGGCTAAC 120
 GGACCTCAGC TGGTCTGACA GGGGCCACT ACTGCTGCTG TCATCAACAG ACGGTTCTG 180
 CTCTATATC TCAATGGAGG ACAGCTATT TGGCGAGCCA TACAGTTCG AGGCACAGCG 240
 GACGGATTCT CTCATACTT CCACTCCAAA AAGCAACATC TTCAGGAACA CCCTGCGGTC 300
 CAACCCGGTC AACGTAAAGC GGAAGCACTC TGTAGGCGGC CACAACGACT CACCCATAAA 360
 GCGGCTGCC AAAAAATGTC GCGCTTTCC CCGTGGTGG TCGATGAGGG ATCTGGGCGG 420
 GCACACAACC GCTACTCTT AGCAAAGATC TCAAGCTCC GAAGGCGCAT CCAACCGTC 480
 CTGTGTTAAT GACAACAACG GGGCACCTA GTATCCCCNC ACGCATCTT ANAAGTTTG 540
 ATTCCNNTAT ACTNAAATAC AAACCCGANA ANCNNTTTTC TTGTINACAA ACTTTTTTTT 600
 GACCTGCATC AACTATATCC GNGNGGTCA TTCTTGCCGA ATGCCCCCTC CCCTTANAA 660
 CNCCNTACN TAAACCTTCC CNCNCCATA TTTACTCATG AATCNCNGCG AANTCNCCTG 720
 GGATCNCCA NCTTTTGGGT AGINTTCCCC TTTTGTGTC C 761

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 728 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1234RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

GATCACAGTG CTGTGGGCAT TGCTGCTGCT CGTGCTCTTG TGCCCCCAA GCGCGAAGT 60

EP 0 866 129 A2

AGACAAGCTG CCAGCAAGCA CTGATTGGTA CAGGAGCTTT TTGTTACGT TCTTAAGCAG 120
 5 GTTCGGGTC GAGTCGGGT TGTCAAAC AGCGCCGGC TGACGCTCG AGCTCGACTC 180
 CCCCCTGGC GACGACGCG TGAATACAC CTCTGATCCC GGGTCGGCAT CCTCGCTCT 240
 CGCAGTCCCC CCGGAAGCAA AAAATTCTC CACGGATGTA TTCCCGTGGT TGCCAGCTG 300
 10 CGCACCGGGC GTACCCGAG CGCTGTGAC ATTGGACGTG ATATTCTCA TCAGCAGCTG 360
 CGAGCTGATG CCCCCGCGG CGCTGTCTT GCTGCGATC TGTAACGTC TCAGACCGA 420
 GTTTTGTTC TGTGGTCCC ACGAACGAG ACGTCCAACC ATGTGTACAA CAAGNCGTT 480
 15 TTGCGCTTCA CACCCATTG CTTTCTG GINGAACGC AACCCCGAT TTCNCAACG 540
 GNATTTCNT ATNGCCCGC CCGCCNNA AATANAACC CAATGNGN TGAAANGNA 600
 NAAANAACC CCTTTTCCC CTTTTCAAA CCGCGCCCN AAGGCCNNT GNGTGNNTAA 660
 20 ANCCCCCCC CCAATTTAA TCCTTTTAA TTGCCCCACC CCGACCTT TTTTNNTC 720
 CCTNNNCN 728

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 782 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
 30

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1234UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GATCCAGCTT CCATATAAGC TGTGTTTC GGTCCGACC TCTACAGAAG TGGTGATATA 60
 TGATACTGTT ACCACGAAAC CCATTGCACT GGTGGGAAAT TTGCATTACA CCGCGTAAC 120
 40 GGACCTCAGC TGGTCTGACA GCGGCACCT ACTCGTCGTG TCATCAACAG ACGGTTCTG 180
 CTCCTATATC TCAATGGAGG ACAGCTATT TGGCGAGCA TACAGTTCG AGGCACAGCG 240
 GACCGATTCT CTCATACCTT CCACTCCAAA AAGCAACATC TTCAGGAACA CCTGCGGTC 300
 45 CAACCGGTC AACGTAAAGC GGAAGCACTC TGTAGCGGC CACAACGACT CACCCATAAA 360
 GCGCGCTGCC AAAAAGTGTG GCGCTTTCC OCTGTGGTC TCAANAAGN ATTTGGGCCC 420
 GGACCACNAA CGCCTACTCC TTANCAAAA ATTTTTCAAA NCCCCAAAG GGGGTCCCAA 480
 50 CCGNCCCTT GTTTTGTGA AAAAAAANG GGGNCTCA TTTTINCCC CCCCCCNC 540
 CCAAAATTTT GGGGATCCCN NNCNAAAA AACACCCCC AAAANCTTT TTCCGGTTAN 600
 NAAANNITNN CNNTGACCC CCNCCCCC TTCCGGGNG TCATTIVINC NAATNGCTCC 660
 55 NCCCCCTNA AAGNCCCN CNAAAAANC CCCCCCCC NTTTTCCC NNNAACCCCC 720

GGGAAAATTC CCNCGGGAN NNNCNANITTT TTCTTGGTCT CCCCCNITTT NTTCOCCTINA 780
GG 782

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1235RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

20	GATCCTTGAG AAGCCAGATA ACGACGAGGA CGAGGAGCCC AGTGACGATG AGGATGCCGA	60
	CGACTACGAC TCGGATTCTC CCCGGCCCCG CGACAGCGGC AGCGAACTCA GAGACCCCTC	120
	TGCGCCGGCG ACATTGCTA CGGAAGTCA CGGATCCAGC GTCTGGCCT CCCCCTTGAC	180
25	CTATTCTTTC CGCTCCGTCA TGTCCACTA TGGCACACAC AACTACGGAC ACTACATTGC	240
	CTTCGCAAG TTCCGTGGTG TGTGGTGGCG CATCAGCGAC GAAACAGCGT ACATCGTGA	300
	TGAAGCTGAG GTCTTGTTCA CACCGGGCGT TTTCATGTTG TTCTACGATA TGACTATGAC	360
30	GAGGCGACCG GGCAGTTGCG TGACGACTTG GCGTGCCTAC AGGAGCCCAG TCCGTGCTGT	420
	CAGATGGGGA CGGAAGAATA CGACTCATTG ACCGGGTCCA CCAAGACCTC GATTCAACGA	480
	NCCAGCTGTT GCTCCCGCCA ATAAACTTTG TTTGGGGCTG GCGGGOCATA TWINCTOCAT	540
35	GCATGTTTCAT GCCCCACCG GACATGTTTG ATCCANATAC TTTTGTGTTN GTINCCCCCT	600
	TTCAGNGVIT CCCCCNAAGC AAGATTCTTA NNCTACTTGC CTNGTGTGTC CCNCTGGTT	660
	TGGNACCCCA AATTCCINTT NNCCVITINT GGGCCANCCC NNGGNAACC CNCCCTTTTT	720
40	TTTCAAACCA GGVTTNCCCT TTINGCN	747

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1235UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

EP 0 866 129 A2

GATCACACCC GTGTCTTTTT CAAAGGTGAC CTGCAACTTC TTGTTATTCA AGATGATAGT 60
 CTCACCTGTCC TTTGACACGC TAGCAGGGTA AAATACCGAC TCCTGGCGGT CAGGGTTTTT 120
 5 TGCAGCCATG TTATCCCAIT GCAAGGTGCC TATTGGGACC AAATTTTCCC CTCTGTGTGT 180
 CAAGGCTCC AAAGCTCTCT CTATGAACCG ATCTGCTAGC TGCAAGACCT TGTTAAGCAT 240
 TGGTATTGCT TCATATTTGT ATACCATTTT TATACATGTC CCGGAAGGA CATCGTGGAA 300
 10 CTGCATAAC AAGATATCTT CCCATAGAGC GTTAATATCA TTAACAGGGT ACGTGTACTT 360
 GTTAGGGCT AGTAGOGAAA CCTTTGTGGC AATCCACTCC AAATCATGGA TCTTAACCTC 420
 AGATAGTCTC ATCAACGGTT TAACGCTGTC CTGTGTGTA TACGTGCTC CTATGGAAAT 480
 15 CAAAGTTACA ATCCGCCCAT CCAAGTTGGC CAATGNGTTC CCANTGTCTG NCTTCNGCAT 540
 AATATCACCG TAAAAACCGT TTANGGAATC CCNACCCCC NACCTINGGG AANAACATTG 600
 CATTCGCGGT TAAAAITGAA CGANACCCC CCATTTGTTC CACNCCCC TGTTTGAACC 660
 20 CCNCCCCGN CNCCGNACCC NNAAAAANAA CGTTGOCNA ANGTTCAITN AAAGTTTGT 720
 TCCCCCGGG TTAAANCC NAATTTINAN AAGGTTCTT TTCCCCGGG GGGTTG 776

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 722 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1236RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GATCTCCCTC CGTGAAGT ACGTGAAGT TTTGAGACTC TGCAAGTGT CTTTTGATAG 60
 CTTCGATGCC TTAGCTCCCA TGCTACTAT AACGCTGTCC CGGCTCAG CTAATGTGGG 120
 40 GCTGCTATC TTAGTCCCTA ACTCTTGGAA GGTGAGAGG CCATAAGCCA CGATGGGGA
 GCTGCTCAA TTAATGCTC TGAAAGCGGT GTGTGGTCC ACTTTCCAG ACCCAAGGCT 240
 ATGCCGGTGA CCTGACCTCC GGTCCGATG TGACGCTGG AGGCGGTGG ATGCCGGCC 300
 45 TCATGGCTGT CGGTGCGAA GGAATATCTA CCAGGACTT GGCTGCTGC GCAATTTGCA 360
 CTGCAGCTTG CAGTGAGGT CTTGGGAAG CTCACGGCA GGGCAGGCA GTTACAGCCA 420
 TGGCACAGG CAAGCCCCG GAGTTGACCG GAGTTGGTTG CCAGATATTG GCGGTCCAA 480
 50 ATTCTGANTA GCCCTTTATA TNAGANCCCC NCGTTGAAC CCCAAGNTT TTTATGGGA 540
 TGGTTGAAT TCGCCCCCT GCGTTAACC CCCCCAACC CTTNCCCCG GCAAAANCAA 600
 55 ATCTNCCCC NGTTNAAAA ANCCGAACN NNAAAAATTT AAAAGAGACA AATCANNNCA 660

CCCGNGAAAA AGAGCCCTNT CTTTGTAGAA TTCCCGGGGG GGGNGTAAA TTNAACCTTT 720
GA 722

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1236UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GATCTTCGTC CGCTTGGGT CAGGAAATC AAGCGGGATG AGCTCTGTG TCAGTTTACC 60
ATAAAAGAGC TGTTTTACAA GGTGGAATG CTGCGCTCT TCATCCAAGC TGAGCGGGAC 120
GGACGCACTC TCAATTTGGT AGAGGACGTT CCAATGCAT TCGTCACAT CTGCTGTCT 180
GCCAATCTCC AATGTGTTTT CTAGCTGGTC GGAATAATT TTGCAACAT AGGTGGAAGT 240
TTCAGGGGCT TCGGCTCTG GACTCCCGAC CATGGTGATA TCTTTACCTG AGTCATCAIT 300
CTCAACAGCC TGCTATCTT CAAGCGGACC TGGCTGGTG TTTTACCCN TTGGNGGNN 360
GAANTCCAAT ANNCCCCCTT TCTGGGGTTC TTGAAAGNA TINGGANAAT TNNITGGGCC 420
GGTINTTACC NTTTTINGANA GAGACCCCTG GNNITCNAN ACCNAAATNN TCCNNGGGG 480
CNCOCGNCG AATNTTTTTN TITCCAAANT TTCCNAAANN CCNCTTTINT GCTTTTCCCC 540
NTTINGNGG NAGCGCCCCA GGGGNCOCG CGAANTATC NGGGGNTGG AAAAAANAAA 600
NAATTTCCCA NAGGGGINTT TTTTTTCCN TNGAGAAGG GNGGTANAA AAACCCATTT 660
TTTCCCCCN NTAGANAACC CCTTTTNCNC CGGGGNTCC NGCCGGGGG ATINTTNGG 720
GNGCNTGN NACCTCCCTT CCCNCTATA NAAATNCCC CGGGGGGGG TTNNVTTTC 780
CCCNNAAN 789

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1237RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

EP 0 866 129 A2

5 GATCCGGGTT GAAGACATTG TCAGGTGGGG AGTTTGCTG GGGGGCACA TCTGTTAAAC 60
 GATAACGCAG ATGTCTAAG GGGGACTCAT GGAGAACAGA AATCTCCAGT AGAACAAAAG 120
 10 GGTAAAAGTC CCCTTGATTT TGATTTTCAG TGTGAATACA AACCATGAAA GTGTGGCCTA 180
 TCGATCCTTT AGTTCCTCGG AGTTTGAGGC TAGAGGTGCC AGAAAAGTTA CCACAGGGAT 240
 AACTGGCTTG TGGCAGTCAA GGGTTCATAG CGACATTGCT TTTTGATTCT TCGATGTGG 300
 15 CTCTTCCTAT CATACCGAAG CAGAATTGGG TAAGCGTTGG ATTGTTTACC CACTAATAGG 360
 GAACTGTGAG CTGGGTTTAG ACCGTCCGTG AGACAGGTTA GTTTTACCCT ACTGATGAAT 420
 GTTATCGCAA TAGTAATTGA ACTTAGTACG AGAGGAACAG TTCAATCGGA TAATTGGTTT 480
 20 TTGGGGCTGT CCGACCGGC ATGTCCCGGA ACTACCATCC GCTGGATTAT GGCTGAACGC 540
 CTCTAAGTCA GAATCCATGC TAGAACCGGA TGATCTTTT CTGCACATT ATAGATGATA 600
 CGAATAGTTG CTTTTANCAT CGCTGAACCA TACAGCCGCA CTGTGTTCAA CGAAGTCTGG 660
 CCCTTCCGCG ATTGCA 676

(2) INFORMATION FOR SEQ ID NO:281:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 709 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1237UP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GATCCCGTAC ACGAAGAAAA TCGGACGGGC CAACCAAACC CAAAGTTCAA CTACGAGCTT 60
 TTAACTGCA ACAACTTTAA TATACGCTAT TGGAGCTGGA ATTACCGGG CTGCTGGCAC 120
 40 CAGACTTGCC CTCCAATTGT TCCTCGTTAA GGTATTTACA TTGTAATCAT TCCAATTACA 180
 AGACCCGTAT GGGCCCTGTA TCGTTATTTA TTGTCACTAC CTCCCTGAAT TAGGATTGGG 240
 TAATTTGCGC GCTGCTGOC TTCTTGAT GTGGTAGCCG TTCTCAGGC TCCTCTCCG 300
 45 GAATCGAACC CTTATTCCCC GTTACCGTT GAAACCATGG TAGGCCACTA TCCTACCATC 360
 GAAAGTTGAT AGGCAGAAA TTTGAATGAA CCATCGCCAG CACAAGGCA TGCGATTCCG 420
 AAAAGTTATT ATGAATCATC AAAGAGTCCG AAGACATTGA TTTTATCT AATAAATACA 480
 50 TCTCTTCAA AAGTCGAGAT TTTAAGCATG TATTAGCTCT AGAATTACCA CAGATATCCA 540
 TGTTAGTTAA AGAATATCA AATAAAGAT AACTGATTTA TGAGCCATTC CGCAGTTTCA 600
 CTGTATAAAT TGCTTATACT TAGACATGCA TGCTTATCTT TGAGACCAGC ATATGACTAC 660
 55 TGGCAGATTG AACCAGATAC TATCTTTAAG ACACCGAAA TGCGCAACA 709

EP 0 866 129 A2

(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 820 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1238RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GATCACGGCA ATGAAAACT ACGCAAACGT TACAGACTTT GAGTGGTACA TCGCCCTGCT	60
TTGGGATCTC TGCATAGTCT CCCAGGACCT GCAAGACAAG ACCCTCGCGC AGAAACTGGG	120
TGAGCAAATT AGAAACATCA TGGTGAAGGT TCCTGACCTG CGGGATCGCA CTTTGGGGCA	180
GATTGTGCAG CTGGTGAAGA GCGAGGACAT CACGGCCCCG CTGCCCCGTG TTCTGAAGGA	240
GTGCATCTGG TGCCCTGGCG AGTATTCTGTC GTTGCTCGAC AATAAGGATG AGTATATTCT	300
GCTATTGGCA GAAAATTCGA AATTATATGA GCTGAACTA CAGCAAACCT TGATCCCTGC	360
CATTTTGAAG ATTTATAGCA ATTGGTGTAA CGAGTCGGTG GTGACACGG GTCCGTATTA	420
AATGGGTAC CGAGCGGATA ATCACCCCAC TAGAAGATCT AATAATCTCG AAGAACTTCG	480
AAGTCAGGA GCGGTCTTC GAGGCTCTCG AATCTTACCC TTNTTCTTGG ACNCCCCCTC	540
CNAAATNNTC TGNATCCCTA NCNGCTGGCA NCTTACNAAT TCCINGCCCA NTTCINCAAC	600
CCTTTGAATT NACCNCNNIN CINTCGGGCC CCCAAAAANC TCNNNNNAAA CINTTINTCN	660
ATGGGAACCC CCTTINCCCN AAANGAAGCC ANANNNNACC GNAAAACNCN CTGAAGNGA	720
TTTCCCGAG TTTTGANAAC ATTTCNCCCN AATTTTCCGG GACGGCCAAA AAGGGTTTIN	780
CAAATTANIT CGGGGGGGGA AGGGGAANGG GGGGGGNNNA	820

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 875 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1238UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GATCAGAAAC GGCCGGCTGC AAGAATGGAT GCGGATGAGC TTCGAGCAGT TGAGGCATCG	60
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EP 0 866 129 A2

CTTATGCAAA AAAAGAAATT CCTCAGATCA CGTGACAAAG TTTCGTGATC TCTAAATGTC 120
 GACGGTTGGG CGAAATGTGC CGTCTCTGTC TATAAAATAT AACTAGTTT CTCTACCACT 180
 5 AGACTGATTG GGAATATCTA AGCTTTCACT TGATAGCAGC AGGAGCACTT CATAATCCAG 240
 TACCTTCTTT GCCTTATCCA CACTAGTCAT CTCATOGAAA ATGTCACAGC CAGTGCAGAG 300
 AGCCGCGGCT CAATCCTTGA TATCCAAATA TGTCATAAG GAAAGCTAA AATACATGCT 360
 10 TACAAAGCAC TTCTGGGGCC CGTATCGAA CTTTGGTATT CCGATTGCTG CGATTATGA 420
 CTTGAAGAAG GACCTGAGT TGATTTCGCG CCCATGACG TTGGGCGCTG TGGTATACTC 480
 AGGTATTTTC ATGCGTTACT CGATGGCCGT CACTCCCAAG AACTACCTCT TGTITGGGTG 540
 15 CCCACTTTAT AAACGAGTCC CGGCAACTC GGACAGCGTT CCGCTGGCT CAAGTTTCAA 600
 TTACTTCGGC GAGAGCCCTG CTGTCAAGC ACCGAGAGA CCGCATAGG TCGTTTGGC 660
 TCCGACACG TTGCATTACA GCGTGACCA CTACATAGAA TATTATTAG CCGACTATCC 720
 20 TACAGTTTC TAGAGCTAGT CGAGATGCGT TTGCTGATA CTGCTCGGT GGGCCAGGCC 780
 GTATCTTGCT CCTCTGGCT TTGCTGGGT GCGCAGCTCC CANTTGNCG TTCNCGATNN 840
 TCTGTGTCC CGTATCCATT GNTAAATGT CTCCC 875
 25

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1239RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

GATCAACTTA GAACTGGTAC GGACAAGGG AATCTGACTG TCTAATTAAA ACATAGCATT 60
 GCGATGGTCA GAAAGTGATG TTGACGCAAT GTGATTTCIG CCCAGTGCTC TGAATGTCAA 120
 AGTGAAGAAA TTCAACCAAG CGCGGGTAAA CGCGGGGAGT AACTATGACT CTCTTAAGGT 180
 45 AGCCAAATGC CTGTCATCTT AATTAGTGAC GCGCATGAAT GGATTAAAGG GATTCCCACT 240
 GTCCCTATCT ACTATCTAGC GAAACCACAG CCAAGGGAAC GGGCTTGGCA GAATCAGCGG 300
 GGAAAGAAGA CCTGTGTGAG CTTGACTCTA GTTTGACATT GTGAAGAGAC ATAGAGGGTG 360
 50 TAGAATAAGT GGGAGCTTCG GCGCCAGTGA AATACCACTA CCTTTATAGT TTCTTTACTT 420
 ATTCAATTAA GCGGAGCTGG AATTCAATTT CCACCTTCTA GCATTTAAG TCCTATACGG 480
 GCTGATCCGG GTTGAAGACA TTGTCAGGTG GGGAGTTTGG CTGGGGGGC ACATCTGTTA 540
 55 AACGATAACG CAGATGTCTT AAGGGGGACT CCATGGAGAA CAGAATCTCC CAGTAGAACA 600

AAGGGTAAAG TCCCCTTGAT TTGATTTCAG TGTGAATACA ACCATGAAGT GTGGCCTATC 660
 GATCCTTAGT TCTCGAGTT TGAGCTAGAG TGCCAGAAAT TACACAGGAT ACTGCT 716

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 793 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1239UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GATCATCTTC GATCCCTTAA CTTTCGTCTT TGATTAAATGA AAAAGTCCTT GGCAAATGCT 60
 TTCGCACTAG TTAGTCTTCA ATAAATCCAA GAATTTCCACC TCTGACAATT GAATACTGAT 120
 GCCCCCGACC GTCCCTATTA ATCATTACGA TGGTCTAGA AACCAACAAA ATAGAACCAA 180
 ACGTCTATT CCATTATTC ATGCTAATAT ATTGAGCTT GCGCTGCTT TGAACACTCT 240
 AATTTTTTCA AAGTAAAGT CCTGGTTCG CTAGAGTACA AGTACCTAG GTTAGOCAGA 300
 AGGAAAGGIT CGGTTGGATC CGTACACGA AGAAATGGG ACGGGCCAAC CAAACCCAAA 360
 GTTCAACTAC GAGCTTTTTA ACTGCAACAA CTTTAATATA CGCTATTGGA GCTGGAATTA 420
 CCGCGGCTGC TGCCACCAGA CTTGOCCTCC AATTGTTCT CGTTAAGGTA TTTACATTGT 480
 ACTCATTOCA ATTACAAGAC CGGTATGGG CCTGTATCGT TATTTATGT CACTACCTCC 540
 CTGAATTAGG ATTGGGTAAT TTGCGGCGCT GCTGCCTTC TTGGATGTGG TAGCCGTTTC 600
 TCAGGCTCCC TCTCCGGAAT CGAACCTTA TCCCGTTAC CGTTGAACC ATGGTAGCCA 660
 CTATCTACC ATCGAAAGTT GATAGGCGAG AAATTTGAAT GAACCATCG CAGCACAAGG 720
 CCATGCGATC CGAAAGTTTA TATGAATCAT CAGAGTCCGA GAACTTGATT TTTATCNATA 780
 ATNCNCTCTC CAA 793

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 836 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1240RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

EP 0 866 129 A2

5 GATCTTAAAA TAAGATAGAA TGGTAATAAA TATCATTCAG GTACAATAGA TGCTGGTGTT 60
 ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT 120
 10 ACAATAATG AAAAGAAAAT TATAAATACA AATACTGTTA CTAATCTTTT AAAAATAAAA 180
 TAACCATGCA TTGGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA 240
 TGTACATGTA ATACCATTA AATGCATAATT ACTATTGCTG CAATAATAAA TGGTACTAAA 300
 15 TAATGAAATA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TCCTCATAAT 360
 CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA 420
 GCACCTCAAT GTGACATTTG TCATATATACT AAACAATAAC CTAAGAAAGC TGCTGCTATA 480
 20 GGTAAAATAA AGATAATAAC ACCAACTGTT CCATACAATA ACTCTAGGTG ATTTATAAGA 540
 ACCATAATAT AAACCTTTAC CAATATGAAT ATACATACAA ATAAAGAAGA ATGAAGCACC 600
 ATTAAGAATG CATATATCTA ATTATCCACC TATTGTACTC TCTCANAATA GTTCCTACCT 660
 25 GATGANAAGC TATCCATATT ANAAGAATAT GCATACCTTA AAAATAOOGT TANAATTGAA 720
 TACTAACATA ACCTATAANA CCNAATTCAC CATAATAATG AGAGGGTGAG GNGAACCATA 780
 CNTACNATAC TAATTTAATT ATTGATTICT TCCCNTTTT ATTATTAAAT TTTAAT 836

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 860 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1240UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

40 GATCTAGAAT TATTAAGTCA ACTATTAACT AATATCTATA ATAATAATGG TTTATCATTA 60
 AAATCATTAAGATAATTAT TAATAAATTA CCATTTAATA ATGATATATT ATTATCAAAA 120
 AATTATGTGA ATAAAATAAA TAAATATAAT TTTACTAATTA ATAATAATTT AAATAATAAT 180
 45 AAAAAAGATT TAATTAATTT ATATACTTTA GATAATAAAT TATTAGATTT AAGTATTCTT 240
 AATAATATAT TATTAGGTAA ATATTTAGTA GGTAGTAATA TCCAATTAAA GGGTAGACTA 300
 TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAAGGTAC ATTTAATAAT 360
 50 TATATATATC AATGAAGTAA ATTAAATAAT TTATATAAAT TAAATTATAT ATCACTTAAT 420
 ATTAATAAAC TTAATAATCT ATTTATTAAT AAAAATGGTA TATTTAATAT TAAATTAAA 480
 TTAAATACTA TTAATAAAT ATCTATAAGT AATTICTTAT TTATTTIATA ACATTTTAAA 540
 55 ATGTTTTATG TTTAAATAGA TAATAACAAT TAAATAATAA AAATTAAGAT GCCACAAATA 600

TTUCCATTIT CCITTTATGAA TCAATTACTT ATGGTTTCCT ATTTATTTTA CTATTTTATC 660
 CTTCATCTT ATGINTTTTA CCTAAGAATT TAANAATATA TACTCCTAAA TATATATTCC 720
 NAAATTATAA TAGTTATTAA ATTTAATTA ATCCANTATG ATCCNTATTT ATAAATATAT 780
 AAGAANATTT TAATATATAT ATATGAATNT TATATCNCN TGAACCATTG NAATNNATTA 840
 TAGTTTACAC CCOCTANATC 860

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1241RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

GATCTAAATA TATATAATTT AATTATATAA GATTAAATATA AACTTTTTTA TTATAATATT 60
 TAAGTATTAA ATTATTTTAA CTATTATTAT CATTTATTTAA TAAATTAATT ATTTGATTAT 120
 TAATACTTAT TATATAATTA TTATATAATT TACTTAAATC ATCATTATTA ATATTTATAT 180
 AATTATAAAA ATAATATTTA ATATGAATAC TATTTAGTCT ATGTTCAAAT TTAAATTTAG 240
 TTATTAAAAT ATTATTAGAT ATTATTATTT TCTTTAATAA ATTATTAAAT AGATTATCAA 300
 TAATTAATAT ATTATTTATT AATTGTTTAT TAAAATAATA TATTTTATTA TTATAAGAT 360
 TTAATTTATT TAAATATGTT AAATTATTAT TTTTATATA ATATCTATTT TTATAAATAT 420
 TATGTTGATT TATATTATTT AATCTTTTTA TAAGAATTAT TATTAAAATT AATTTTAACT 480
 TTAATTTCTT ATTATTAATT TTTATATTAT TTAATAAATT ATATTTCAAT TTATTTATTT 540
 ATTTATTTAA TTAAATTAAT TATTTAATTA ATATTTTATC ATTATTTAAT TAATTAATAA 600
 AATATTATTA AGAATGTAGT TAAAAATACT TATAAAAGGA TCCGAACCTA TATTATTGTT 660
 TATGAGACAA ATCCTTTTAC CCATAAGCTA TATAGTTTGA CTATCATTTG AGANTTGGGT 720
 NNNCCCCCTA TGCTNNCATC CTGVTGTCOC CNCTAAANGA ATTINTTINT TNANANATGA 780
 AAAANITATT TATCAAAGAA TTATAATTTT TTAANAAGGG GNANAAGGAA AGACCCG 837

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1241UP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

GATCTGTATA CTAGAGCTTA TTTTACTTCA GCTACTATAA TTATCTTAT TCCTACTAGT 60
 ATTAAAGTAT TTAGTTGATT ACTAACTATT TATGGTGGTT CATTAAAGATT ACTAACACCA 120
 ATATTATATC TATTATCAAT TTTATTTTTA TTACTGTAG GTGGTTTAACT TGGGTAGTA 180
 TTAGCTAATC TATCATTAGA TGTAGCATTG CATGATACTT ATTATGTAGT ACTACATTTT 240
 CATTATGTAT TAAGTTTAGG TGCTGTATTG TCTATGTTTG CTGGTTATTA TTATTGAAGT 300
 CCTCTTGTTT TAGGTTTAAA TTATAATGAA AAATTATCAC AAATTCATTT CTGATTAAAT 360
 TTCTTAGGTC TTAATATTAT TTTCTTCCTT ATGCATTTCT TAGGTATTAA TGGTATACCA 420
 AGAAGAATTC CTGATTATCC TGATCTATTG CTAGGTGAA ATTTAGTATC TTCATTTGGT 480
 TCTATAATAA CTATTATATC ATTAATGTTA TTCTTTTATA TTATTTATGA TCAATTAAATA 540
 AATGGTTTAA CTAATAAAGT TAATAATAAA TCTATTAATT ATATAAACT ACCCTGATTT 600
 TATTGAATCA AATAATATTT TCTTAATGAA TACTACTAAA TCACATCTAT GATTTATATG 660
 AATCACCCTT CTTAATCNAT CAATTAAACC CTCTAATCCA ACTTTAAATA NNCITTAATTA 720
 TAAATTANNA ATAAATTTAG TGAANAATTT AATNGTAANC AATNTTTTNA NGGANITTTAT 780
 CTCNNTCCAA CCGAAACTAC TTTTATCCTT AANNAAAACC TTAAATNAAT GGACCNCANA 840
 NTCNNAACNN GTTTTC 856

(2) INFORMATION FOR SEQ ID NO:290:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1242RP

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GATCAGTGC TAAATGTCG GGTACATTAG TGCACCGTA CACCGCATTG CGACATTACG 60
 ACGCTTCTTG ACTAACCAGG TTATCACGTG TATATAGTTA CATACGAACG TCTGGTACAA 120
 GGAAGAGCCG GCGGAAGTC CACTTCACCC TTAAATTGCC ACATTTTCATG AGCATTTACA 180
 ACAGAAGCAC AGCTGTAAAC GTTCTCGAA CTCGTGAAGT TTCATATTGT TCCTTAAGGG 240
 CCCTTGATGT TGCAGTTCAA GCTAGTTCTG TTGGGAGACT CGTCGGTGG TAAGTCGTCA 300

55

EP 0 866 129 A2

ATTGTTTCATC GCTTCGTGAA GGATTCGTTT GATGAGTTCC GGGAAAGCAC AATCGGCGCC 360
 GCAATTTCTGT CCGGTACCAT CAAGCTGGCG GACCAAGAGC ACGCAATGAT CAATTTGAGA 420
 5 TCTGGGACAC CGCGGGACAG GAGCGGTACA AATCGCTGGC TCGATGTAT TACAGGAATG 480
 CGAACGCGGC GTTGGTGGTG TTATGACGTT GACACAGGAG GATTCTCTAG CAAAGGCACA 540
 GAGCTGGGTT GAACGAATTA AGAGCAGGTT GGTAAGAGA ATTCTGGTAT CTTCCTGT 600
 10 GGGCATAATT GATTNGGGGA NGAGGANOGG AACCNAGGTG ATTGAACOGA GAAACNAGGC 660
 TCCCCAAACC CNGGGTGANT TCCCNAGGT TTNNNOCAAA CCGGCGGTT NOCGGATTIN 720
 TTCNNGGAT TGGGGGAANN CTAAACNNG GCNATTCNT NCGGGCCCC CCGNTCCCC 780
 15 ANITTCNTT CAAGNCCCC CAAAGAACAC CCTGGGNTT ACCCCCTCC N 831

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 878 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1242UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

GATCTGTGTC ATTGTGAAGG AGGAGACGAA AAACGCTACC ATCAGTGTG CCGTCGAGAA 60
 CAAGCAGCTC ATCCCATTC A TTTCGCTGGC GGAAGTGGAG ATTTCGAGG ACGTACTGT 120
 GAAGGCTTC CCTAACGGCT CTGAGAAGAT CGTCTTATG GGGCCACGG ATGAAGCGAA 180
 35 GGAAGCAAAG GTGAATGTT AGAATTACTT GAACACTTTA GCAAGCAAG TATCTGAGAA 240
 AAAGATTTG ATTCTCGCA AGTTCAGCC TCTGATCGAT GCAGAGGATG TCAGGGAGAA 300
 ATACAAGGTC TCGTTATCT TCCCAACCGC CCTTGGTGAT GATACTGTGT CGTCTACGG 360
 40 ACTGTCCGCT AATCTTGATG ACGGATCGC ATATGCTCGC CAGTCGTCTA AGCAGTACAT 420
 GGTAGAATCT TTGGAGGTAT CCAAGGCTCA CGAAAGAAT GTCGCTCATG CAAAGAATTT 480
 AATGTTCTAC TTCGCCAGTT ACGAACTCCT CCAAGGATAT TAAGGAATTC GTTCCAAGGG 540
 45 ANITGAANTT TTGINCTACC CACTCCCGGA GGGATTTCG CCGTTTAAAN AAGNTTTTNA 600
 ATNCACANTT TTCCAAAGG GNGAATTTG GGNACAAAA AAAANTGINT TCCCCGNCNA 660
 TNCCTTATTT NTTAACNACC CCCCCTCCCC NGPTTCNCC GNTGAANACC NAANTATNAC 720
 50 CCTTCCCCC AGNGATTTAC CNGGGCCNIN CAGGGGANTC CACTTTTTIN CTCCGGANTC 780
 AANAAAGGGA AANACCNGN GCTTTTGCCA GNTGANAAA AAATCCNCC CCCCAGAGG 840
 TAAGANCCNN GNAAGGNGG CCGTTTGGGA GAATNCCC 878

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1243RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GATCGCTAAT CCCGAGGTTT GTTTTGAAGT CTGTGATCAG TTGGTCTCC ACATCTTTGA 60
 GAATTCTAAT AGCCTCCGAT GGCAGTTCCT CCAATTCCAT TCGCACTGG GCAGACTGTA 120
 TCTTTAGAGA GTAAATTTTC ACACACAAAG AGTCAATCTT GTCTTGAACA TCGTCAATCA 180
 TATACTTCAG TACATCGTTC ATGTTTGGTA GATTCCTGA GCTTTTGAGT GCGCCTTTTC 240
 CTAGCGCCGA AAGGTTCCCC GCTTCATTGG ATGAGAAGCC TAGAACTGAC ATCATGGCGT 300
 GGCAGCATGT CTTCCGCAAC TGTGACAACC AATAATTCAA GACTGCGGGG CCTAGATAAC 360
 AGGGCCCTTG CCCGTCGAG TCATAGCCTG AAGCCTCCAA GAAGGATTTT CATAGGTTAA 420
 CATAATTATC ACGCTCTATC GGTGAGAATT GAAGTTGGAT TAAGTAATGA TGCTGCTTTG 480
 GGAATTTAAT CTGATATTGG ACATCATTCT TTGTATGACG GATACAAAGG TTGAAACGTG 540
 GGATGATATC AAGAAGTTCT CTTGCGGTGA AAGTCACACC GTTGACACGT TGGAGCTTTG 600
 CGAATTGTTT GCGGGATCTA GATGCATCGG ATTGTTGCCC AGTTCCCTGG TATTCTGGCA 660
 GACTGTGTTT GATATACTTT GGAGATCCCT TGAAGGGATG CACTGCCATT AGAAATACAC 720
 CTTGAATCCN CTAGTGAATG ATAGGTTTAC CCGAACCCCC ANTTTGTATA CCGNCAGAG 780
 TTTGTCATC GGGCCCTTCN NCTTCTGCC CACATTGCCT CCNATTTTA TCCTGAAATG 840
 CTTA 844

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1243UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

GATCTGTCC CACCACGGGC GCAGGAAGT GTACTGGCCT TTGAGATCA ACTCTGTCAG 60

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GACGTGATC TTTCGTGCT AAAAAGGCGG GAAGCCGCAC AACACGGTGT ATAGGAAGCA 120
 GCGGATCCCC CACATGTGCA CCTTCATGGA GTAGCGTTG TCTTCACCA CCTCGGGGCG 180
 5 GGTGTACCCG ACAGTCCCGC ACGGCGTCTT GGTGTGCTA GCATAAATTT GCTTCGAGAG 240
 TCCGAAGTCT GCGAGCTTTA TCACACGAT CCGCGCGCCC CCGATGCCAG GTCGGAACAG 300
 GCGCTGCTCT TGTTTTGTCT TTGGTCTGTC CCACTGTCTC AGCTGCTGGC GCTTGTCTGG 360
 10 TATAAATCA ATTGGGGAGA ACAGCAAGTT TTCTGGCTTG ATATCCCGGT GGACAAATGCC 420
 AAGCGAGTGC ATGTGTTTTA CCGCGAGTGC CAGCTGCCTG ATTACATGTC TAGAAAGGTC 480
 CTCGAAAAA TAAGTGAGTC GCACGATTTT TCCAAAAATC TCCCCCCCCG GCAAGCAGCT 540
 15 CCTGGACTAT GAAGTAGTAT GACTCGGTCT CCTCGAAGT CGATAAACGT CACAATGTTT 600
 TCGCCCGAGG ACACCGCCTT GTGGATGGTG ATCTCCTTCA GAACTGCTCT CCGGATGTG 660
 CCTGTTCGCG CCGCTCCNCC CACTTNNNNC GGGCCCCCCC NCGTGCCCCC ATCGTTAANA 720
 20 GGNCCCTTTT GCTGATCNC TTGACGGCNC CGTTTNNNTAC NGNCNAAGTN CCTTTTCGGN 780
 CGNCCCTCAG CCGNCCNNG ANNCCNNGN AAACCCCNCC CATTNNCC NAACTTNTCC 840
 CNCAANCCAA GNNCCGAANC CCCCC 865

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAGL244RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GATCCTGCCT TATCAAGAGC GCCATCGAA CTCCCCCGG GATGTGTTG AGAGGTAGCG 60
 AGCTCACTC CACAACCTC TCATCTGAAT CGTCTTCGTA TGTACTATCT AGCTCTTCAG 120
 CGTCGCGCGA TGCAGATTCC GCGCTGTCTT TCACCTGTTT CAGCACCGCC TGTGCGTTAA 180
 45 GCTCAGAGAG GCAGGCATGT GTGCGACCCC CGTATATCTG GCCCAGGTAA TACCCGTTG 240
 CCAGCGAAGC CATGTAACG CTCAGTATGA ACGTAAAGTT GATACCTGCC ATCCTAGTTT 300
 CTGTTTGCTA TTCTGCATGC TGAGTGCGCA AGCCAAGTTG GTTGAAAATT CCTTCAAGCT 360
 50 GACAATCGCT GGTCTGCGC GCAGTTCAAC ACAGCAAAC TCAGAGAGAG GTATAAACGC 420
 CATATATAGG AGGAGACTAC TCTATTCATC GCTATCTTT TCAGCCACA GTTCTCTGCG 480
 CTGCAAAAT GTGTGTGAT TCGCCAGCA TTTTGTTCAT CGTCTGACA TATTCGTGCG 540
 55 TTATGATTG GAATCCGTGG AACATTCCG CGCCAGCTG TTAGATTAGG CCACACCGCC 600

CTTGTTAGAC CATAGTGGGC GAGTGGGATT ACAGGTTATC CNTCGAACAC CATCCGTAGA 660
 ACCAGTGGCT ACNCTCCGGN GTTAAACCCC TACGCTNCCC TTCCACTTNC CGATAGTCCA 720
 TACGGGAAT TTGGGGGGCC AAAAAAGTGC CCNGCAGGAA CNCAAACGAA GNNTCAAAGC 780
 CNTGINTTGG GCNGGTGCCN TTTCNCNAAA NCAGTGGGTA NTINTAANCC NGCCNCTTAT 840
 TTTCCCAT T 851

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 859 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1244UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GATCAATCTG ACAGTTGGAT TGATACCAGG TGCTATCTCC TTATCAGCCT TTACAGTGAC 60
 GAAGGAGGGA TTGGATTGGG GAATGGAGAA TAAAGATATT TTTGATCCAT CACCAGAAGG 120
 ATTTGATCCC TCTTTCAGTG AGCATGCCCA ACTTTTACTC TOGGAACGTA TAATGGGAAA 180
 CTTTCTCGTT CCAAAGTCTG GCATCTGGAA TTATGCATTT ATGGGTGCTG GATTTAACAG 240
 AGAGCTACGT TACGAGCTAT CTCTCGACAT ACCACTOGGA TTTTATGATG AACAGCACCG 300
 TGCAACGCAT TTTCTACAAT TCAACGAAGT GGCAGCTGAC GATACTTTGG AAGCAGAACA 360
 GGAAGATTTA TTCTCTAAG TACATATTAA GGATAGAGCC AACTTGCAA CTAGCTTCAG 420
 TTGGGTATGA ATCCATATA TGTATATATC AATACACGGG CCACTCATGG CTGGTGACCC 480
 ATTTAAGCAA ATACCATATT TTTTAATGTT GCGGTGATTT TATAATCTCG ATATCATGAT 540
 TTTATTTATA GGAGATGACT TTTCCCTCTA CAACGCCACA TTATAGAAGA CGTCAATGC 600
 AGCACCCAGG CTGAAGCCAG AACGGAAATG TTGGAACCAG AACAGGCAGG TTTGAATAGC 660
 TCGACATATG AACCTCCCA GAACATGTTT TTTTGAACA TCNAATGANT TTCTGCCAAA 720
 AACANGAAAA TGGACNCCNN GCATCATCA AAAAAACCN TCCTTGAACC TGACAAAAAA 780
 TATGCACCN GATTTTTTGA TCACGGANNG TTTTCTTTAC NCCAATTAAA TAGGNCOCOC 840
 NGAGATTTTT ACACCCNCC 859

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1245RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

10	GATCAAAAC AGAGTACCCCT CCGCACGAAC TTCCCATATG AGGCCAGAG AGAACAACAT	60
	CGCCGATCAC CTATATCAAC AACGAGACC TTGGTCTGCC GAGAAGTCA CAGCTTATCT	120
	TATTATCGAT CGAATGGATG TTGGAAAGAA GATACAAAAT AACGCATAAT TGCTGAATAT	180
15	ATTGCACGCT TCTAACGCAA ACGACGAGCC TCAAGCTCAG ATTCCATCAA GACCAAGATG	240
	TCGTTCTCTC TAACTGGGCC CTTGACGTTT CTGACAATGG TTCTGGAAGT GTCTGCAAG	300
	AACTCAACGC GGACCTGGGT GACACCACCA CGAGAACCGG TTCTACCTAG AACCTTGATA	360
20	ACCTTAGCTA GAGTGACTGG GGTCTTGGAG TCATTTTGA TCTATTGCTT CTGGATATA	420
	AAATATCTAG TAAAAAGTGC TGAATAGGTG AGAGGAAGAT ATCATGAACA GGCGTTTIT	480
	TTTGATGCCC CGAAAAATTT TTCAGGTCTG CGATGCCCAT CCGAGGTGAA ATGTGCTTGG	540
25	GTTCCTGAAA AATCACATCA TACGATAACT ATGGGTGCAC CCAAAGGCTT TGGCAGCAGC	600
	GAAGTGGCGG AAGGTTAGCC AGCCCGAAC GAAACCTGAG AACAGGTTAA GCTCAGGTGA	660
	ATTGTTTGCT TCTATTGCTT TACAGTTCAT CTTCGGTAA TTGCAGTATC CGTTGATTCC	720
30	CCNCAGCTGA CCAGCGGTIN ATTCCCGTTT GAACCTTCAG AGNTCNIGAA ACCCTNGINT	780
	TTTCAACCCN TGACACNTAT ATNCCCCCT TATATGACTT CCGTGNATNC CCG	833

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1245UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

50	GATCCGGGTA ATACAACGCC TCGGACCCCT CGCGGGCTAA CGAGAAAATC GCGCTAAGCT	60
	TCCAGCCTAA TCATAATAAA AGGGGCATTG GTGGAAGCTT TCTGGTACTT ACGCGAGTAA	120
	ACAAAAGGCG CAAGGACGTT TCAGAAGAAG CCAGAAGCAG CAATGAGOGA GATCAACTCG	180
	ATCATTCACA GAGTGAATGT ACTGGTCTCA AACTGCCCA AAGAGAAGGA TGCAGGCTG	240
55	GAGAAAGAGT GCGCGCTGAT CAAGTTGGGC GGCATGGTAT CTAACCGCGA ATCGGGCCTG	300

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TTGTTTGGAG AACTGGGCGA GCAGATGGAT CGCAGAGGG TGCTACGGCA GCCATGGATT 360
 GTGAGTPTTG TTGTGCGCTT GGGCAACGAG CTATGCGGGC GTGGGAGGTT GGGCGAGAGC 420
 5 TTCTGGGGCA AGATATTGGT TCGTTGGAT GGACAGACCC CGTTATTGAC AGTTACTAAC 480
 AAGAATCCAG GGTGCGAAGT TTTCGGGTAA TGTTGCGGTC CATGGCCGGT TGGTGGAGGC 540
 GCTGCTGGAC GGGGCGCTGT CGGTACGGC TCCCTGTGGG TGGCAGAATA TGGCGTGTGT 600
 10 GCTCCAGCTG TCCTATNNAC CNCCGGATT NTCGGAAGT TGNIGNCCCC CCTTTACCCC 660
 CCCCCTNNCN AGNATGGTTG GNGACNNTT GNNCGNTNC CAACTTCCTT NNNCCCNCT 720
 TTTTGTGNAC NITGAANCNA TTTTCCCCC TINAANICAA CCNACNGTT NNNCAACCC 780
 15 CCCCCCCTT TGGGAAAANN AGNAAAAAN ACCTTTTCCA CCNCGATNC CCTTTGNCA 840
 NCTGGAACNG NNNNNTCNC CCTC 864

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 830 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1246RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

GATCAACAAT GATTGTGGCG ACGGGGGGCG GGGCGTTCAA ATTCTACGAC GTGCTGCTGT 60
 CGGAATTTC GGGCGTGTC GATATCTCC GGTGGACGA GATGGACTGC CTGACGAAGG 120
 35 GGTGGACTT CTTCATCCAC AAGGTGCCCT ACGAGGTGTT CACATACAAC GACCTGGACG 180
 GCGAAGGCAC GGTGGATGCG GTGGCGGATG ATGAGATGTA CCGTACATG CTAGTGAACA 240
 TAGGATCCGG GTCTCGATT CTGAAGGTGG AGTCGCCCAA CGAGTGCAATG CGTGTGGGCG 300
 40 GCTCGTCATT GGGGCGGGC ACGTTGTGG GACTACTGTC GCTAATTACT GGGCGAAGA 360
 CGTACGACGA GATGCTGGCC TGGGCAAACC AGGGCAATAA CGGGAACGTG GACATGTTGG 420
 TAGGCGACAT ATACGGCACC GACTATGCCA AGATCGGCCT GAAATCCAGT AATATGTCAT 480
 45 CGTGTTCGG GAAGGTCTTC CAACGGGAGA GCGTACCGC GCCCCCTGGC GGGCCTGACT 540
 TGGCGTCTG CGACCTGAC GTGTGAGATC CGAGATTGGA AATGAGAAAT CCNCAACGCC 600
 GAATNTTCCC ATCCCTCTG TACCATCTC CAACAAATCG GCCAAATGCT TNCTGCAGCC 660
 50 AAATCCCCAA CTCGAAAAA NNTCTTTGG GTCNITATNT CCCCCTTTT TACCCCTGA 720
 CCTTTACCC CCCCCTAAT CNGGTCAAN GNTTTTACA NCCNCCCC TNAGGNTTAA 780
 55 GGTNNTGGCC CCNNGGCCCT TMTGCCCCA AAAATTCCC NNCNNTCTN 830

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1246UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

GATCGTAGAG CGTGAGACGG CACCGGCGGA GCGGCCAGCG CCGGACGGTG TGCAGCCAGG 60
 GGGGTTCCTT GAGCTGTACC GCGCGGCAGC GATATCTAGC TGCGGCCAAC GCTTCAGAA 120
 GAAGAATGGG CAGCGCAGGC CGCCCGCGGC GCGCCTCGCC GCAAGCGAGG CGGAGAAGAT 180
 CCACAAGGAA AACATGGCGT ACATCGAGGG GCTGTGGAG GAGCAGCGGA CGGCAGAGCG 240
 CCGCGAGCTG TTAGAGAGCC TGGACCCCAA GGTGTGTCAG GCGTGTACC GTCGGTTGGA 300
 TGCACGTGCA GCAGCGGACG GAACGGCGCC CTTAGTGGCG GAAGTCAGG GAGCGGCAGG 360
 CACGTGGGTG GCGGCCACCC GCGAGGAGCC GATGATGCCG CGCTGGATG ACGGACCGT 420
 CGACGCGCGG CTAGCGCGGC CACAGGCTTC GATGCCAGAG GCGCGGCCA CGTAAGACCT 480
 GCCAGCGCCG CTGGAGGATG CGGACGACAT CGCGCCCCAG GAATACCACT TCATCAGCAG 540
 ATGGACCATA TGAAGGACAG GACTTGCTAC GAGATATCCA CTTCCTCGC AATGAGACTG 600
 TGGCGCCCGG ACTGGACATC AACGACCCCA ACTTTATGAG CAGCTGCAAG AGAATACTTC 660
 CGGATNITCC GAAAGAAANA AATAACTINGA ATGGATGAAG GCCACTGAAC CCTGACACTC 720
 TTCINCTAAC TCNCGATTT TGCCGAATGC CCTCCAACTT AGGGCCCATG TCCCCCCCCC 780
 CCGGAATTIN NCCCCNNAA CNGCCTCNC CCTTCGAAAA CCCCCCTTIN CCGGCNTTCC 840
 TCCCATTTGC ACNITCCCCA C 861

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1247RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

GATCTGGCGG CGCAGCTGGG GCGCTGTATT GCTCCCTGTC GTTACTGTGG CGCGCGCGGC 60

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GTGTCTTATT CGGCATCGCG TAGGGTTCAC TAAGCCCTC CAGGACGGGC AAAAAAGCG 120
 CAGGGGCTC ATAGAGCACC ACAGGCTCTG GGTGGGAAG CACGTGCATC CGCGGGTGT 180
 5 GCTTGCTCAC CGCCTGTGC GCCTTGCCCC GCTCTGCCAC CGGCGCAGGC GTTCAGGCC 240
 CGGGGGCGCG GGGGGGCTG TGCACGTAG CGGCACGGGC GGGGGGAGC CTGGCTTGC 300
 GGACCGCTT GATGACCGC TTGTGGCCG GCGCGGCGC GCTGGCCGA GCGAGGCCA 360
 10 GCGCGGCTG CACAGCATC AGCATCCAT CCACGCTTT CCTGTGTCT TCCACACGC 420
 TGTGGCTGA AGCAGACTCT GGGCTATCT CTCGGCTCG GACGAAAGC CTCGTGCTG 480
 CTGACTGC TCTGCCGTA CTTCGGTGA AGTACGGCG CAGTGGCGC GCGGCTTGC 540
 15 CCTCGCGGC CGCGGGCGC GCGAAGGCC CGTTAGGGG CCGAGCGGC GTCAGACCT 600
 CCTCATCGAA TCGAACGC TCGCGCGTC GCGCAATCG CCCACGGAAC CAGCCCCCG 660
 GGGGTTNG NGGCGCGGC GCGCCCTC TTTTNAAAAC GACNACNCT TGNAAANCCG 720
 20 TTACCCNCN CNNTCAAAC NCCNGGAAA ATTTTCGN CN ANNNNNNNN CCCCCCCCC 780
 NTNCINGAA ANAANGNCN GGCCCTNNG 810

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 630 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1248RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GATCAGATAC CGTGTAGTC TTAACATAA ACTATGCGA CTAGGGATCG GGTGGTGT 60
 TCTTATGACC CACTGGCAC CTTACGAGAA ATCAAAGTCT TTGGGTCTG GGGGAGTAT 120
 40 GGTGCAAGG CTGAACTTA AAGGAATTGA CGGAAGGCC CCACAGGAG TGGAGCTGC 180
 GGCTTAATTT GACTCAACAC GGGGAACTC ACCAGGTCCA GACACAATAA GGATTGACAG 240
 45 ATGAGAGCT CTTTCTTGAT TTGTGGGTG GTGGTGCATG GCGTCTTA GTTGGTGGAG 300
 TGATTTGTCT GCTTAATTC GATAACGAAC GAGACCTTAA CTTACTAAAT AGTCTGCTA 360
 GCATTTGCTG GTTGGCACT TCTTAGAGG ACTATCGGT TCAAGCGAT GGAAGTTGA 420
 50 GGCAATAACA GTCTGTGAT GCGCTTAGAC GTCTGGGC GCAGCGGC TACACTGAG 480
 GAGCCAGCA GTATAACCT GCGGAGAGT CTGGTAATC TTGTGAACT GTCCGTGCT 540
 GGGATAGAG CATTGCAATT ATGCTCTTC CAGGAAGAAT CCTAATAGC GCAGTCATCA 600
 55 CTTCGTTGA TACTTCCCT GCGCTGTAC 630

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1248UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GATCGCTAGA TGCCCAGGAT GAGACTGTC AGGTTAGGCA GGTTGTGTAT GCGCCGCCAG 60
 AGGGAAACCC AATGACTTTG CATAGAACAA ACCCGCCATC ACCCATGTCT TCGCTGTAT 120
 AGAGACTAAG GTATCTGACG ATCCCTTAGC GACTCTCTCC ACCGCTCGAC GAGGCCATTG 180
 AGCTCTTAGC AACTGCACAA ACCTACTCGA ACTCTGTTTC CAGACTTCTT TCTGTTTGTG 240
 TTCAACTGCT TTCCCATGAA GTACCCCCCA GGCTATTTT CTTACCCGCC TGGTGTGTGT 300
 CTATATACCC GGTGTATTT TTGATAAAA ACTCAGCTCT TCCTCTACGG CAGAAATATA 360
 TATCCAGTCC TTAGCGCCAT GCGAAAATCT GCCTTTTAC CGCTGTTTCT CCCAGTCTTA 420
 GCACTGGCAG AAAAAAGATG TATGGGTAT AGGCGCTGGC CCGCGGAAA AAAAAAAAAA 480
 ATAGAAAAAT AGAAAAATAA AAAGACGTGG GCGCCCCGC GGCAGACGA AGAAAAATA 540
 GCGGCCACC CTTCCCAAGC AGACGAACAG GCGAGACATA ATAAATCCCA CACCAGGGAA 600
 GAAAGTCTTG TGCAAGCTCC CGGCTCATAC GCTGCCATCT GTTCCATCCG GNTTGCAACC 660
 AGTATGGATG TTCAAGCATG TCCGANGCTC CGCTGCCCTG 700

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1249RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

GATCATGCAA CATTTCTTCT TTTCCGCTT TCTGCCTGTG CCGGACGGTG TGTCCCGCC 60
 CCGCACTCT GAGGAAGAGC TTGGGACTG CAGCGAGCAT GCGACAGTA CCTGGGGCGA 120
 CTGCTGGGC ATTCCGATAC CCAGCGGGT GGCGGCTCC GAGGCACTC GCAAGCATTC 180

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TAAACCACTT CCATTGATT GAATCAAATT ATATATACCA TTAAGTAGAG CTACCATGCG 240
AACCTTAGCT GGGACGCAGT AAAGATTGGC GGTTCOCAGA TCAGCTTCTC GGGGTGATC 300
5 GATGGCCTTT TCTTCGCTAT CAGCTTCTCG TACCTTAGCA GCACGTCTC GTTCAGGTAC 360
AAGATGTGCT GGCCCTTGTA ATATCGCAGT ATGTTAAGAG CCTTGGCTGT GTGCAGTATG 420
TCTGTAGTCG TGAGCGATGT CATGCTACTG ATTTTCATCGA TGTGATCTC GGTGCGGTTT 480
10 TCGACTAGCA GCTTGATCAG GGTATCGGAC CAATAGGCTC TGTAGAGAGC AGCCCAAGAT 540
CAGAGAGCGG CTTCCTCGGC ACCCAACTTG TTCTCCTTCT TAGAGAGCTC CATACGAAAC 600
TCAATCAGCA GCGTGCCGTA CCCCATCCGC TGGTACTGAG GGAGCGTCCA GAATACACGC 660
15 CACATTGTAC CCGTCCGCCA NTCCTTTCCN TTGGANAATN CCCACCAAGT NGGTGCCCCA 720
CTCACTCCCC TGTGTTCTTG CANTAAAAA AAGGTCAANT TCCTATNACT CNTGTGNTCC 780
AAAAAACTTT GANAAAGNTN GTTGGNACC ACTTCCTNNT NCCCCGTCAA TTCAAAT 837

(2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 853 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
30 (A) ORGANISM: PAGL249UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

35 GAOC TGCCGA TGGACNGCCG TTGGCAGGTG ACTGCOCTAC GGTCTTTAGT CCCC GCAAAG 60
CGGATGGCCT TTGTGGGCAC ACGCAAGAAC TTGGCAATGA TGTTGACCAC GTCCATGGTG 120
TCCTTATCTT CCTTGATCAT TGTGAAGTGC ACGCAGTTCT TGGAGGGGCC GTACCCCCAG 180
40 TTAATGACAC CGTCTCTGTC TCTTGCTGTC TCACATAGT CCTCTTTGCT GACTCTGGTT 240
TTACGGTTGG CCAGGGCAAT CTGGAATGTG TTGGACGCGG AAGTGACCGA TTCAAGCTCA 300
TTGTTGAACG CCTTTCGTAG CAGCTGGTGG ATCTTCGTCC GTGCAGCTTT GTCGTCAAAG 360
45 CTCTGGTGG TTTCATTTTT CGTGACGTTT CTGTACACGG CCTCAATCTG CTGCATGTCC 420
TCCTGCCCCA GTAGCTCTAC CAGCTGGTTC CGCAGCTCTG CCTCCACCGC GTGGTTGTGG 480
CGCCGTTCCG GCTCTTCAGC CTGCTGTGCC TTCACCTGGT CGGCAGAGGT TTGGGTTTAG 540
50 CAGGCATTTT GAACCCATTG TCCCGCAAGT ACACCACTGT TCCATCCTTC TGGATCTCAT 600
TGACCATGAA GTCCGAATAG CGCTGCTTGA TCTGCCCCGT AAACCCCTGGT ACTCTGCTGA 660
GAGGTACTCT GTGATCCAAC GTGATTCTT TGAGTCCATC GGTCTCCGNT TTGGCCCCCT 720
55 NCCNCAAAG TTCCTGGCTG CTCNNANCC GCTCTNTAAT CCCCCGAAAN TCTGTACNNT 780

TCNCNATTTTC CNNNINNNCC TACCTNAACC CTTGTINAAC CTTCCACCCN ANAANTCATA 840
AATATTCCCC NOC 853

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1250RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

ATCTTAATTT AAAATTTTAA TTAATTTT ATAATTTAGA AATATATAAT CTAGAGATAT 60
ATAATCTTAA AATCATAGGT AAAAATACAT AAGATAGTAA GAATAAAATT AGTAAAATAA 120
ATAGAAAACC ATAAGTTAAT TGATTCATAA AGAAAAATGG AATTATTTGT GGCATCTTAA 180
TTTTTATTAT TTAATTGATT ATTATCTATT TAACATAAAA CATTTTAAAA TGTATATAAA 240
TAAATAAGAA ATTACTTATA GAATATTTAT TAAATAGTAT TTAATTTAAT TTTAATATTA 300
AATATACCAT TTTTATTAAT AAATAGATTA TTAAGTTTAT TAATATTAAG TGATATATAA 360
TTTAATTTAT ATAAATTATT TAATTTACTT CATTGATATA TATAATTATT AAATGTACCT 420
TTCATAATAT TTATTTTTAT TAGTCTAGTA ATATTTCTAT TTAATAGTCT ACCCTTTAAT 480
TGGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAT ACTTAAATCT 540
AATAATTTAT TATCTAAAGT ATATAAATTA ATTAAATCCT TTTTATTAT TATTTAATTA 600
TTATTAAATTA GTAAATTATA TTTATTATTT TATTAAATA ATTTTTTGAT AATAATATAT 660
CCATATTAAA TGGTAATTTA TTAATAATAT CCTTTAATGA TTINATGATA ACCNATTTAT 720
TATGANATTA GTTAATAGTG ACCTTAATAT CCNATCCNA ATATATNTAT TTATTNTAA 780
NAACANANAA CTTCTTATNN CATATTTANT TTANTATIN ACCNINCCN NNNT 834

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1250UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

EP 0 866 129 A2

5 GATCAAAATT TCAACAATTT CCATTTTCATT TAGTACTACC ATCAACATGA CCAATTGTTA 60
 CATCATTTAG TTTATTAGGT TTAATAATTAA CTTTAGCTTT TACTATACAT GGTATTATTG 120
 10 GTAATATTTA TOCTTTATTA TTATCTTTAT TAGTAGTTTT ATTACTAATA ACTTTATGAT 180
 TTAGAGATAT TGTAGCTGAA CTACTTTATT TAGGTGATCA TACTTTAGCT GTAAGAAAAG 240
 GTATTAACTT AGGTTTCTTA TTATTTGTTG TATCTGAAGT ATTAATTTTT GCTTCTTTAT 300
 TTTGAGCTTA CTTCCATTC A GCTATAAGTC CTGATATTCT ATTAGGTAAT GTTTGACCAC 360
 CAGTAGGTAT TGAAGCAGTT CAACCAACAG AATTACCATT ATTAAATACT ATTATTTTAT 420
 15 TAGCATCAGG TCTAACTATT ACATATAGTC ATCATGGTTT AATTGAAGGT AATAGAAAAC 480
 ATGCTTTATC AGGTTTACTT ATTACTTTCT GATTAATTGT TACATTTGTA TTATGTCAAT 540
 ATATTGAATA TAGTAATACA TCATTTACAA TTACAGATGG TATTTATGGG TCCAGTATTT 600
 TTGCTGGTAC TGGTTACATT CTTACNTATG GTTAGTTTAC TAATTAGGTA GGINCTATTA 660
 20 NGAANAACAA GAAATTNCT TTAACNCCN CCCCCTCGTT NGANATNNAA CCNCACCTAT 720
 TATTACNNT TTINAAAATA NTGAANACCC CANNATGTT NTAANGAAAG GNNTAACGTN 780
 25 NACNCACCN TAGNNTTNG GTCCCCCCCC NTGCTACCC ATTTTGNCCC CCCCCACAN 840
 AACCCCC 847

(2) INFORMATION FOR SEQ ID NO:307:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 825 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1251RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GATCAGGAGG GTTTTGCGGT GCTGCGGAC GGCGGGTTAG AGGTAATGCT CCTGCGAGAG 60
 GATGACAAGA CTGTCGCTGT GTACCGGGAA GTGCAGAAAT AGTGTATACT ACATAGTCAT 120
 45 AGTTATAATA AACAAGCCGC GGCGGGCTCT AACGAAATGG GGAGTTGCCC ATGCCACCGG 180
 GGCCGCCGGG GCGCGCGGG CCGCCAAAGG GCGGTTTCCA GCGCGCACCG GGGAGGAAAC 240
 CCGCGGGCTT GCGCGGGTCC GCGGGGTCCG CCGGGTGGAA CTGGCCCGCG TAGGGCAGCG 300
 50 GGGCGGTGGG CCGTTGTAGC CCGGATCGA ATATCATGCC GCCCTGCGGG TTGGGCGCGG 360
 GAAAGGGGTC AAACGGGTTT GCGCGCTTCT GCGCGCTGG ATACAGGTGG CTGTGCGCGT 420
 AGCCTGCAGG GCTGCCAGG AGCGGCTGG CCGCGCCGGC CCGGGGGAG AGAACCTCGT 480
 55 ACTCGTCTC GAAGCCAGG ATGTCTGCTG GCAGCTGG TGCAGGAACC TGCGCGCGGA 540

TTGGCGGAGG CGCGCCTCCG CTGAGGGCGT CMTAATCACC GGGCTGTGCT TTTGCGCNGG 600
 GCTTCTCMT CCGCCACCAG GGNAAATTCC CTNGNAACT TNCOGAATC CNCCCCCTTA 660
 5 AACTGGCCN CNCCCTTTIN CCTNNNGCT NTCTCTCTGC NNCCCNMTT CCCCCCAAN 720
 ACCCNOCTAC CCNNTCTINT NGNTTCNNC OCTACANCT TTCNNCTNC TCCCCCNCC 780
 ATNTCTCTNT TMTATCNAA AATTTCTIN CTTTTTACCC CCCCC 825

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1251UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GA CTGTTCG TGTGAGGAA GATAATCAAT ACCGGAATCC TCTGAGCTTT GCTTCGGCCT 60
 CCATTGCGCT ATTACGAAAT TCGGTGCTG CTCTAACGA TGTGTACCG TTTATACAAC 120
 CGCTTGTGA TCGCTTTTGA GCAGAAGCCG GTTTTGCAC CGACAGAGAT GACAACCTTT 180
 30 GCTACTTCTC CGATCCAGTA TTGTTCAGTG CTGTAGTCAT CTTGCGATCG TTGGTAAACA 240
 CATATACCCC ATCGCAGTTC GAGAAGATCG ATACCAAGTT GCTTTCGCTC TCATTTCAAC 300
 CATTAATTTC GCGCCTTTTA TTGTAAAGGT GCAGCACCAC AGAAATACTT GATAAAATCT 360
 35 TAGGCAATGG CCATATTGGG AAGTTTATAT TACTAGCAGC ATGGTTGCTC ATCCCGGCTT 420
 TGTGCTGTTC GTTCAGGGG GCGCTGTAC TACCTTTAGT CCTGTGTAC TCACAGCTTG 480
 TTACCGGGCC GGGCTTCTAT GCAACTATTA TATTTGCTTC TAATATATAA GTACTGACAT 540
 40 TTTCATACGC GCCTAGCTAC CGCTGCTTTC TCTTGGTGA CTCTCTCAG AACAGCTTCT 600
 TGGAATTATC TTGTACTATC AACCATGGAG AACTGTTC GCCACACCC GACCAAAGG 660
 AGAACOGAAG GACAATTTTG ANCTCCCTT TCCCCGAAT TANGNTINT GAANATATNA 720
 45 ACCGGGACCG GGTTCCTTNN TCCCCGGGT ANTTNCCNT TAAATCGTN TAAANTTANN 780
 AANGGTINTAT GGGNGAANG AACCCANCT GACCNAAN GTINGNIGG GTTTAACCTN 840
 CTNNINCGCC GTNCCG 856

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

EP 0 866 129 A2

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1252RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

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10  GATCTOCTAT TAGTGGGTAG CTAGCTAGTC GGCOCGGCTG GCOGGGCCCG AACTGGTACC      60
    GGGTGGAGG CCGAGTGACT AACACTCCGG GTTCTTCTGT CTCCTGCCAT GCGAACATA      120
    ACCATGGCGA CTTATATAAG TTCCGGCGGC GTGCAGTCGT ATGAGCCCGT ACGAGCAAGA      180
15  CGTCCAGCAG TTTCAGGCGC GGTAGTCGGG GCGTGCAGT TGTGTATATA TTGCCACCOCT      240
    TCGGAAGTTG GACAGCCGTA TGCTGGAGGC GGTCACTAGT AAGCAGGAGC CCGTGACTCA      300
    AAGTAGAAGT CGATTGTAA AGGACAACAG ACCAGTGGCG GTACGGACAG CAGCGGGCCA      360
20  ACGTAGTAAT AAAATATGAC GAGAGATATA CAGAACCACC TACTCTTGA GACGGCCACG      420
    GAGGTAGCGA ACAAGGTCCG GGCATCTAC TCGGTGCTGA AGTCGAAGGC ACCGGTGACC      480
    TGCGCTCAGT ACAAGGACCA CTACCACTGT ATTGGGCCCC TGAATCCAGA CTCGGTGACG      540
25  ATAGAAGTGG AGGCGCTGGA CTGGGAGGAT GACAGCGTGT TGGACCCGGG AGATTGCTGC      600
    CCGGTAAAC GTCCCTGCA GCACATGCGG AACCCCGCGT TGAATCCGT ATATGCOGGT      660
    GGTGTGTGAA GGTNCCCCCG GTTATCTTGT TCAACCTGTT CCGGTACCC CTOCTCCAC      720
30  AATTGAAGCC ACCTGTTGAA CACTGCGGAT CCCCCCCCC CAAANAACCA NAAACAAAAC      780
    CCATCCGTTA GGTNCCCCNG NCTGTCCCG AAATTAANGC CGANCCNCCN TCAN          834

```

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 858 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1252UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

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    GATCTTTATC GCAACNTTTT GGTCTGTITT CGAGTTACGG GCGTGGGGA CCACACCGAA      60
50  AGCGCCAGCT CCGAGTGTTT TGCCGAATAT GTAGTCGGCT TTGTTACAT ACGAGGCTGG      120
    TTGACCTGTC ACCTTGTGGA AGAACTTCGT CAACATGTTG GCGTGAGACG GAGGACGATC      180
    CTGGGCTTTC GATGCGTCTT CGTCGTGCTC CCCTACACCC TTACCGAGTT TTCGGTGGA      240
55  ACTAGTGAAC ACTGCCATAG CCTCGCAGTT AAAGTGATGT GGCAATATTA TATTGTAGTT      300

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EP 0 866 129 A2

TTGTCTTTT CTGTATTGTT TTAGGCTGCC GATAGCCAC GAGGTGAAGT TTTGTACACT 360
 TCACACATCC CAGCACTGCC ATCAGACAG ATGTTGAAGA TCAAATTTG CAGCTACATG 420
 5 CTGCATTGTG GTGCTTGGGT TAGCAGTAGC GGCTAAGTTG CAACTACATT GTCCCCATTC 480
 ACTCAGAAGT ACCTCGGTTA AGCTCACTAT GCGCTTATTG CCGAGCGAAG CCGAGCATTG 540
 TTACAGCAAT GATGAGAAGA GGCTATTGGT ATGTTAACAT AACGCCAGTA GTGTTATATT 600
 10 TACCACTAAC CATAGAAAAA GTACAGAATA TCGTAGOCT ACGAACTGAA TGAATATNTT 660
 GCTTCCCCNC CCGGCCNTA TACCAATGAA TAATAAATTG GATTTGCTAA TATCTNCCCC 720
 ATATCCNGCC GGGCCCCGA NNCCCTNCAA CTATTGGTN CACNCCNCCN TGCCNCCN 780
 15 TTTTNTTTIN TCNNGGAACC CCCCCCGT CATCTCGNN TGNVINAANA TGANTACCT 840
 CCTTGNTCC CCNCCCT 858

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 841 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1253UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

GATCCTAACC AAGCTGATTG ACTCCAACIT TOCACTTGGC ACATTGACA AGCTGTTGCA 60
 35 GAGCTCGAGC GCGGTGGGG GTGGTGGCTC CATATTGGGA TCAGATGGTG GGTGTACAGA 120
 CACGGAGGCA TTGGGACATG ACCGAAACG CAAGAAGTTG GAGCCCCGCT TCCCGGGCC 180
 TCCCGGAGC GTGGCACTG GCGCGGCCA TCGCGATAT AATCTGAAT TGGGCTCAA 240
 40 CTACTTGGC GAGAGCAAC GCGAGCCAG CGTGATGCTC CCGAGGTGC AGCAGGCTG 300
 GAACACAGCT CCTGACAAC AACCCAGCA ACAGCATAGA CAACATGGGC AGGCGAGGA 360
 AACGGGTCA CCACCAATGG CTCTTGCTA TCCCTCCCA ATGTTAATGA ACAGCAATTA 420
 45 TACATTCCCT GCGGCCCCC AGCAGCGCT CCGCCGCAT CCACAATGC GTGCTCGAC 480
 GCAGCAATCT GATGTCCAG CTACCTCCC CGGAATATG GGTAGCACC ATGTCCCAA 540
 CTTCCACAG CCCCCACGC TGACTAGTCT TTTGTCTAAA CATCAGCTC ATCACTGCA 600
 50 GCTAATGAG CTGCCTACCT CCCATGCATA TGTACAACAG ATTTGCTAC TCCAATAGCC 660
 CAGTCTGAA GTCTGCTTC TTACGTTGG CCTCTCCCC TTGGCAATN TATCCTGTN 720
 NNNAACCN AACCCNGTT CCGTGTGCC NGAATTCTA CTTTACCGT CCGTTATTC 780
 55 NTAAATCATA ACCCGGTCA ANAACCTTT CTTGACNAT ATCNCAATTG GCNANCCNT 840

C

841

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1253UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

```

GATCGAOCAG TTCGATGTTG AGAOGTCAA GAAGCTGTTT GCGAACTGCA TTGCAAGGA      60
TGTGGATGTTG CCGGAGGTTG TOGCGGAGTA CCGACTGATA GTGCGGTGTG AGGAGCGGG      120
TGGGGTGGG CCGCGGGGG CCGGTGAOCG GCGGAGGGG GAAACGGAAC CGTTTTCGCA      180
CGAAGAGAGC AAAGAGATTA GGATCATTCT GCTCCAAAG CCAATTGCGA TTGAGTTTGT      240
AAAGAATGTTG TGGGAGAACT GCTGTGTGCT GTACCGTTTC TATCAOCGCC CGACTTTCAT      300
CAGGAAGCTG GACGACCTGT ATGAGACAGA CCGCGGTGAG TACACGCACG AGCAGCTACG      360
CTTCTTGCG TTGTGCTACG CTGTCAITGC AGTGGGTGCG CTGTTCCTTA GCTCATGCT      420
CCCTGGTGGG GGAAGCGAAG ATGCGGGCTC TCGAGCAGA ATAACAGCGG CTACATTGGC      480
GGATACGGAC ACACGGCAGC CTTATCTGCA CGACGAGGC TACCGGTACT ATGTGGCTGC      540
GAAAAAGCTA GTGATCTCAC GAACGCGGT GACACCGAGG CGAATCAAAC CTTGTTCGG      600
TTGTGTGTTT CCAAGTTCC GCGCGGTGNC CCGGCATCC GTTTTCTGCG CCGCTATNA      660
ATTCCNCCCN CTTNAGANT CCACCCACCC CCCCCGANA ANTAAAAAAA TTTCCTCCCC      720
CAACCGGAAN TCCNCCCG NTTTACCCC CTANAAANG AGGTTTTTTA AACAAANCGG      780
GGNGCCCCNC NCCCCGGNN CNNNACATCC CCCCCTAAA TCGGAANATT NNCCGAAACC      840
GC                                                                                   842

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(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1254RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

GATCGGCCAC ATTGTCCCTG AGGCTTATGA AGGGGGCCCA ATTGGGCTOG TGCAAGACGG 60
 TGACGACATT GTCATOGAG CCGAGAACAA TGCCATCAAC CTCCTTGTGC CAAAAGAAGA 120
 5 AATTGAGTGG CGCGCGCTC GCTGGACCCA GCGGCTCCA CGCTACAAGA GGGGCAOGCT 180
 CGCCACCTAT TCTAAGTTAG TCTCCAACGC CTCCAAGGGT TGTGTCTTGG ACAGGGACGA 240
 CTAGCACCTC GACGCAAGTC ACTATTATT AACAGATTA TGTATATAAG CACCCCGCCA 300
 10 TGTOCATTGA ATGGACGGCA TATGTAAACAA AAATCGAGGA TGCTTCCCTA TCGTCTACAA 360
 ATCTCAGGAT GTTGAGTACC TTTTCAGTGT CTGACTGAAA TAAATGTTGA ACTTTGATAG 420
 TACTTTTATG TTTGAAAAAT TTTAAATTT TATTGTATGG CTGTCAACCAC GAGTACTCAT 480
 15 CTTCAACCGA CATTACGGGT ACGTGAAGAG CTTATCTATC GATAACATGG CGACTCAGGA 540
 GCGCGTATTT ATCGGGCGCA ATAGGCAGAC GAAGGTTGG GACTTCTATT TGCCGACCAA 600
 GACTGTCCAT TCGACTGGAA AGTGCATCCT CTATGGAATC CGTTGGACGA ACNCATGCG 660
 20 GNGTTTNGC CATTGAAGGC CACAACCGA GNTACTCGN AATTATATGG GCNAAAACT 720
 TTTGGTCACN CTGNCGAAG CACAATNCTT CGCAAGNAA NAAAAANGA ATTGNCNAT 780
 TTGGAGCCN AAACCTNTAC NTGNCNTGGN GNGGGTANC TCNNNTCCN ANGTN 836

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1254UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

GATCTCTGGT ACCCCAGCAG CCTGGCGGG GACGTGGCAT TGGTGAATC TCCCCAGGT 60
 AACCGGGTGT GCTCTCAGC CCTTCCCCAC ATTGAAGTTA AGCTTGTAG CGGTACTCCG 120
 CTTCAATTTT TGTGCCCCGT CGACCGGTAG CGTCATAGTC CCGCGGTGTG GCGACCGGG 180
 45 GCGCGCCATC ACAGGTATCT ACAGTTCAAC GCGCGGCTOG CGATCCCAAG CGCAGTCTGG 240
 AATCTCGAAC GGTGCTACAA AGAACGGATG CGTGGCAGAT CGAAGCTATC GAGAAGGTGG 300
 TGGGGGAATT GAGTGAAAGT ACACGAAGGC AGGGTGTGAG ATCTGTATCC TCTGCATAC 360
 50 AGTACGAGAA GGAGTGGCG ACGGTGTTC GAAATCAGCG CAGTGTCCAG TGCGGGGAAG 420
 CGTGCAAACG GAACCTGGAA ACAATCGAC GGACCTACTG CCAGGTCCAA GCCCTTTCCA 480
 CCGTGTACAA GCTAAGATGG TGAATGGCA ATAATTGTG ATGCTGTAT TCGTGTGTGG 540
 55 ACGATTATCT ATTCGGTTCA GCGTTTCATA TTAGGTGG CTGCAACGT GTGACATCA 600

CGATTGCACT GTATATATGA TGGAGTAATT CGCATACACT GAAAATCNTA ATAATCAATA 660
 ACCCATGCCN CNACTCGNCA ACTTCNCNC TTCTGCTCCN GGTGAAATCC CCTTCACTAN 720
 5 TTTTTTTCAT TGOCCATTNN ACCGAACTTT ACNAATNATG CAATGANAAC CNCCCCCTCCC 780
 AAACCTANAT CCTTTTINTIN NGGGTCCCN ACNGTTCNCN TTCNGNCNA NCCCNCTTIN 840
 ATTCCAANAC 850

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1255RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

25 GATCGTGTG TCAGGGTGCA TTGCAGTGGG CCTGAAGACG GTGGGGACTG ATCGGGGGCC 60
 GAAGAAGCTG TCGCAGCTAC AGCGGATTGC GGTGTGTGGT CAGGGCCGGC TTATTGCGCG 120
 GTGGGACTCC CTCTTCAGAC CGTTCAACGA GAAGATTGCG CAGATTTTGT TGACACGGAA 180
 30 CGACATAGTT GACTGTGTCG AGTATAAGAA CGCGCAGAAT ACGTTCCACG AACTGCTGGC 240
 GATGGGGGTG ACGCCGATTG TGAACGAGAA CGACACGCTC TCAATCAGCG GAGTGAAGTT 300
 TGGGGACAAC GACACGCTGA GTGCGATCAC AGGGGGCTG ATCGGGCGAG ACTAAGTGT 360
 35 CCTGATGACG GACGTGGACT GCGTATACAC CGACAACCG CGGAAGAAC CGGATGCAAA 420
 GCGATCTTG GTGGTGCCGG ATCTGTACA GGGACTGCCC GCGGTGAACA CCTCTAGTGG 480
 GTCGGTTCA GGTGTGGGCA CCGGGGCGAT GCGGACGAAG ATCCTTGCTG CAGACCTGGC 540
 40 AACGAACGCC GGGTGCTAC GATTATTATG AAGAGTGAGC GCGCGTCGAC ATGGTGCGGA 600
 TCGTGGAGTT CATGGAATGG CGCAGCAGTG CACTGCAGTT TCTGCTGACG CGAGACTTGC 660
 AGACGGACGA GCTGAATTTG TTGCAGAGCA CGGCGTCCCA CTACACAGCG NCTTNTGCA 720
 45 ACTTTGCACC TCCTGAACNA CNGATTCTTG ATCCNCGTC TGTGACNCGG NCGTATCTAA 780
 CAGGGGCTNA GGCCCCCA ACAAAGTGT CCCACGTINT CCGTCAG 827

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: 1256RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

10 GATCTAATGG CATTCTCCCT ACCAAATGGG CCCAATTGTA TATTGCCGAT CTTCCTACAG 60
 GGNACTGGTT TACGGATCCA GCGAAGATCG GGAGAGTTCA GCTCTTGGTA TTGCCGACAT 120
 TGTGTGAGAA ACACCAGCTG CAAACTTGAG GCCATATGTC ACTGTTCATCA CAGGTCCACT 180
 TATCCGTGTT GTTGGCGAAA GGTCTAGCAG TGATATTAG GCTGCTATCC TATATGCOCT 240
 15 AAATGTTCTC TTTTCGAAGG TTCCACAATT OCTGCGGCGA TTCATACCTC AACTACAGAG 300
 AACATTGTGT AAATCTCTTT CGACTCAAC CAATGAGACC TTAAGATTGC GGGCCGGGAA 360
 GGCACAGGT ACTTTGATAC AATATCAACC AAGAAATGAC CCTCTGGTGG TCGAGCTAGT 420
 20 AACAGGCGCT CAGCAGGCGA CTGAAAGGGG AGTAAGGACG GCTATCTTGA AGGCATTGTT 480
 GGAAGTTGTC TCCAAAGCTG GCAGCAAGAT AAGCGAAGCT TCCAAAGCTA ACATCATTAG 540
 ACTTGTGGAG CAAGAGATGG CATCCACAGA CAGCAAGTTT GCAGTCGCTT ACGCCAAGCT 600
 25 TCTAGGTGCA CTTTCTGAAA TCATGTCTCC GGAGGAGGCG CAGACCATAC TTCACGAAAA 660
 GTGCTTGATC CAATTTTGAA GAGCAGCTG AAATTTGCGT CAGACCCAC TCTATCTTNC 720
 TACCCTGTA CTTTCTCCCG CCAATACCCN ATTTTGACTN TTTTGGTGC ACGGATCNCN 780
 30 ATCCTTCNN CACAGTTTIN CCCNNGNAT TCCCCCNAA NGAAAGTNAN CCCCC 836

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 841 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1256UP

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

50 GATCAACTGG TCGGGGGGCG TGCAACAGC CAAGAAGAGC AATCCTTCGG GGTCTGTGTA 60
 CGTGAACGAC ATTGTTCTGG CGATTCTGAA TCTGCTGCGC TACCACCCAC GCGTCTGTGA 120
 CATTGACATT GATCTGCACC ACGGAGACGG TGCCAAGAA GCATTCTACA CTACTGACCG 180
 CGTGTTCACG GTCTCGTTCC ACAAGTACAA TGGTGAGTTT TTTCCGGGAA CCGGGGATT 240
 GGATGAGATC GGATGCTCGC GCGGCAAGCA CTTTTCGCTG AATGTGCGC TCAATGACGG 300
 55 CATCGATGAT GATTGCTACA TCAACTTATT TAAGAGCATC ATAGACCCGC TAGTTACATC 360

EP 0 866 129 A2

ATACAAGCCA ACAGTAATTA TTCAGCAATG TGGAGCAGAC TCTTTGGGGC ATGACAGACT 420
GGGGTGTTC AATCTAAATA TCAGAGCCCA CGGCGAGTGC GTCAATTGT GAAGTCGTTT 480
5 GGGATACTTA TGCTATGTGT CGGTGGTGGG GGTACACCC CCAGGAATGT GTGCGGGCTA 540
TGAAGTACG AGACAGGCAT CCTTAATGAT GTGCTCTTAC CTTTCAGATAT CCCAGAAGAT 600
ATTCCGTTCC GCGAATGGTT CGGTCCAGAC TATCTCTGCA CCGGTCTCTT GGATGANTTN 660
10 TCCAAAATAA ACNCCCAAT TACTGGANAA NATACGTCG GNTTTAAAN NTAAATTNIG 720
CNGGGGCCAT TTTGNCNIGA NNCGAATATC CTCAGATTT CGTTTAAACN AAAAAAAT 780
GATCGGAANA ACCAAAANAT NCCTTGNTAA CANINAAGAA NTTTGCCGNN ACTTNTTANT 840
15 C 841

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 841 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1257RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

30 GATCACTGGT GTCACCAAGG GCTACAAGTA CAAGATGAGA TATGTGTACG CGCATTTTCC 60
CATCAACGTC AACGTTGTGG AGAAGGACGG CGAGAAGTTC ATTGAGATCA GAAACTACTT 120
GGGTGACAAG AGAGTTAGAG CTGTGCGCTGT CAGAGAGGGC GTCAGCGTGG AGTTCTCCAC 180
35 CAACGAGAAG GACGAGATTG TTTTGTCCGG TACCTCCATC GAAAACGTTT CTCAGAACGC 240
TGCTGACATC CAGCAATCT GCGGTGCCAG AAACAAGGAT ATCAGAAAGT TCTTGGACGG 300
TATCTACGTT TCTGAGAAGG GTGTCAATGC CGAGGAAGCC TAAGTCCCTT ACTGACCGTA 360
40 TCTTGATAAA TAATATGAGT ATTATGTAAT CAAAGAACTC ACTGCTTTTT ATTGGTGGTG 420
TTTTGTCAA ACGCTCTTAT TAGCGCCGGG GTTAGAGTGT GGAATACTG GCGTTATATG 480
CTTTAGAAGT TATGTTAAGT AAATTTAATG TCCTATCAGG GCCACAGCCT TAGCAACTAG 540
45 GTGCAGGTAC TCCTTTAGCT TGCCACTGTT CTGGAACAGA AGATATATTT TATCTGTCTC 600
GTTGSCACCA TCGTAGACAG GTTCACCGCT TCCTTGACAG AACGATGGAA CGCCAGCTTT 660
CCGGGTGGG AGTTATAGGA ATTATGGATT OCAATGACAG TTGGTGTGTT AACNANCTG 720
50 ATTTGTCCAN TTTCCCGTCT CNGAAGCTNC ANTGNPTCCN TGACCNANCA AACCGGGAN 780
ACCCCTAGGG CTGNNAGGCT TGAATGCNTT AAAANANITT CNITGANAAA NCATTGNTAA 840
55 841

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1257UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GATCGGGCCG CTCACACACT CAGGTACCTC AAAGGAATAC GAGTTTGTGG CAOGCTTCCC 60
 GTGTCCAGAT GCACAGAAAA TCGATATGTA CATCAAGGAG CCGCAAAACA AGTACCTCTT 120
 TTGGGAACA GAGTACACTT TCCAAATCAT CTGCAGCCCT GCAGACGGCC TCACTCAOGA 180
 TCCATACGAC GCGCAAGCCG CTGCGCCAAA TGTGATAGTC GTCCAGTCCC CATCCGGCAA 240
 GATCTACCGT CTGAAAAAGG CCGAATCCGA TGTGGAATTT GCGGTATGCG AAGCTAGGCT 300
 AAAAGTGCAC GAGCCAGGCG TCTGGCTGGC CCTAATTACC TCTGAGGCAG GTGCTGGTTG 360
 GTGCACTTTC GCGAAGTGA TCTGTGTTTA ACACCTAGAT GCTACACAGT CATCCACCCC 420
 ACGAAATTAA TAGATAGTAC GGGTACATAC AAGCCCTATA GTTCTTTAAT ACACTTGGCC 480
 TATATTGAAT ATGTCTACGA AGTATATGGG CGAGGCACTT TCAAAATCGG TGAAAAAANA 540
 TGCACCACTT CGAAATCCAT GTTTTATGAG CTTAACAAC AGTGGTTGTT GAAGAACAAT 600
 ACCCTGCCAA GGAAATGTCA GGTACTCGAA CCAGCTCTCA ACAGATTCTT AAAGATTGCC 660
 AGTGTGTGTA CCGAATCCAC GTTGGCTGAA TGCTGGGACC GACATCAGAC CTTTGATTG 720
 GTACAAAATC AGTCTATAAG GAGAGCGCCT GTNTGCCNA AAAANAAANA CCACGGAAGG 780
 ACNCATTGTC ACTTGAACNG AGNCAATGTG TNCNGTACG CGGVNTTTC GNTTCAAGCC 840
 CCAAGGACAA NAAAGC 856

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1258RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GATCCAACT TCTACTAGG TATTTTTC TACCTCAGC TGCAATTCCA TGCCATCGCT 60

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AACCAAGATA ATATTCCTCT CCAGTAGATC CATATTCCTCT CCGACTTCG CACTAATCGG 120
 GATGACTGGC ACGTTTCAC CCAGATCTTC AGCATGTATT TCATGCTGTA GCAAATCAAT 180
 5 CATTATTTTG TTGATCACAG TTTCCTTTTC TTTTGCCGAC CGGAGTTTGT CCACCTTGST 240
 TATGGCGACA ATCAGCTCAT TCCCTGATTT TTTGACATGC TTAATCGCTT CAATGGTCTG 300
 GGGTTTAATT GAGTCTTCGG CAGATACTAC CAAGACAAOG ATATCGGTAA TATTGCGGCC 360
 10 CCGTTCCCTC ATCTTCAAAA ATGCTTCGTG CCCGGGGGTA TCCAAAAACG TGATCTTCOG 420
 CTTCGAAACA GGTGTGACAA CCTGGAAOCG ACCAATGTGT TGTGTAATGC CACCAAACTC 480
 CTGCGAAACG ATGCTCGACT TCCGAGATA GTCCAATATG GTGGTTTTGC CGTGATCAAC 540
 15 GTGACCCATA ATGCTCACA CAGGTGGCOG GTCCCTCAGG GCGTTCCGGT CTGAGGCTG 600
 CTTCAATTCA TGTAAACGT TCTCCGAGT GACAATTCCC TCCCGGAGG CAGTTGGTAG 660
 CTATCTCCTC CCAATATAGC TCGATGTAGT CTCCTGGAAA TATGTAGTCC GCGTGGCTTT 720
 20 TCAA 724

(2) INFORMATION FOR SEQ ID NO:321:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 853 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1258UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GATCCTGTTT ACAACTAAGT TCGCATCCCT ACCAGGGGAA AATATGAAAT ACCAAGTGTT 60
 GTATTCCGAA CGCTAGAATT CTTGTACAAA AACCGCGGCA TTCAGGAAGA AGGTATATTT 120
 40 AGGTTAAGCG GATCCAGTTC TCTCATAAAA TCTTTGCAGG AGCAATTIGA CAAAGAATAT 180
 GACGTGGATT TGTGCAATTA CAACGATAAA GTTCTGTGTA CACCAGGAAA CGAAAATCAG 240
 GCGGGTCTCT ACGTCGATGT GAATACCGTT TCAGGTTTAT TAAACTATA CCTAAGAAAG 300
 45 CTTCCTCATA TGATCTTTGG GGATGCTGCA TATATGGATT TTAAGAGAAT CGTGGAAAGA 360
 AACGGAGATG ATAGCAAAC AATAGCACTC GAGTTCAGG CATTTGGTTAA TTCCGGACGA 420
 ATTGCCAAAG AATATGTGCG CTTAATGTAT GCATTGTTG AGTTATTGGT GAAGATCACC 480
 50 GAGAACAGCA AATATAACAA GATGAATCTG CGGAATTTGT GTATCGTATT TTGCCAACG 540
 TTGAACATAC CCGTGAATAT ACTACATCG TTTATCACTG ACTTTGGCTG TATATTCCAA 600
 GATAAGGCGC CGATGGAGAA CGGACCGGT CAACATACAC ATCCCGCAAT TTAGTTCATA 660
 55 CTAAGTAAAA TACTATTAAC TTAGAATATG TGATAAGTGT TTTAATTACN TAACTTGGTA 720

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TTAGTCNAT TGINTAATAA TTGAATATGA ATGCNITATT NITCTINANT CAATNTGTCA 780
CGATTGGATT TACACNGCG TCTGTAANGA CNTCTAGCTT GGTCATCCCA NITCTCANIT 840
NCTCCCGCTT NCA 853

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1259RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

GATCACACGA ATATTGCGGG AGTATTTCTC CATGTTGCG CGCAAGCGG CCTGCGCATC 60
GCGGTGAGC GATTGCGCCT CGTTGATGAT CACACTCTTG TACCTCGCG CTAGCCCCCTC 120
CGATCCGCTC TGGAAATCCA CCTGCTCCAT CTGCGCAATC TCCTTCAACA ACTCTGAAT 180
CACGATCCGG TCATGTGCGC CCATGTGCT CGGCGTGATC TCGATGIGGT ATGGGCTGCT 240
GACGACGTTG AGCTGAGCT TCTTGTAGA TGGGTAACA AATTGCGCA CATCAATCTT 300
TAATTTGTAT ACACCTGCTC CAAAGATACT TGCAAGGAGC CCCATGCACC GTGTCTTCTT 360
CCCACTTCCA TTGGGCGCGT AAAGTAAAT ATGCGGCAGG TCCTTCGAG AACCTGCTAA 420
AGCTCGAGC TGCTTGTAA GCGATGCGT ATGTGAAAGG CTGGTCAACG ACTCGGTCT 480
ATGCTTGTC ACCCAAAGTG ACATATTCCT GTGTATCCTG AGATGGGCTT TTGTGTGTTG 540
TAGGGAAGGT GAGCAATTCA GTGCAATTA AATTCATTA GATTGCGTT TTAGCAGAAA 600
ACGATATGCC CTCAGTAAGG CCAGAATACA TACAGTACT TGGCTACTA CTTTGTACAG 660
AAGTAAAGCT CTCAGAGAT CGCTGAGGA GATGGCATGT ATATAAOCN CAATTACTCT 720
GATGCNAAAA ATGTTGCACC CNTGCTTTT TANTCTGTC GACAACTANN AGAGCCTNTA 780
TCNAGTCCAA ATTTTNCNAA ANCTGGGAAA ACCTTNTNCC GTGGTNTATN AACACA 836

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1259UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

5	GATCACCCOC CAAATCAGCA ATAACTCGAA AACTGTGCCC AGTAOCTTTC AACGCGCATG	60
	AACCTAAOGG CGCGCAGOGG TCATGGGTAC TCGACTGCCT TTGTATCCCT CACACTGOGC	120
	CTCTTCGTGT GCCGCACGTG CTTGTGTGATG GTAGCGGCGC GCGCCGGTGG ATCTAAGGCG	180
10	ACGTCTCTTT GTACGTGGGT CTCACGTGCA CATGTCATC CATCCGCTTG CGAATGAGTA	240
	GATCAGCACG GAGAOCATGC TAGGCAGGGC GGTGGGCGA GGTGGAAAGG TTGCAGCATT	300
	GAGGTGGAGC AGCAAGATGA CATCACAGGA TAGTAGTCGG AAGAAAGAGC TATGTGCAGC	360
15	GTACAGCGTA GTGGATGAGC GGGTTTCGGC CAGCATGGAA GAATGCGGAC GTAGAAGGTC	420
	GGAGTTCTTA TTGCTTGCCG TTTCTAAACT GAAACCTCGC TOGGATGTGG CGATACTGTA	480
	CGAAGAAATG GGGCTGCGGC ACTTTGGAGA GAACTACGTG CAGGAGCTGG TGGGGAAGGC	540
20	AGCAGAGCTG CCGGGCGATA TCCAGTGGCA CTTTATCGGG GCGCTGCAGA GTAACAAGTG	600
	CAAGGACCTG GCGAAGGTAG TGAACTCAT GCGGTGGAGA CCATOGACTC GCTAAGAAGG	660
	CGCGGAAGCT GAGGAGGCGG TCGGAAGTTC CAGCGAGGCC CCGGCATCTG TGTTACATTG	720
25	AGTGAACNCT CTGGCAACNC AAAGNNGTIN CNGATGAGC NACNGTGCAC TGTGATTCTT	780
	CTNCCAAAAC AAACCTTCCC TGCCCGACGA TAAATGGTCC TGGACCCCTC CCGCGAAGGG	840
	AACCGATCCC C	851

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1260RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

45	GATCCTCAGA GGGCCCGCAA GAAGCTTCGG CCGAGACAGT AACGATGTTT GCGAGGTTG	60
	TGCTGTATCA CAGTTGAGCT CTAGGTTGCA CTTTCGGAAA GAGCGCTACC GTAGCTGCAT	120
	GAAAAAAAAG TAAGGCTCAT CAGTTTATGC AGAGGCAAGA ATAAGTTTGG TAGAGCCTTA	180
50	CTTCACAAGC GTGCTCTAG CGAGCCATAT TATTCTATGG CCGGCAAGAG AAGACCGAAG	240
	AAGGCCAGAG CTCATATCG AAAGTACGTG GCGGTCAAG GGTTTGTGCA TACCTACGGG	300
	GTTCACAGTA CTGAGAGTTC AGCACAGAT GAAAGCGGTT TGTTCOCGC AGACAGTGGG	360
55	GTGCAGGTAT CTGACGATGA TATTGCGAGA CGACTTGTG ATATGACACT TTCGCAAGC	420

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GCAGCGTTTG CCGGTGGAGC GGCACCCATA CCGTATCCCG GACACTCAAT GGTGCTTCCC 480
 TGGGAGCTGC AGTTTTTGGT TCTGTCCAAA TGCAAACTA TTGAAACACA CTTCATGCAA 540
 5 GTGTGCAGGC GGTGGTATAT CATGTGTCTG CCATTGATCT AOCGAGCACC AAGGCTCTCC 600
 AGCAAGACTT CTACAAGTTT GTGAGACAC TGGTGGCAGC CCGTAAACAG AATTACCGGC 660
 AATATTCCTC GATCTCGACC GTCCATGAAT ACCNNANCGC AAACCTTTTC CAAGGTCTC 720
 10 CCGTGTCTCC CACCCCTGAC ATTCCGGGCC CAAACACTCG TATCCCCNIG AATCTTAGGG 780
 CNCCCCNNTT GCAACCGATT TGTCTNTTCC CAACGTTANC GAACNCTG AG 832

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 846 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1060UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

GATGACCCG CCGCCACGC CCGTCCGTC GGTGAAGTC CCGCCCTGGA TCATGAAGTT 60
 CCGGATGACG CCGTGGAACG TGGAGTTGAT GTAGCCCGCG GAGGCGTCTT GGCTCTTTTC 120
 30 GAGCGTGACG AAGTTGGOGA CCGTCCGCGG AGCGACGTG CCGAACAGCC CGAGCAGCAG 180
 ACGGCCAGT GGCTCGTCC CCGTCTGCAG ATCGAAGAAG ACACGGTGTG TGACGGTGGG 240
 GTCTGCGAGC CGGAACCGCC AGAGCAGCC CTGTGCGAGA ACGAAGAGGA CCTGCATTGG 300
 35 GGTGGCTGC GGGAGCGCG GAGCGCGCG GGAACCGCC CGCTTTTATA CGCGAAAAG 360
 CTGCTTCGCG TACGTAGCTA GAGATACAGA GCGGTGACT TGAGGCTCTG CAGCATCAGG 420
 CCGTCCATCA TCTCGGGCGT CAGCAGTCC GAGTAGCCCG CCGTCCGCGC GTCCAGCGCC 480
 40 GCGTCAGCG CTGGCGCAGT GCGCTAGAC GCGGTCTGTC CACTGGCCCG CTGCACCGAG 540
 TTCTGCTCCA CCGGCACGAA GCGCGCGCC TGGCCAGGCT GGAAGCGCG CAGACGCTGA 600
 TCGCGCCAG CCGCGCCGAC AGGTGGAAGC CCGTCCGACAG CAGGCGGTTT TGCAACCGCC 660
 45 TGTAGCGCGT GCGCGCTGTA CCTTCCCNNA ANANGTNTAT CTGACGCAT CACCGTTCCG 720
 CCCCCTGTC TTCCGAACCA AATCCGTCC NCTTAACAC CNITTCANGC CNITCACTTC 780
 ACNCTGNCCA CACNCTTNC GGTACGTCC CAATGCCGTC TCCCCGGGC GCTTAGCNGG 840
 50 GCTCGT 846

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 835 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1261RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GATCATAAAC GAAGAATTCC TAATTAACAA TTTGTCTGTC ATGTACTTCC TCAGTGAGAA	60
ATAGCGATAT AATCATTAGA AAGCTTCCCC GAGCACTTTA GCAGCACCGC ATGCCAGCAT	120
AACCCOCTGG ACTCAGGGCA GTATGCGGC TGGCACTCG GCACCTCATC GCAGGCGAGA	180
CAGTCCACCA CTGCGAGCAC CGTAGTATTT ATACTTTTCC AGGTTGAAAA ATTTTCCAGC	240
GCCCCACGCC GCAGAGGGCT GGAACGCGAT TAGGGCTCAC AGCGGTGAC TGGCACTGCT	300
GCCCCAACAG CGCGCGCAT GTAACTGAA ATGATATATT ATACCTTCTG ACTACAATGT	360
GAAATATACA AAGGTGGCTC ATAGGCGCAT TGCATTTATT CAGACGCGT AGCTCTGGTG	420
TAGATAGCCT GCTTGGAGTG CTTGGAGATT GGCTTGATGA TGCCCTCGGT CTCCAAGTGT	480
CTCAAAGCAA CTCTGGCCAT GGAACGCGC ATCTTCAATC TGTCGACCAA CACGGACACA	540
GAGACGTATC TGTAGGTTGG GACCTCCTTT AGGATTCTGT CAAGCTTGTC CTGGTCCAAG	600
ATGAAGGGGT GCTGGGCCTT GTCCTTGTGG GACTTCTTGG ACCACTTCTC TTGGACTTCT	660
TACCACGGC CATGGGCGC GCGCCTTCTG GGCCTTAAAN ATNTTGTTTT TGGTGCATAT	720
ACNGTGTGCC CNTATACTGT CGCACCACT GGCNTCTCTG CGNAGGGTGG TGAGCTTCCG	780
TACTCCNCCC CCTAACCNC CCCCCNNGT TGTCNPTTC NNCNNNOCTA ANICT	835

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1261UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GATCTGCAAC AACACCATTC CATCGGAAG TCCTTCCAAT TTCTGTTCTG GAATATTATG	60
AGGAAGTTTG AGAAGGATAT TGGGAGCGAT GATGAGGAAG ATCCCTTCCA GATCAACGAT	120
TTGGACGAGG AGAAGACCTT GCGCATGCTT TCTAACCAAG CCTGTTCCTT CCGCTACCTG	180
ATGGCCGAAG GTCAGGTAAA GTTAGATGTT TTAACCATG TATCCATTAT GGGGTGAAC	240

TCTGACGGGA GACTTTTCTT AGAGAATCTT CTATTTTCAGT TTCTGTTGGC CTCAGCCAAA 300
 AAAGCAGAAA CTA AAAAGAA GGTGGGGAAT ATCAAGGAAT GGTCTTACAG AGATGACTTG 360
 5 TTGCAGGGCG CCTGTGCGA TGGGATCCAG GCGGAAAATA AAAAGATAAT CTGCAAATCG 420
 CTCAGGATGT TTATGAGGAA TTTTAGATAC ACGAACTATA TTCTGGGTCA GCTGGCTCG 480
 AAGGAGTATC AACGTGACAT GAGAAGGTTG GACTGGGCGG TTAAGCGTTT TTTGGAACCTT 540
 10 ATAGATGAAG AACTGGATAG TGCAGATTGT GAAGAGCTTC TTGTCACTAG TCTGAATGCA 600
 TATTACGIGT AACATTGAAC ATACGTACTC TATATTAAAG TGGTGAAAGT GATGAGAGTA 660
 TGACGTCCNT GCTTTTATTG CATACTACTT NIGAAITACA GTTATTGGT GAATGACNAC 720
 15 AAACANGTTC CATTACTTAC TTGTGTGACNT CCGCNCGACC ACCACCCGCG CCACACCTTT 780
 GTTACCTTA TAAAATCTC CACNCCGNC GTATANAGCC TNAANAATTC NTTCGCTCAT 840
 GCGGTTTTGA CN 852

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1262RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

35 GATCTTTTGA CACGCTGGTA ATGTTTCCCA CTAAGTGGTA TTTTCTCTTG TCTAGATAGT 60
 CTGCGGTAAA GACTCCCGAC GTGATCGGC GGCACGGAC GCGCATCTGC TCCAAGGCCG 120
 TCACAAGTTT CAGGTTCTGT TCCAGAAAGC ACTCGGGAAC TACTGTCTATG GTCACAGGAT 180
 40 CAGTTACGCG AATTCTCTCT ATATATGAAG GCTCGATACC CTGAGCCTCC AATTGTGTTAT 240
 TCACCTGCGG ACCCGTGCCA TGCAGCACA TCGGATAGAG CCCCACATGG TACAGGAACG 300
 CCAGGCATGA AGCCAGTTCC GCAAGTTGT CGCTGATGAT GGCACCTCCA ACTTTGATAA 360
 45 CCGCGAATTG CTGCTCCGAG ACGGAAGTAA AGTACTTCAG GTACTGTCTT ACTTCACGCT 420
 TAGAGCCAAT ACTGTTGAGA AGCTGGATCA CGGTGGACCG TGTCTGCAGA GACCCAACGC 480
 CCTCGTTGTT CCGGTTCTTT GCATAGTTCA GCTTCTTTAT AGCGGCAGTG CTGAACAATT 540
 50 CCGGCTTGTA TCGGACACGG ACAGCCCATG GCGTCCGGTT TTAGATCTTG CTACCAGCGA 600
 AGCTCTACTA AACAGTAGAG AGTGCTCGCA AGCATCTTGG TACTCCGTTT ATCCAGTGC 660
 CCGGAGTTCT AGCTCTCGAA AGCAGTCCGT GTGGCTTATA GCCTAANTTC TCTTCGGTTC 720
 55 CATAACCACA AACCGTCTCN TIGNCNTCC TGANTTTCAA GACCCCNANA TTTTCACAAT 780

TTNTGCAITTT NTCNGNGNA AGGGTGCNAT TTATTNTTGC ATNCNTTTAA A

831

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1262UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GATCACAAGC TTGTTGAAGC CAACTGCTGA AAATGTCCTC TACGAGAAGA AACGATTCTC	60
TCCACTAGGA GACGTGTGGC AAATTTTAAA AGGAGCCAGT AAGACGCAGA CTAGCCCCAG	120
CAGAAGCGCC AGTAGTTGTT AGGAAGCATT CCAGAGCGTA TACGACACTT TGAAGACGGA	180
CAGCGTTCAG AGAAGACAGA GACAATCAAC ACCAAACAAA CATGGAGAAT CCTCACGTAC	240
ATGATAATTT ACAACACATC CAGGCGGTGT TATCGAACTA CGACACATCG TTTCTCTCGG	300
ACGATGAAGA GGACTACTGT CCGCTCTGCA TGGAGCCTTT GGACATCACC GATAAGAACT	360
TTAAGCCGTG TCCGTGCGG TATCAAATCT GTCAGTCTTG CTACAACAAC ATCAGACAGA	420
ACCCGGAGCT AAATGGGCGG TGTCCTGGT GTCCGCGAAA TATGATGATG AGTCGGTGG	480
GTACATTGTT TTGAGCCCCG AGGAGCTGAA ACTTGAGCGA GCGAAGCAGG CGCCGAAGGA	540
GCGCGAGCGC AAGCAGCGCG AGAAGGAGCG AAAGGAAAAC GAATATGCCA CCGCAACATC	600
TGCGCGGCAT GCGCGTTATC CAGAAGATTG GTATACGTTA TTGGCCTGAA CCACCCGTAC	660
CGTACGAGGA GGTTGGTGGC CTGTTGCCCT CGGACAGTTA CTTTGGCNGT TNCGGGANAT	720
TTACNNATCN TCCGTGAACC GCAAAGGCC CCATGACCCC NACGGTNTGG ATNTNTTTC	780
TTCCCGGAAA AAGAGCGGCC CNNTTNCGGC GTGGATGINT TTNTGANGG CNGGTGAGG	840
GGGTACGACC NATNTGCCIN TTTTG	865

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1263RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

	GATCGGCGCA TTGCTTCTG AATGGTTCCT CACAGAAGGA TGTGCTACC AATGGCATTA	60
5	GTTCAGGAG GTCTCGCTA CTAACAGAAT CGTCTGTGG AACTCTCTT AGGAAGGTGA	120
	ACAGTTCATC TATCCTTTCA AAATTGATAC TCTGAAAGG TTCATTGCG GGGTTAAACA	180
	TACTAGATGC AGTCATTAGG GCGGCACCTT CTGGTTAAT ATGTCAGCT ATCCTTTTTA	240
10	GTGCTTCTTC CTCATTTTCA TTGGGCTTGA ATAAACCTCT AGCTATCAA AACTCAATTA	300
	GTATCTTCCT GACCTTAGTA GTGGTTCGT CTGGGGGCT AGTCATACTC ATTAAGTGAT	360
	GACGGAGCTT TTGCACACCT TTGCCAGAAA ACACACAAA TATTTGACGT TGGTTAAAGG	420
15	TAAATTCATC AGGAGGAGGT CTGCAAAAT GTGTGATATC TGGCTGAGA AAAGAAGTAC	480
	CGCAGTCAAT GACAAATGAG AGAGCTTTGG ACAAGCCATT ACCAACTCAT ATATTGGATA	540
	AATAGTCAAA TTAGTACAAT ATGATAGGTG AACTCTTTC AATGTGCAT TCCTACCAG	600
20	CAAAGCAATC ATATTTAATA ACCTCATCTG TCATCTGAGA ACATTCACCA ACCCTATCTT	660
	TTTAGTTTGT TAATTCOCCA ATCATATAAG TATGAATTGT CCATTTTGTA CACAACNATC	720
	CNCTCTGAT CNNGGANATC CTGATTCAAC CTTATCCCN CCNGAATGA ACNTGGCCAA	780
25	NGANATTNIN GTTTTTCN CTGAAANCT CNAATNCAT ACCCGCTTA CC	832

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 851 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1263UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

	GATCTTAAAA GCTGGCTCC GCAGATAGAC CTCTGCGCA GAGGCTGGAA ACCTCAACTA	60
	GCAAGTCGCC ACCCGAATCA GATAAGCACT AGAGTGTTC CAGTAACAGA GGAAGCGATC	120
45	AAGGAAGATA GTAGAAGAGG AACTGCTGC CAGGCTTGAT CGGACAGAGG GTTTAGCTTT	180
	CTGTTGAATT TTAGAGTTTC GGGCTTTGT TTACTTCGTT TCATCTTTC GTGTAAGAA	240
	GCTGTTTGA GGTGCCATC ATTTGCCAGT CGCCAGGTAG GGTATTGCAG GCGACGGAG	300
50	TCGGTGAAAC AGAGCAGGAC CGAGAAGCC GATAGACAGG CGTTTGTGTA TAAGCGGTGA	360
	GAGCTGAAGC AGGTCAAGAG GCGGCTTGG CGAGGTGTG CCGCGCGGC AGAGCACAGC	420
	AGGCGATCCG AAGAAGGGG AGCGTGGGA CAGGAGCGCA GCGCGCGAA CAGCGGGGTG	480
55	TGATGACGAG CGAGACGAAC AACAACAAC GCGCGAGCTC GAACGCGGG CAGCTACCGC	540

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CATCGGGGCT TCCGGGAGC TGGTTTACGA CGCCATTTCCT GCGCGCTCGA CCACAGACAG 600
 ACAGCAGTAC TCCAGAGAAT TTCGGGAGCG TGTMTGGCGG TGAAGCCAGC GCGCCAGAAC 660
 TATTTTTCCTA CTTACCAACC GCGCGNAATG CCCCCACTTT TMTTGNCCAA ANACCATTTT 720
 TCCNCCAGCN CCCNCCCTNC TAAAACCAAT TCTTACNGGG NCGAATGAAA TGGGTGTGTT 780
 TTCCCGCCCC NGAGAACACA TTTTTCNCNA CTGTGACCCG ANINNTTANT CTCCNNAACA 840
 TTATTTTTTTC C 851

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1364RP

(>i) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GATCTCGTTT TTGTAATGCT CTAGCTCATA TTGTGTGAAG GAGAAGGGTG AAAACAGCTC 60
 CGAGGCTGCA ACTACTGCAA AGAATAAAGA GCAAATATG GCACATAAGA TGCTTTCOA 120
 ATTCAATTGG TACAGCTCTA ATACTGTGAA CCTTAATCT CCGGTAGGCG CAACAGTTAT 180
 GCGGCCAACC ACGTTAAGT GATAATGATG TAGGTACCCG GGTGAAAAAA AGAGTATGTG 240
 GAACCGGCCA GCTGAACCAA GCGGATGAGA CATGCCAACC ATATCCAAGC ATACTTGACC 300
 ATGATGACGC AAAACTATCT AGCATAGTGA GTCTTGACG TGAGACAGGC TTCAATCGTA 360
 AACCTCCAC CTTCACTATT GTCACGTGAG AGGCAACATA ATTGATCTTG TGAATACCAC 420
 CCATACATTT TGCTACCACC CATACATACT AATTAATGGG GAAAATAGCG GCTGGTACAG 480
 ATTCTTGCACT CTCCCTGCCC CAGAGGGGCG CCGGCTCTTC GTTCCCCAGC GCGGCAGGC 540
 GCGGCAGGC CGACTGTCTT ACTACGCTCT CCTGTGTGGC CCGTGGTTAC CGGCTCAA 600
 ATTACCAANC CTCCAATTTT TGAATATCCC CGACAGTTNT GTNCTNTTT TTTACCCCAA 660
 TTCCGGAATT TCCTATTAA ANGTAAGAC CCNNNTTAC TTTTGTGGAN TAACCTNNGG 720
 CGTNCCTTNG GGNVNCCTT TTTTACNGG CCCCNTTCA GGCCTTTTGG TTCCCTAAAA 780
 CCGGINAAAA AAAAAAGAT T 801

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1264UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

10	GATCTCATGT ATCACAACCA GACTATGATG CGACTTGGGG TGACTATGTC TCCTTTGCCC	60
	AGCGGTTCAG AGAACGAGTG AAAGACAAGG ACCTTATTTT GATCGACTCT GGTGACAAAC	120
	GTACCGGTAA TGGTCTCAGT GATCTCACTA GTCGATGGG TTTGAAGTCA ACGGTATCT	180
15	TTAAGCTTCA GAACTTGAC TTGTAACTC TCGGTAATCA TGAAGTAT ACAGAAGATG	240
	TGGTTGCTTT GGAATACTAT GGAACAGCA TGGAGCTGA GCTAAGTAT AAATATGTCA	300
	CAAGCAATGT GGAATTTATC ACAGAAGATG GGGACGTGT ATCGTTGCG CAATAAATAT	360
20	AGGTACTTTG AAACGCCAAA CCAGAATCTA CGTGTATGG CGTTGCAAT CATGTTGAT	420
	TTTCCCGTGG GCTGCTAAAA ATGTTAGGTT AACCCCTCTG GCCGAGAGG TTAAAAAGGA	480
	CTGTTTACC CAACTGTGG AAAAGTACCC GCTGACAAGC TTGATATTAT AGTTGTCTTC	540
25	CGTCATTTAC CAGTCACCG TGGCGAAAG AGAGCTTCTG CAGTTACACC AACGACTAAG	600
	GGAATCTTAC CCGGACACTA TTATCCCGTA CTTCGAGTG NNTACTCAGT CNGAAANTCC	660
	CINGTTTNG ANAAAAAGAN TGCTTTACCA ACGGCGAAT TCTTGAAACA TGGAAATCNA	720
30	TCAANANNG TTTCNCAAGA AACCAAAATTT TCATTTCAT ATGACTTACC CAATTCCTTT	780
	TCCCTCTCNG NTINANACTC CAAATTCNT CCAAGGAAGA ANANTACNC CC	832

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1265RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

45	GATCTTGCTC AGAAATAACT TGCAATGTCT CCACTATTTT CTCAGATTA GCATTTATGC	60
	ATGTCAC TAG GCATTTGCTT TCAGGTAATG CATTCOCAAC AAGTGGCTTA CGATCTGGAA	120
50	CAGATTGTGT TCTTTGTGAT TCTGGTGGAG CCGTACCTCC AAAAGTTGAA TCTTCGTTTT	180
	CCGCCGAGCA GGAATTGCAT GGACGAGACT TCTTGTGAGA CATAACTCA AGTGGGCGCG	240
	CTCTATCTGA CATATCTTCC TGAATCTCTT CTGCATACGT GCGTTACCT GGCCTAGTT	300
55	CGTCTCAGT CCTAGCTCT CTCTTGCAT GCATATCOCT TGCTGTCAGA TATGTTTCTC	360

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TCTTCGGGCT AGAAGGGTCC TCATTGTAG GATCTTGAAC AAAAAGTAGT TTGTTATTCT 420
 CCAGCTGGC AGTCTCTTCC AGGTTTACT TCCGATGCTT ATTAATACTG GTTCTTTAGA 480
 TGGTTCCCTG ACTTTGGCTA TAGGCCATTG GTTCCGGCGA CTGTGAAGG TATGCATTGA 540
 GAGTCTCTCT GGTAAAGCT GINGTCCCC CGTTATTTTA NCACGGCTTG GCCGGAATGG 600
 TACACNGNTG AGTTAATCNC NGCGGTTGC NGTTCCATOC TGTGGGGGGC CCACCCAGAA 660
 CCCNAACTTN GGCGCCACNA TTTCCTNTCN CCAAACNNTT TGGCCNAAAA AANAATINTT 720
 CCCCCAAGN NGGANNACGC ATACCCCGAN ATGNNGTATN TTGTGGGGGN AACCCCNNA 780
 ANCCCNCCC CCNGNGGAA 800

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1265UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GATCCGGTGG CCGCTGGTGA AGGCAGCGAC GTGGTTGTAC CGGCAAGGCG GCCTGGGGCG 60
 GTTCTACCTG GGCAACGGGC TCAACGTGAT CAAGGTGTTT CCGGAGTCGG CGATGAAGTT 120
 CGGCTGGTTC GAGCTGGGGA AGCGCGTGCT GGCGGGCTTG GAGGGCTGGG GCGAGACGGG 180
 CGAGCTCTCG CGCTGTGGA CGTACGTTGC GGGGGGGCTT GGCGGCATCA TGGGCGAGTT 240
 CTGGTCTTAC CCAATGACA CCTTGAAGTT TGGCATACAG TGTGGGGGCC TGGATACGGG 300
 CTGCGGGGGT CTGCGGCTGC TAATCAAGAC GGCGAAGGAC ATGTACCGCG AGGGGGGTCT 360
 GCGACTCTTC TACCGGGGCC TTGGGTTGG CATTTTGGGC GTGTTCCTCG TACGCGGGCG 420
 TCGACTCTCG CACCTTCTCG GCGCTCAAAC GCTGGTACAT TACCGTCCG GCAAATGCGC 480
 TGGCATCTC CCGAGAACGA AGTGGTCAAG AGCATCTCCG TGTGCTGCCG AATGGGCGCT 540
 TCAGCGGTAC GTCCGGGCGA CGTGTCTAOC CTATCAACCT TCTACNGAG CGNTCCAGC 600
 CCCAGGAGT TNCNCCNCCC CCTCTTACA ANGNITCAAN TINTTCCGAA AACACCNCNN 660
 AGGCCCCCCC GCTTTTACAA GGTGGTTC NACATGCGA GGTNNCCNC ATCCACNCT 720
 NTTTTTTTNC NAAANTTAAA NNCCANCCCC CCNAATAAAG GCGGCTTNTC CCCCCNACCC 780
 CNGGAATAAN GGTTCGCT NNAAAACCAA NACNCCCCC 820

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: 1266RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GATCTTATCT	GGAACACCA	TTCAGAACGA	TTTATCTGAA	TATTTGGCCT	TACTAAATTT	60
TAGTAACCCCT	GGGCTTCTCG	GTACGGGGG	ACAATTTAGG	AAAAATTTGG	AAATACCCAT	120
TCTACGGGGT	CGGATGCTG	ATGCTACTGA	CAAGGAGATC	GCTGCTGGTG	AGGTGAAGTT	180
ACATGAGTTA	TOCCAGATTG	TGTGAAATT	CATTATCCGG	AGAACCAATG	ATATCCTATC	240
GAAGTACTTA	CCTGTAAAGT	ACGAACATAT	TCTATTGGTC	AATCTCTCTC	CGATGCAAAA	300
GGCAATTTAC	GAACACTTGG	TGAGGTCACG	AGAGGTTGCC	AAGTTAATGA	AAGGTACAGG	360
GTCGCAGCCA	CTGAAGGGGA	TAGGTTTGCT	GAAAAAGTTA	TGTTACCACC	CTGACCTGCT	420
AGATCTCCCG	GATGAGATCG	CCGGTCTCTAC	AAATTTAATT	CCAGATGACT	ACCAGAAGTG	480
CTAGTGACAC	AACTCCGCC	GCCGAAGAA	TTCCCTTTT	GNATTOCAAC	GANACATTCC	540
ATCNAATTTT	GCNATTOCTA	GAACGTTTTC	NGTTTTAGAA	TCCAGCCNTG	ATTCTAATGA	600
AAAAAATGTC	CCNGATTTCT	ACNNCCCCC	ACCTTGGATT	TNTCCAAAA	AATNINNNCCN	660
CCCNCCCCCN	GGTTTNTTCC	CANCTGAANG	NNCCCGNAA	ATTAAANNAN	TTTNAACCTT	720
TTGAAAATTC	CAAAACCCCC	GGGAGAAATT	NTCNTTNTT	TCCCCCGGN	CNGGGNNGGG	780
NTCCCCCTTT	NGCCCCCGG	NGAANTTTGA	CCCCAAAGN			819

(2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 807 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1266UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GATCTGTCAG	CATTACAGA	AACCATCGCT	ACGAAAAGTT	TCCTACAAGT	AATCCAGCC	60
AGCCGAAGGA	CTCCCCGTG	GGTCTGTAG	CCGTCTTGGC	AGGCACAGT	TTCCAGGACT	120
TGCTTCTGT	TGGTCAGAGT	ACTAGGCAGG	ATGCGTTTGC	TTATTCCAAT	CACAGTGTG	180

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5 TGGCTAATGA TCGCCAGGCC TCTTTACCGC GAAACCTGC CCCAGACTOC ACGTTCACTG 240
 CGGAGTTTAA CCAGCTGCTA TCTGAATCCA GCAACTGCOCT TGAGCTTGAT TCTATATTCT 300
 CAGGCAACTC AGTTCTCTGG AATGGGAGAG CCTTAACTTC TGAAGCAAGA GCTAACCTCG 360
 AGGGCGATGT GCCATCTGTC TCGGAAGATG CCCGGAGCGA CAGCCAGGCA AATTCTGCAC 420
 AGAATGGCOCT GAAGTATTGA GTCTAGCGGA CACTGAGTAT GCGGACCTGG ATAGTTTGAT 480
 10 CACTAATTTG TACTTCTACC ATGCGAGGGT TCGTCCCGCG GGTCTGAACG TTTTGTATATA 540
 ATGATCGATT TTAGAAAATA TAAGAACCCO CTTGAATATG AATACTGNCN NTTAACCCOC 600
 GGGGGTTGCT GATACCCCCC CTNTCCCCCN CTNGGNTGAA TTNTTACCCC NOGGNGGGGN 660
 15 GANAAANAAT TCCTGCCNNC TTGGGTTCCN AANCCCCATT CCTTTTNNAA TNAAAANTGC 720
 TTCCNNGNCN TTTTAAAAA AAAAACCGTG TTGCCCCNAT AACCAAATOC CCNCGCANGN 780
 AATTTCCTGG GTTCAACANC CGCTCAC 807

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1267RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

35 GATCCATTCC ACCGGATTGC AGCAGCTAGT GCATTTGGCC ATACGCCCGA TTGCCCTTTC 60
 TTATAATGAA TCCCGGCTTG TAGAGCATCA TCCGGCACTT CACGTGGTAT TGAATAGCTC 120
 CTCATAACCG CACCGGAAGA TTTCAGGAAT ATATCTGGTT GTGTAGTGTA GAGGTATCA 180
 40 CTGTGGATTG TGATATGGCT GTTGCAGCTT GAACATTCCA CTAACCTCGG TTGGAATCCG 240
 AGCAGGAACA ATTTTITGNC TNAANCCNA NATTTTNNCC CCTANAATAN TGGNCTNNCC 300
 AAAATCNTCN NNTTTNAATT TTTTCCAAA CTTTGTCCGT GACCGGANIN GAAATGNGGG 360
 45 NAAGTGAAT GTCCAAGNCG GGNCCGNAA ATTAGAATTC CAGGGAAAAT TCCTACANTA 420
 NANAGGTGNC ACCNCGGNA ACCCCGGGNN GGNNNACTG GNOCTTTINA ACCTGNGAAT 480
 GCGGTNTTCC AACCTTTTNC CGGNGGCTT GGGCCCCCN TTAATNCNAT TACCCNCCCC 540
 50 TNCITTTCCC NAAANNGATN CCCCCCNCG GAAAGGTTN TTNNNNANCN TAGGAGGCC 600
 CTNGGTCCG GAATTNGNN CCTTTCTNN TCCCCCCCCA AATCCNGGAC CCTGNAANNC 660
 CCTTNNCCC CCNFTTTAC NNTTTCCNN GNAANINCTT CCCTTGGCCC ATCCCCGGAC 720
 55 NNNAATTGGG GMITTAANGG CCCCCCGGNC CCCCNCNTGN AAAAAGNTNN GGNCCCCCCC 780

CCCCCCCCCTTN GN

792

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 824 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1267UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GATCCGCATC GTTTTGTGTA GTCATACTAC CTGGACGCCA TGTTCGCCGA GCTGGCGCCG 60
 CCGGCGAGTC TCGGGTCACT GGTCCGCTTG TGCAACGCGG ACTGTGCCCC CTCCTACTGG 120
 TTGGAGCTAC CCAAGGACCG TATCCTGTTC CTATGTGCGA TTGOGAACCT CGTAATCAGG 180
 CACCTCGTGA ATGTAGACCC AGCAGCAAGG GACATGCACG CTTTCTGGGA GAAGGTGAAT 240
 GCGCTCTTCT TCGAGAACGG CTCAGGGCGG ATGCTGCAGA AGGAGGCTTT GGTGCCGCAA 300
 CCGAAGAGCT GCGAGAACGA TGGCGGGGAG GCGAACGTTT CTGGGTCCCC GATTTCCTGT 360
 TCGCAGACAC AATACACATC GGACCCAGGC AGCAATTACA TGAACCCGCA CGCATTCGGC 420
 ACGGGGCCCC ATGGGGCCCC CACAGGGGCC TCGTCTGTG CGCTTAACAG CGACACCTTC 480
 TCTGTGGGAC TGGCTTCACA CAACGCTGC GCGCCAGAAG CGTGGGCGAG ATTCCATACC 540
 AGACTTGTCT ACGCAGGCTC GAGGACGCCA TCAGACAGGG AGCTTGCTGC TTTGACCAGA 600
 AGGGCTTGAG CAGGATTCCC AGGACGACAC GACCGCCTG TAATGCAACT GTTGTCTTTC 660
 CNATTTCGCG CCTATCCCC AATGGAACGC CACTCCCCNG AAAAAAAAAA AATTTTCCGN 720
 TGGATATTTG ATGAATGAA TTAGAAAAAT TACNTTTCIN NNATTCTTGC GGIGCCACAA 780
 CAATTGCGAN TNCTAGACCC GCGNCCTGGC NTINGGTTTT AAAT 824

(2) INFORMATION FOR SEQ ID NO:340:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 787 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1268RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

GATCCTGAGA ACACFTTTTC TGTCGAGGCT TATCAATGCT CTTTCTATCC GCAGCTTCTT 60

CCAGGCAGAT GAATACTGGC AGTGGCTGGA GCGTGGCAT GTTAAGGCGT TTGGATATGG 120
 TGGGCTGACT TGGGAGTGGC AGCATGGGCT GCGCAGCTAT GCATTCCCGA TGCTCTTTGA 180
 5 AATGTGCTAC TATGTGGCGT GGATACTGGG TGTGGCCACC CGGATGGCGC TGCAGGGGTT 240
 GGCACATGCG ACGGCGCTGT GTGGGGGGGT GGTGGCGAGC GCGCGGGGGG GGGTGGCGGC 300
 GATGAAGGCC GTCTGGGAGC TGCCGGAGGC AGCGCAGGAA CTGGTGGAGT ACTACGGGGT 360
 10 TATTGTACGG GCGCGAAGT GGTGATGGCG GCGGTAGCAG CGTTGGGGGA GTTCTACAGC 420
 GTGCTGCTGG TTGGCAAGC TGTATCTGGG AGTGGCGGAT AAGGGGGACA CCAGAAGGGC 480
 GACCGCGGCC GTGAGCGGTT GCGCTGATGC TGACCATGAC AACTTCTTCA ACTGTTTCTT 540
 15 CCGGACGCGA ACGTTCATCA CTCCTTCGAG ATGAAGCTCA CCGGTGGCGC TCTACCATTC 600
 ATTGAACGGG CCTCAGTTGG TTCTCTGCTT TGNCCCAACT TGCGGTGGCT CTTTTCGCTG 660
 CCTCAGCGCA NTACTTTTTA TCTGGCNCCT TGCTNTTCTT GGTGNGANCC TGTTCGCCCN 720
 20 ANNGTGCNCN CCTTTTAACC CGNCCCAAGT TGCCCCGAGC CCGTGGGTIN TTTCAATCCA 780
 ANNANNC 787

(2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 840 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1268UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GATCCAGGTA TACCCGCCCTC CGTGGCGCAG CGAGCTGGC AGCGCTTCA TGGCTGCAAC 60
 40 TGAGAATGCC CTCGACCTGA TGTGGGTAT GCTGAAGATG GACCGGCACA AACGGTGGGA 120
 CACGACTCGT TGCCTGCTCA GTCAGTATTT TGTAGAGCTT CCGGAGGCGA CACCTCCTAC 180
 GGAACCTTCCA AAATAAATA AGTAATGACT ATGATAACCT AGATGGTATA CTCGGAAGTT 240
 45 TTGTGTTTGT GCTTTGAGGC GATGACATTG GCTTTTATGG TATCGCAGAC GTTGCTGAA 300
 AAAGATTCAA CGTCTGGTA ACAGATTTC GCAGACTACT TGTGAAAGA ACAAGACCA 360
 GAGCGCTGGG ATGCTCAGCC CAATGACGAA CCGACTCCGC CTTATTGGCG CTGGCTGCAG 420
 50 GTTCTTAGC ACCAACAATA GCGCGCCACT GCACAAGATC TTTCCCTCCC AAGAAGCTGG 480
 TGAACAGGAT GCTGTTGAC CTGATAGCC GACTGACCTT CCGGAAATT ACTGCTGTGA 540
 TACGAGCAGT TGTACACCC AATTAGACAG TAGTAGGGCG ATTTGTAGTA CCGCGCGGT 600
 55 TGAGGGCGCC ACGAGCTTGA TGATTATGA AAAGGTGCTG AGAAGACTCG CCGCCAGAA 660

CGAGAGCTCC CATCGCCNTC TACTTGCNCC GGANAACAAC TGCTTTACTT GCTGCCCANT 720
 GGANACNAAA ATGCACGNGC NCTNCCCTTG ANCCCGTGCA CCGNMTGGCC NAAGGNNOGA 780
 5 AATGAATTTG CAATTTAGNT CNGATTTTAC NCTCTGGNVC CCCCCCCCCA CTGANNGANC 840

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 787 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1269RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

GATCCCACTC TTGGCAAGCT ATACGGTGAC ACTATCATAG CTCGCGGTGG CCTCTACGAG 60
 ATGGAAGACA ACCTGGGGGA GTTCTTGAC AGAGAACCA ATAACGAGGC GTACCTCAGA 120
 25 GATCAGGGCC TAGCCTAAAT GCTCCTTCTT TTGCGGGCTT TCTGCCCCC CTATGTATAT 180
 TCCAGCTAGA GAATCGCAAG CAAGCCATAC TTAGAAATAG GATATTGTTC CGGGAACACT 240
 GATTTACTGT GGGTACTGC TCGGAAACT CACTGTGTTG GTATCGAATA ATTAGGTTTC 300
 30 GACTACCGCC AGTGTGATGC TTTCTTTATA CCGGCATACT AAAACAGGGT CCTCAGTCGA 360
 ATCGTGTGTC ACTGAATATG AGCCCCCTCA TGAGTTCCTA TCGGTAGAG CGTCTATGT 420
 GCAGACCATA TCAACACCT CTGTACAGC GTGGAGTTCA ATATACGGT ACGACGCACA 480
 35 TACAATAGTA CGTGTGCGCA ACCGTATAC GAAGAGCTGC GTTCTGATTG CAGCAITTC 540
 CAAGCCCCGG AAATACAAA CCGCAITTTT AGCCAGTGC GATAGATGTC CTGAACCANG 600
 GAATTACANC GAAGGNGAT TGCTACTACN ANCATCANCC AGGGCTCGNG TATTTCTCAT 660
 40 CCATCCCCCT CNAACNAAA ATCGGANIT TTAAATTTT CATGCAAACC ATNCANATCC 720
 CCNTTTNGAT ATTNCCCAC TGGCCCCCCC NCCCCANNT ANCGTCGGG ATCCNGNATT 780
 45 CCCCCGT 787

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 820 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1269UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

5 GATCGAACTC CATGAAGGAG CGTAATGGCC TCGTGGAGCT GCACCGCACT GGGTGGGTAC 60
 ATAGCGGGAT GTAGGAATGC GGGGATAACG ATTGGGAAAA GCTGACTGGG CTGCGCCTCT 120
 AGCTTCAGCT CAAGCTGGCG CAGCAGCGTT GCTATAGGCT GTTGTGGGGA CAAGGTGAC 180
 10 ACTTCAGTTG CAGTAGGAGC AGGTAGCATA CGACTAGTGA TATCGAACTG GTGCGGTAA 240
 TGAGGATGAG GGTCAATTTC TGGCTCGAG CGCTGGCTAG CACCACAATT ATCACCAGT 300
 CCATACCTCC ATGCAATTCT GAGATCTTGG CTAAGTGGA CCGTTTTCG ACCCCCTCG 360
 15 GCTAAGTTTT GCACCGTGAC CTTCGATCC TCCTGGGAAA TGCGAGATT CTTTACCTCT 420
 TTACGTGTGC CCTGGAATAT CCCCAGCAGC TCCTTCGCAT ACTGAGTGT GAGCGTATG 480
 ACCACCAT GCGTTATCC CCCCCCTGN GGGCCCNAN TTTCCCCCG GGTATTCTCT 540
 20 GTCCCTGGC CTGCAANAC TTCCANTTAC GAGCAATCT GGTCCCCCTG TTCTTCCCC 600
 AAAACATCTG GCCCATTTGA NCCATATGC CCTAGAACCN ATCCAATCTG CACCCGNGA 660
 NTTTTTGAA ANNAATTACC GGAAGGANC AACCCGAAG NAAAGCCGC CCCCCTGTG 720
 25 GAGCNACTT CCCCCCCCC NAAACNGA ANTTNTTTT TNNTTTGGC CNANCGNCCN 780
 TTTTCNGCC NGCCGGGANG GCCTTAAAN TTCTCCCC 820

(2) INFORMATION FOR SEQ ID NO:344:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 806 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: DNA (genomic)
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1270RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:
 GATCATATGG TGAAGTTGGC ACATACAGTT GAATCATCCC AATAGCAAAG AGAACGTAAG 60
 45 ATTTACCTAG CGCGGCATCA CCTGGAATAT CTAGCATTTG CAGCGCAGGT GAAAAGAATT 120
 TCTCATGAAT TGATTGGAAA TGTGGTCCG TGTGTTCAT TGCTAAGCCC GCTAGTACAC 180
 GATAATCATC ATTAGACTCA CAGGTAGAT GGGCCTTCAC TGTGCTTA TACCAGTCTA 240
 50 ATAGAACCTG CCTGTACGA GCATATTGAT CCTGAAGAAT AACCAACGAT GGTCAACCA 300
 TOGAATTGAG CAACAATGTC GGTTCATTCA CGGTTTGAGT GATGTGACTT CCGTGAAAT 360
 TCTCAAAGGA ATTTAATTTC GGTATCAACC CCTTCAACAA GGAAGCTGTG AAGATATCAT 420
 55 CAACATGCGA TTTGTAAGCT AAACCTTCCC GCATCCATAG GAAATCAAAA GTGGCTGGGA 480

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AAGCATAGTT TGGCTATTG GCTTTGACTA ACTGCGAAGT TAGAATACTA CTTGTGGGOG 540
CCAGTTTGAA TAGCAGAGTT AGACATTCAA CGGATTCCNA GAATATAATC CTNGCGAATT 600
5 TATCCATCCN CCTANAAAAT TTTTCCNCC TTGATCCANA ACNANAAAAT TCCGTTGACC 660
NCTGAAGACC TATTCCINCC TTINAAGAC CTGCNCATTC TTCNATTTC CNAANGNNTC 720
CCGTTCTACC NAGAAANTTC TTGCATGCCN NCATGGTTTN AACCNAAACN TCCTTTGANG 780
10 NPANTINACTT CCCCCNCCC AATTTA 806

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1270UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

GATCCGATTG TCAAATTTTC TGAATGGTAT GGTAAGAAGT TTGGGGCTGG AAAGGCTAAC 60
AGTGGTGTTA TATCTTTGCG TGATATTTTA GCTTGGGTG AGTTCATTAA TAGTACCTAT 120
AAGGCATTGG CTTGCCCTTA TGCTTCATTA ATCCATGGGG CGGCAATGGT ATTCAATTGAC 180
30 GCGCTTGAA CCAACAACAC AGGTACCTT GCGGAGAGTG AGGAACGATT AGAACACCAG 240
AAGCAAGAAT GTCTCAAATA TCTGTCTGAA CTAGCAGGAA AGGATTTAAA CAAATACATG 300
TCTGGTCCAT TGATGTTAA GATTGACGAT GAACTCTCC AATCCGGGCT TTTTAGCCTA 360
35 CCCAGAGTTT CTTCCTCATC TGTCCAACCG GTTTTCAATC TTGGGCACT ACTACAGCCT 420
ACAATCTCAT GAAAGTTGTC AGAGCAATGC AAGTACAAA GCCATCTTAC TGAAGGATC 480
ACCTGGTGTT GGTAAACCA CATTAAATTC CGCATTTGGCT GACTGTACCG TTACGAATTA 540
40 CCCTTTTAA TTATCCGAAC CAACTGATTT GAATGAATTA TTIGGATCCG AAGCNCCCCG 600
AAAAAAAAN GNAATTTNT TTTGNGTGA TCCCCCNIT TTINAACCTA TGCCAAAGTG 660
GATGGTTTIN TTAAATAAA ANNANATTC NCCCCANCN TTTTAAAGN CNVACCTGT 720
45 TTGINNCCNT GGNGAACCA NCCCCAAAT TAANAAATTT TTTGCCCCC ATCCGCTTTT 780
TTGVINCCA AACCCANACA GGGNGGTGA AAAGGGTTC CAANCTTCC TC 832

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1271RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

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10  GATCATTATA TTATAAAATA TAATAAAGAA TATATTTAAA TAATAATAAT AATATGAAAT    60
    ATTATATTAA TTCTCCATTG GAGCAATTTG AGATTAGAGA TTTATTAGGT TTAACATCAC    120
    CAATAATAGA TTTTAGTTTT ATTAATATTA CTAATTTTGG TTTATATCTT ATAATTCCTT    180
15  TATTAGTAAT TTTACTAATG AATTTAATAA CTAATAATTA TAATAAATTA GTAGGTCTA    240
    ATTGATATTT AAGTCAAGAA ATAATTTATG ATACTATTAT AAATATAGTT AAGACACAGA    300
    TTGGTGGTAA AGTTATGAGG TTATTATTTT CCATTAGTTT ATACATTTTT TATTCTTATT    360
20  TTTACTATAA ATTTAATTAG TATAATCCTT ATTCATTTGC TATAACTTCA CATGTAGTAT    420
    TTGTAGTATC AATAAGTATA ATTATTTGAT TAGGTCTAAC TATTATTGGT TTTTATACTC    480
    ATGTTTAAAT CTTTGTTTAT TTTACCACTA GGTACACCAT TAATTTAGTA CCATTATTAG    540
25  TATCCATTGA ATTATATCCT ATTTGCTNNA ACTTATTCCA TAGGTTTTTA AAATACACTA    600
    ATATATACCG GTCCATTTAT AATGGTTATT TAGNNGGTTT AATATINAAT TNAAAACCAN    660
    AATATTTTACA TTTTATGGTN NOCNCCCAAN AAGGCATTGG TTTGGTINIT TAAAAAGGCN    720
30  ACCTATATCN CCTANITGAT NTTTTTTATN CCCCCTTTTA AANANCNATT TINNCTTAT    780
    TAAANTAAAT C                                                    791

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(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1271UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

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50  GATCAATCTT TCGATCATTG TCCAATATTC CCCACTGCTG TATCATATAG ATATTGATTA    60
    TAATTTCTAA ATCAACGTGA TTGTTCTAAC TTAAATTAAC AATTATGAAT TTTTGGCTAG    120
    TTATTATTTT TTAATTAAC TAACTCTAAA TCATTATAAG CTGACTTAA AACAAATAAT    180
55  TATTACATTA TTCTTTATTT ATTATTTAAT ATTTAGTTAA ATTTAAGTT CATTATCTT    240
    AATTTTACT CACGAGTACA CCACTTATTA ATACTATTAA TTAATAATAT TAACGTTTGA    300

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TTGCGATGTG TAATGTCTTT AGTTAGCGCT TAATCTGAAC CAACATCATG TTCTCATTAT 360
TATTAACATAT TTTTAATAT TTTAAATAAT TATTTAATAC GAAAGTTATA GGATTGGAAC 420
5 CTATGAAATC ATAAAGATTT ATAATAGCTC AAATATTACA CTTTAAACCA CTCAGTCAAA 480
CTTCTTAAT ATATATACCT TATATATGGT TTGATAATTT ACTTATAATA TATAGTATAT 540
AATTTAATGA TAACTCTTAT CATTTAGGTG CGTAGGGTTC ACCCCCTAT TGCTAGTCAG 600
10 CATATGAGGT ACCTCCCCC AATGATAAAA GTTATAATAT ATAATATTAT ATTAAGTATT 660
TAAAGANAT AATATAATTA TTTAATAATA TTTTATTTTA GGNAATAAA AAAAANTTTC 720
ANNITTTGAAA NANGGTGNG AGAATTANAA AAAGCNAATA ATATGTTCAA TTGACCCAT 780
15 TAANAATGTA GINCCTGAC ATCNOCTATT TCCTATANAA ANITTANAAN AANA 834

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1272RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

GATCAAATCT AGGTTCTCG ACGCAACGG TGACGAGTTC GTGAACGGC TCAAGCTCTG 60
TGGCTTTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCACGAAGT TTGAGTTCTT 120
35 CAAGCCTCCA AAGGAGATCC TAGAAGAACG CAAAGCCAAG CTCGAGGTA AGCAGAAGTT 180
CATCGAAGTG GAAACAGAGA AGGAAGCTCT AGAGTCTAAG CGGTGGGAAA ATCCAGAAGG 240
AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCTAGTC TCCTCTCAGC 300
40 ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA CCGACAGCTT 360
CAACCGTTCC TAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG 420
AATGTAGGCA TTTGTGGCCA TATGCTGCTT GTCTCCGAGC TTTTCTTGTT GGGCTCCCAT 480
45 CTGTGCCAG GAGCGGAATC CGTACGCAT TGTACCTGTT ACCCTGCTGC GAACAGCACC 540
AGAAGAGGCT GATAATTGTA GTNCAGCAC ACCATAGACG CGAACAATG CCCCAGGCGC 600
AGTCTGCGT TAGTTTGAAA TCCAAAACA CTTCGAATCA TCGGTTCGCC GGAGGCCCAA 660
50 TTATCOGAN TTGGCTTTTA AANCCNAAT ACAANGANTG CGCCCNVGT CCGCTGTACA 720
TTGTGCCCCN CTTAGGNGC CCACTCCCN CNGAANITT TTATTCATTT AATCTCNG 780
NCCCNCTTT GTGANAATG AATTCANITT TIN 813

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 844 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1272UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

```

15  GATCGACCCC GCGGCGCATCG GGCCCTCCGG CCTGCTGCGC CCCTCGGGCC TGGGCTGGCA      60
    GCTGCTCTAC ATCCTCACC GTCGCATCTT CACCAAGAC TTCTTCATGT CCGGCTTCTG      120
    GCTGCGCACC TTGCGCGCGC GCTCCAACCG CGAAGCTGCTG CTGGGCTGCT CGCTGGCGCG      180
20  CGTGCTGCTC GCGGTGCTGC TGCTGCTGCT CGGGGTCACC GGCTGCTCG CGGTGTGGGC      240
    CGGCTACGGC CCGGTGCGAG ACCTGACAG CGCCAGTTTC TTCTGCTGC TGGCGGGCT      300
    GCGCGCTGG GCCAAGCGCG TGCTGCTGCG CCTGCTGCTG GTGCTATCCA CCTGCACGCT      360
25  CGACTCCTTC CAGAGCGCAC TGCTCTCCAC CATTTCCAAC GACCTCTTCC CGCAACCGCC      420
    TGCCCCCGCT CTACGCGGCG GCGCGGCTCG CCGTGTGCTG GTTCCCGGTC GTGCTGCTCG      480
    GCGTGTGGC CACCGACAT CCTGGCCATC TACCTCATCG TGAAGCTGCT GTCCGCGCGC      540
30  GTGCTCCCGG TCATGCTGCT GGCTTCTGGC CGCGGCGCGG CGGGCCCTGT TCTGCTTGG      600
    AGCTGATCGG CGCGGGCTCC GNGGGGCTGT CTGGGTCTTC NCTTTTCGG CCATCTATAA      660
    CGCTNTNCCN CNANGGGGNC GCTGCTATT TATTGNAANG NCCCTACTTN AATAANGGGG      720
35  NNCTTNNNGN GCTTNGTCTT TCCCCCNIN GGGAACTGTT TTTCCCGGNA NAANTTNGC      780
    CTGGGNCCC GTTGGNCCN CCGGANANT CANGTAACC NCAGGGGAAN TCCAAANTTT      840
    CTNC      844
  
```

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 792 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1273RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

```

    GATCCAATA CAAGCAATAT TGTCGCTACC AGAATGCCCC ATTTGCGACC CATATAATCA      60
55  CAAGCGAATC CCATCCCCAC CTGCCCTATG ATAGTCCCTA TGAGTGATGC ATTTGAAACC      120
  
```

CTGTAGATA CATCTGCACT ATATTCTATC TCACCGTACT GATTTCGTAA TACACGGTTT 180
 AACATCGACA TGACATTATT TTGGTAACCA TCTGAAATAA GCGCAAATCC TGCCGCCAGG 240
 5 ATACTGAATA GATGTAGCCA TTGGCCCTTC TTCCOCACAG CAAAACGTGC TTTCGGAGCC 300
 TCCGGGTCAT ACTTTAGTAA CCTGTGCTG GACATCGTAT TTCTGCAAGC CCGGCTATC 360
 CGAATAATAT CTAGCGGGTC AAGCGTTAGG TTGCTGCATT CTATATTATA TATTTCTCT 420
 10 CTCTACCACG TGCAAATTTA CCTGTATGAT TATGCTGCAA TCTCCGGT CTACTTCCTT 480
 TCTTGAGAC CGCTACCGAC TGCTTTATGA TTATCGGTGC ACCATATGGC GTCAAGCAGC 540
 ACTAGCTTTT ACCTGTGATA CCTTCCTTTA CTAAGTGNAT TCCGAAGTAN TTGNNCCCA 600
 15 TACTATATCC TTCCCTAGA GTGAAATAAC CTTCCATTTA GGTNNTOCC ATTCCNGAA 660
 ACAGTTTTTA AANAANACA ACCTTTATCC TTNAACCCCA AACGCCCAA AAANAAAATT 720
 TCCCATTIN CTAGGTTTTT TNGCCNGGA GGAAGAAC CCCCCCTAAC CCCCATAANA 780
 20 ATTCTCTTNC CC 792

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1273UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

GATCGGGCTA TAAAACTGAA AGTTCATGTA TGCTGTCTTG AATGCAGAGA CGCGGGGCAC 60
 TTACACATC GGCAAGCCTT GTGTGCGAA TGAAACATTA AGCTTATGTC AATACCATG 120
 40 AACTGTATGC CAAATTTAGT AAAACTCGTA CGTGTGGCA GCATAGATAG AGCTGTTACC 180
 GATATCTOCC TTGAGGCTAA AGCCGAGCAT TGGGTATTAA CTTCCTGGA CTATTCCGAA 240
 TCAGAGCTTT CAGATTGCTC TTATCATGG TCAGTCATCA AAGTGTGGA TGTAGGATGT 300
 45 TCTATTTTCC CACCGCAATA AAGTGCAGTA TTATGCAGT ATTCAATAAG CTACCTCTC 360
 ACCTGATAT CTAGCACATC AGCTGGAGCG GAACCTAACC AGACCGAAG TTATAGTGGC 420
 AGCTCTTGA GGAGTGAAA TATTTCTTGG TCCGGCAATG ATCTCATGC GCCATTATAT 480
 50 GCGTAAAGT TAGGTACATA CCTGTGACAC CCAACAAAGT ACAGTTGCTA AGTCCCAAT 540
 ATCTTAAAG ANCCGTTTAA ACCNCATATT AAGGTGAAGT TTATGAACCT TTGANAGTAA 600
 CTGNNCTT ATAGCGGAAT ACCANANNAA TAACGNCCTT GTTANGGAT CTATCGAAGG 660
 55 NPTACTTCN NITOGANCA TTTATAGTTC NINTATTAC CCGGANAAA TTGAACAAC 720

CNTGAGAAAA GTTNTNNCCN CNGGGAAANG AAAANTVINC TTNIGANTCC CCCCCTTTAC 780

5 CTTGAAGNTT CTCCATTNC GAGATTCAAA TTTTNTAAN AAGGANTTN TAA 833

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1274RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

20 GATCAGAAC AAAAAGCAGT TCGAGTATAT CAGTAAGCAC TGGGAAGTTT GGGAAATAGC 60
AGTGCTGAGA GTTACGGGAC AGATTGGCAA AGACACATTT GCGATGGAAT TTAATTGCCC 120
25 GCAGCCAGAG CACGCACAAT TACACATTCA CCTTAAAGGT GCAGCCCGGC TGCTGGGAAA 180
ACTGCACGG GAGGGTGGC TGATGCACCA CGAAGATAAC CAAGAAAACC GGGGCCGGGA 240
AGGACCGCTG ATTCCGTCAC CGCCGCTGTC ACCACGAATC GGGCCGGGAG AGAACCGGGG 300
30 CGCCGTINGGA ACGGAATCCC CGAACCCCTT TTNITACCCC AACTTGGNTC CCNGCCTTAN 360
TTTCAAACCG NTINCAAACC CCNCCCTGG GTTNTINGC CCNNTNCCA NTANTTGGGC 420
TNGGGGGGG GGGGCCNGN CCAAAAAAA ANGGGNTIN CCNGGGNGC CCCCNGTTTT 480
35 ANCAAAANAT TTNCCCCCGG GTTCNCCC CNVAAAAGGT TTTTCCCCC CCGGGGTTTT 540
ACCAAAAANC CNGCCCCCCC TTGGANGGT TTCCNNTCC CCATGGGGGG TTTTCNCGG 600
GCTCCCCCN GGGGAACCC AAAAAGGGC CCCCCCTTTT NIGGGCCCC NAAANNCCCC 660
40 CNTNNTTTT CAGANGGTT NCCNCCCCC TTTTPTTTC CCATTANNOG GGAANTCCCN 720
NNTTCCCCC CTTTNCCCC CCCCCAAA ANNAATTTTT TTNATTAAAA GAGGGCCCN 780
NGAAAAANAA NACCCNCCC CAC 803

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1274UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

	GATCAATTGC GGATACACGA GGCACAGGCG GATAGGCCAA GCTTCCAAGA ATGGGAAGAG	60
5	TACCTAGTCA GGGTCGTCTT GGTAAAGCTG AACCGCTGCA AGCAGCTCTA TACACAAAAT	120
	GTAGAGATTC TATTGATAT ATATCCGAG ATAGACCGCC CATAAACACT AATGATACGC	180
	TAATTCATAC ACCTACAGCG TGTACATCAA ACACACACAC AAGTTTGATG CACACGCTTT	240
10	ATTGTGTTCT TGACACACT TGATTTAGAC GGTCAACACC CTCAAGGTGT TAGAGTGGCC	300
	AACACCAGAC GCGAAACCTT GAATAGTGAC AATAGTGTCA CCTCGCTCA GGATACCAAG	360
	CTCCTTGGAC TTCTCCACAC CGAAGTTCAA TCTGGCTCG ACGTCATCG TCCACTCATC	420
15	AGCTGCTCC TGTTGTAGA CGAATGGGAA GACACCTCTG TGCAAGTGGC AGTATCTGGC	480
	CGCTCTTGG TTTCTGGTCA CCATAACGAT TGGAACTTT GGCTTGTTACT TGGAGCCAT	540
	CTGTGGTGT CACCCGAGGT TGATACACGA ANATGCTTG GCTTCTGCTC GAANTNCCGC	600
20	GAAAGCAGCA CACAAGNCCC CGAGGTGAA TTGGCTTGNT CATTCTCTGA GTCACCGTAT	660
	TTGAACGTTT GGAAGGCTTG CACCACTATC AAAATCTGCG CAGNCTTAAA CGTNAATGGT	720
	TGANACCTTG GGGTCCCGN AAAAATAANA TCNCCCGCN GAAAAGTTCC ACTTCGAACN	780
25	CCCCNGTNGT CTGGTTTTGN TGGTANCCCA ACGG	814

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1275RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

40	TGACTCGGCT TCGTGAGGAA CTGACGCTTT TACTACATGT AGATTGAAAC CGTTTTCTCT	60
	GGATCGCCTC GTCTCGTTGC TTGGTATCTT TGCCAATCCT CCTGAGTGGC CGCTGCCCTGT	120
45	AGAGGATCTT CCGATGGGC CAAACAAGCC CCACAGCCC AAAGAAGTGT GAGAGAGGCG	180
	TGAAGAAGGT TCATTGACCT CCTTTATGCG TTCAAATGCT GACGGAAGTG ACAAATCGTT	240
	CCCAAGACGC ATGTCGACA ATTCTCTGAC GGTGGACTCC AAGACCTGGA TGGCTCTGC	300
50	CCTGGTCTTT GATATCTAT GGATAGTGGC AATGTCTTT GAGAGTGCA TGTTCTGTT	360
	TGTGAGGTTT AGGTTATCAA GTTGGCAAT AGGAGCTGC TCTGCAAGTT GGTGGTTTTT	420
	TCCACAGCT GTGCTCTGT GTGTTTCAGG TCTGTATCA GTTCTTTAA GCCTCTCTT	480
55	ATCGGCCGAT CGTCCACTG GACTGNTATN TTTTINCCAC NCCATINNN CCATAATTG	540

NTNAAGNAGG TNCCCCNCCG GAATTINGNT CCGTTTCCA NAGNTOGGNC CGGGGATAAT 600
 TTAAACNITT AAAAATTANC CCGGCCCTA NTCTCTTTIN CCNAATNNNN GNNCCCCCN 660
 5 GNAANNITTT NCAANNCTIN TGNCCNTAN CCTTTTINNC CCCACGGTTT TTNNTCCCC 720
 CCGNTCCCN ATTNNGGANT TCCCCNTIN CCCC 754

(2) INFORMATION FOR SEQ ID NO:355:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 842 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1275UP

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

GATGCCCCAC ATTATGTC TC AGGTACTTT GTACGTTAAG AAGACCTGCC GCTCGATGCT 60
 25 GCCTCAGAGC ATGTCGAGC ACTACAAC TT GGACGTCCT ATTGTCGATG CCGACAAGAA 120
 CGAGGAGTTC GAGAAGAAGT TOCCATTGAA GCGCGCTCCA GCGTTTTCCT GTGCGGCTGG 180
 AAATCTAACT GAGACCATGG CCATCACTA TTACTGTAAG TTGCCACCGA CTACACACCG 240
 30 AAGCATGGAG CCTAGTGTG ATGAGAAAAC CTTTCGAAAA AACAGTTATC CCTGTCTGAA 300
 TGGGCATAAT ATCTGGTTC ACATGTGTG AGAGACCATA CTCTGATTTA GAGCTACATG 360
 CGAGGTTCG AGGAACACGT ACTAACCGAA CAACAGTGGT CAACCTAATC CAGGACGAGA 420
 35 AGGCCAAGGC TGCTCTGCTT GGCTCCAGC TAGAGGAGCA GGCACAGGTG TTGCGCTGGG 480
 AGTCTTTGAC CAACACCAAC TTCAATGACG ACGTTGGCTC TGCTCTCTAT ACCTAGAGAG 540
 GGTGTGTTCC CMTINACCA ANNCNACATG GAAAACGNCN TTCCCGNGG CGAAACNTIN 600
 40 CCGNAGTGT TINNAAAAAA GAAATAACCN CTTCCTCC TTACCCCGG AAANTTTTNT 660
 TINCCGGAN NCCNTGNCN TNGGGGGT GAACNNANTT CCCCACANTT NGGGGNCNN 720
 NTGGGNCNG GCCCCCCCC CCCNNNNANG GTTACCCCTT GGGTANCCCC NNNINAAAAA 780
 45 CNCCNCCCC CCTTNGGTC GGACCNAAAG GGGGGNCCC CAAANGAAAA AAAAAAAAAA 840
 AA 842

(2) INFORMATION FOR SEQ ID NO:356:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1276RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GATCGTATTT GTTGTGACC AGTAGCACTT TTTTCATCTT CCTTGGACG ACCAOCCTCG 60
CCAOGTTACC GAGGATC 77

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1276UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

GATCCTCGGT AACGTGGCGG AGGTGCTGT CGAAGGGAAG ATGAAAAAAG TGCTACTGGT 60
CAACAACAAA TAGGATC 77

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1277RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

GATCGGTCAC GGACAGACTG AATGGTCAAA ATCAGGTCAA TACACAGGCT TGACAGACCT 60
TCCGCTGACC GAATATGGTG TCGGCCAGAT GCGGCGCACT GGTGCTGCGA TATTTAGCGC 120
AAAATACATT GATCCTGGGC ACATAACATA CGTATTTACT TCTCCAGGCC AACGGGGCGG 180
GAAGACTGTG GACCTGGTTT TGGAAAGCCT CAGTGAAGAT GAACGTGCAC GCATCCAGGT 240
GGTGGTGGAC GAGGACCTAC GGGAGTGGGA GTACGGTGAC TACGAAGGTC TGCTGACAAG 300
CCAGATTATC GAATTCGGTC GTAGCGGTGG CTTGGACTGC AAGCGCCCAT GGAATATATG 360
GCGGAGCGGC TCGGAGAACG GCGAGAGCAC CCAGCAGGTG GGCTGAGGC TATCACGAGT 420
GATTGCCCGG ATCCAGGCAT TACACCGGCA GCACCAAGCT GAGGGAACGC CGAGCGATAT 480

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TCTGGTGTTC GCGCATGGCC ATGCTCTCCG TTATTTTCTT GCGCTCTGGA TGAAGATGGG 540
 CGTCGAAGCG CCGACGCCAG ACTGCGCCAT GCGCTCGAGT AACCGGAATG ACGATCCGTG 600
 5 CCGTTGGTGC GGCTGGAGCA ATCCGTACCT GCAGGACACC CCACTTCTTG CTAGACGCAG 660
 GTGGCATCGG TGTGTTGTCC TACCCCCNEN ATTTGAGACC ANICTACTON CCTGGCCNTT 720
 CNITGCCCCC CCGAGATCCC CCCACGGTNA GTCCACCGA AAATTTTAT ATCTACAAGN 780
 10 GNGTCCCCC ATGAATATAC CNTATCTTCT TAATCGTCN CN 822

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1277UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

GCGTCTTC TGCGGCAGC GCGAGTCCAG GTGCGCAGC ACGCCCCAG AGCGGACCT 60
 GCGCAGCGA TAGTAAGGT ATGCGACCAG GCGCGCGCC AGCAAGTTC TTGCGCGAA 120
 30 GAACCAGAGG AACCGGCAGC GGCTAACAG CTGCACAGC TGTCGTAT CTGCGCGCAG 180
 CGGTCCCCG GACGCCAGC CCATGGTGT GCGCACAGT CCGAGCATCA CGCGCCCCC 240
 GCAGATCAGC ACCGTCCGA CGACGTAAG CATAAAAC GGCTCTGGA GCAGCAACA 300
 35 CGAAAACAG CTGTTGAACA GCAGTCCGA CGCTGCAGC GGGGCCAGCA TCACAGTGG 360
 TAGGTGGCA ATCTGCATG TGCTTCGAA CAGTTCGCT AGAATGAATA GGTGAGAC 420
 CATCTGCCAT AGCGGCTAC GTTACACCAC CTGCACAGT CCGGTGCCA CTGCGAGGC 480
 40 AGCTTGCGC TGAAAGTACC AGGCCAAAA GACTGCATAC GCTTGAACT ACCGCCACA 540
 CGACCCATAA TAACAGTTG ATCGACCATT CGCTTGATA CCGTCACCC TTGCTGCAG 600
 AGTACTCTAC TGTGGCGCC TTTTGGCTCT AGGTCTCTAC GCTATGCCAA ACATACTGGC 660
 45 TCCGGTGGT CATGTTGAT GCTGTATGTC ACGTGACCGA TGACAGGGTA CCTGTGGTT 720
 CTCTCCGGT TCAGGATAT GATACGAAA NCGGAATTA NCGGATGAA TTCCCGACC 780
 CTGCGATAC GACNCCAACN GGAGCGCNG TTTTNGT 818

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1278RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

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10  GATCTTCAAC CTGCTTCOCG CTATGAACAT TCIGTTGTGA TTGAGAGGCG ATACCGCCTC      60
    CACCTTTCTT CGAGCCTGCC CGGTTTGGT AATOCATAAG TTCTTCCCA TTCTTTTGGT      120
    ATTGGTATAA GCGATGCAA TGAAAACAGC CTCTTGAATA CAAATOGACT TGCTTACGTA      180
15  TAAAATTATA TTTTATCAG AAACITGGCG AGCATCAAGC TCGGCTTCAT TGATTCATAT      240
    ACTAAACAGA ATACACTACA TGCTACCGTC CGAAAACGAA TAATCTATTT CCAATATATA      300
    TATATATATA TATATATATA TTATAGTGT ACTTTATAAA TCTGAACTAG GTCATACAAC      360
20  TCTCAAATCA AACGATATTT ATCTACATA TAGCACGGC GACGCACCA TTGAAGACTC      420
    TAGGGCGCCT GAACTTGGCG CTGCCCTGTA TCCTTAGCCT GTTCTTTAC AGGGTCATAA      480
    ACATAGTACA TACCGCGCTC TAGTTGCTCA TACTGGATGT TCCTCTGTTT CAGCTGCGGC      540
25  CAATTTTGTG GAGGGATATC CCACCCACAT TTCTGAGCTA TGAAAGCTGC AACGTGCTCG      600
    CACAGCCCCA GTAACCTAGG TCAATTCGCG TGCTTAACGG GTCTCTATG ATAGTACTTG      660
    TGGTACGTGA GCTGGACCTT GTTTACATCN CGGAAACTGC GGNCTTCAN CTNITCNATC      720
30  ANCNCAATCG CATNCANNTT CTGGCNANTT TTTTIGANTC CATGACCCCC CCNAAANNTT      780
    TTCCGGTNG ACCCACACCC CTTGAAATN NCTGATNTGN AGANGCNC      828

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(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1278UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```

45  GATCTTGGAT GTACTGGGGG CTCATACTTC GGCTTCGTGT TCCTGTCTTT TTTGCCCTTC      60
    TGGCCCTTGC CATACGTGGA TGCTCCTTGG CCCATCTTAG AGATATCTGC TGTGCGGCTA      120
50  TGGAGTAAAG CTCTGCTTG CGAACTCTAA GTAGTGTTAT CAACTTGTGT GTATCATTTT      180
    TGCCACCTGG AATCCATCAA TTTCACCTAG CCAACCCAA GCTGCGAECT ATCAAAAAAC      240
    AGGAGCAGGA AGCTGCCTGA AGAAGCGCTC CAGGGGCTA CCGACGGGA AACTACGAG      300
55  GACTGGTGCT ATGACATCCT TCCCGGGATC CATCCCGAGT TCAGTGCTTT CGAGCTGTAC      360

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AATTGCGTCC GAGCGGTGG AGCGCAAGCG TOGTGACAAC ATCAACGACC GTATCCAGGA 420
 GCTGCTCAAC GTGATTCCAG AGGAGTTCCT CCAGGACTAC TACCAGAAGA AGAAGGACCA 480
 5 GGAGTCCGAG AGCGGGAGCG CGGGCGCTCT GCCCAAAAAC AAGGGAACTG GGACGCGGGA 540
 CGGCAAGCCC AACAAAGGCA GATTCTCAGC CAGGCGCTCG AATATGTGAC CTATCTGCAA 600
 ACCAGTGGAT CTGCGCACCG CGAAGAGGTG GAGCTGATCC TGAAGGTCAG GAGCTGTGTC 660
 10 GGCAGACGGG CAGCATCGTG AACGACGTGA ACTAGAAACA CCATTGCCGA CTCGCGCTGG 720
 GAAATGGGT TGGGCNCTGC AGCGTGCTCC GGAATTNTGC GGCNCAGGG CAGCACACCC 780
 NGGCAGCACA CGCCCCAGA CCACACACTC ATTTGGGTCC CATTCGGACG CNTAGATTTT 840
 15 CNCTGGNCT GTTTT 855

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1279RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

GATCCTTCCTG GATGCTGGTA GCTCCGATGA GGAAGTCGTA CTTTGGTAA TGTCACTGCT 60
 GCTTAAGCAT CTACTTTCAA AGCGTGATAT ACAGAGAGCG TTTGCTAAAA GTGGTGGATA 120
 35 TAGGTTACTG TTCTCCATAT TAAAAGATAT CCAATCCGGG CTTACAGGAA AAGTCACGAA 180
 TCTATTGTGC ACCTATGCAT TTGGAAATCA TATGTGCCA ACACACAGCG AAAGCACGTC 240
 CCTTCTTATT AGACCGCAAG GCGATGGGCT ACAAAGGATA GTTTTGAAC TTCATTATTT 300
 40 GGCAATTGCA TTGTTAGAGA TAGCGGTGAT AAAAGCCCCA AAGGAGGATC AACAAGAGTT 360
 GAGTAAAAAC ATTATTACGT ATATCAACGA GTTGGCGTTA CTTCATAGTA CTCACTCTCG 420
 AATATOGCTT TTTGATOCOA GCGTATGCCA ACTTCATGAG AGATTGTTAA CTTTGTATT 480
 45 AACTTTGACA GATCCCAAAT ATCAGGGTTT CTATATACAG GCTATTCTGG ACATTGAACT 540
 TCTATTGAGT AACACATAT CTTTCACTTA AAGAATGATG ATCCACCACC TTTTGAAC 600
 ACTTGCAAAA TATTTTGGTA ATGAAAGGGA CATCCGATTA GTCCTAGCAG ATTACAGTTA 660
 50 GTAACAAAGG TCCAATTATA TTGAGACCAC TATATNTTAA AATTGTCCCC NIGTTATTGA 720
 AAACNTNIGC CCNGGTACA CTTATTGCTN TTCNACACCG TCCTGNAAAA ANTGTGNTTT 780
 GTTACGATTA ACTCGTTTCC TTGATTGAGC AACTTTTGN 790
 55 TTTTATCATA G 831

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 841 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1279UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

GATCAAGAGT ACAGTTGATG AAAAGGAGTT CCATGATGAA ATATGTAAGA TGGACTTGCT	60
TAAGAAATTG ATAATATAAA AGGCTACGAG CTTCATATT ATAATACGCA TTGCATAATT	120
TATTACATTA AATTGATATA GGTATATTTT TCTTGAAGA ATTAATTTCTA ATCATTTCOA	180
TGTGAAGATA TGGCCCTCTG TGTTACCTGC GGATATTTTC ACTCTTAGTA TATCTACATA	240
TTTTGGCGAG CCATTATTTA AACTGGCCAG CTTGACTCTG GACCCAAGAG CCGTAATGGC	300
AGCAGCTCTT CCTGAGCGCA ATTTCTTCAA GCAATTGAGG CACCATGTGC CGTCTTTTAA	360
TTCAAGCACA TATAAACAGA CCGTCCCGTC AATAAACCCCT AGCACAATTA TATCCTTTTC	420
TTTCCAATAC ATGTGCGGAT ACGTGGACAT TTCTGAGAT GCAAAGTTAA CAAAGCTTAT	480
AGCAGTGATA TCTTGGGTTA GAGACATGCT TGCAAATTTT GAACCGTTGA GGTATATAAC	540
ATGAACGTTA TTTGAGAATA TCAACACCC ATTAAATGAA CTGTACCTGT TTGAAACCGC	600
AATGCACTGG NNINNCTINGA AATATTNCC AACCCNCCCT TAAAAGNGTC CCCCTTTATT	660
NNGNCTNGC TATTCCCAAA AACNTACCCG NTCNTGTG NGNCCAAGN NTTTTNNCT	720
TNTTGGCAGC CTTTTAGAGN TTAAANATN TTCCAANCC CAAATCCANT TTTTAAAGN	780
CTCCCTTAA AANNCTNIGA ATGANCAGN GAATTGTTT GCGNTTAAAC TTCCAGINA	840
G	841

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 826 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1280RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

GATCATCAGA CCGTGGGAG GGTTCGTTAG TGAACCTCT TCGTAGGGG GAGCCGCTGT	60
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TGTGAGCCTT GAGCGCTCT GGAGACGGCG GCTTCGAGTG AAACGGAGCT CGTATCGGGG 120
 ATCGCGAGAT GTACTGGGGC GACCTTAATG CAATTTTCTT CTCGAAGGAC TTGTGCGGGA 180
 5 CGGAGGAAAG TCTTTCAAAT ATTGACGCAG AGCGGCGCTT TGAGATTGTG CTCTGGAAAG 240
 ACGTCTTTTC CAAGCGCGCC GGCAGCTTTT CTCCCGTGCT TGCAGCGCTT GCGCAGGTG 300
 CAAGCACGCG CGCCTTCGCA AGAACGGGAC TCTGCTTCAG TAGGCTTGTC TTGGTCATCA 360
 10 TCGGCTGCAC CACCAGCGGA TCTTTGTGTG GCAGGGGCAC AAACATGTTG GACCGCGGGA 420
 GGTGCGGTG ACGGCTCGGC GGAATCAAGG CTGCGGTCCG AAAGTGAAC GTGTCTCGG 480
 GGCTCTTGA CATCGAAACC TTGCTCTGCT TGATGGGACT TCTCCGAGTC CACCTCCTGT 540
 15 ACCGTGCTCT GCTCCCGCTC CTGCGTGGC TOCGGCTCCN GNCNCCNGT TCCTGCCCTC 600
 CTGACTNTTC CCCCCCTTT AGGGGAACAC GGAAGAAAA NAANINCCCT TTCINNCCG 660
 GCGCTTGTG TCGCCCCCN NNNNCCCCN CCCINNINN NNNNNNNNN NNCNNNNN 720
 20 NNNNAAAA NTAGGGGNGG GAAAAATNG GTTAGNGTC CCACCGAA CCCCCAAAA 780
 AACCNCCAT GINTCCAGG NCTTATGAN CANCTTCN NITGGA 826

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 840 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1280UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GATCATAATG CGACTATGCG CCATAAGCAG GGCAATACG CTATCCACAT CAAAGTCCCT 60
 40 GACCGTCCA TTCTCCGCGA CCGTACGTG CCTGTGTACA AAGGCTCAGC GCTCCAGGG 120
 CCGATGTCA TCCCGTATCA CGAACTATCA AACTCGAAT ATTTCACTGT GAATCCTGT 180
 GAAACACTAA CACTTCCTGT GTATGAACG GAGTTAAACA TCCAAGGCAA CATTGTGAG 240
 45 GGGGGCAGA TTACCAATTT AACTCAGGT GTACCAGGCG ATGTCCCGAT TTCTATCTA 300
 GACGGGAACA ACTATACCA CTGGCAGCG TTGACAACT CTGAGAGGGC ACTCTGTGTG 360
 ATTGATTGG GTTCGAAGA GGAGTACGAG ATCACAACG GTTAAATTT TGTGGGGCGC 420
 50 TGTCCCGCG AAGAACTTCT CCATCTCTAT TCTCCCCAAC TCAAAGCACA TCACAGAGAT 480
 ATTGACAAA CTGACGGCCA TGATGGACG CCGGAATAC GACTTGTCTC CTGCTCAAAG 540
 TGCCAGCGG TCTCTTCTC GCAGCATCTG CTGGGGGGC TGGCGAATGT CACCGATTCC 600
 55 AGGGAATCG CGGCCATTGA TGAAACGTG GANNVTGTTT TAAAAAATTT CNGTTGGACT 660

TTCANCTCCN NNNITTCACN TTTCOCNAGG CGCCAATNCN GANCTOCTNA GGCCCTGNAA 720
 CACCATTNAN CNITCGACCTA CTCAAAAGIN TTCTATCCCC CAATNTCNIT TOCAACACAA 780
 5 CGATCTGCTA ATTGNGGNC CAACCATCAC TTNNVGCATC ATTTTGCCAC AACAATGNGA 840

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1281RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GATCCGACGT TCAGTGGACT CTTCCCATTT AAGGTTTTCA ACAAATTOCA AACTCATGTG 60
 TTAAATGCOCT TGTACCATAC CGATGAAAT GTATTTATG GAGCTTGTA GGGCTCGGT 120
 25 AAAACTGCAA TGGCAGAATT AGCTTTATG AGTCACTGGA GAGATGGTAA GGGACGTGCC 180
 GTCTATATAT GTCCATCTCA GGAGAAATTT GATTTTCTGG TGAAGGATTG GCGAAACAGA 240
 TTTTAAATG TGGCAGGTGG AAAGGTTATT AATAAACTCA CATTGGAATT AACTAACAAT 300
 30 CTTGGAACGC TAGCCCACTC GCATTTAATC TTAGOGACTC CAGAGCAGTT TGACCTGCTT 360
 TCTCGTGGCT GGAAAAGAAG AAAAAACATT CAGACATTAG AGCTGTTGAT TCTAGATGAT 420
 CTTCATATGA TCAGTAGTGA CTTGCTGGC GCAAGGTATG AAAATATAAT ATCCAGAATG 480
 35 CTGTTTCATTC GGGGTCAACT TGAAACGGCC TTGGGTATAG TGGTTTATC TACCTCCCTC 540
 GCTAATGGTC GCGACTTTGG AGAGTTGGCT CCGAGCTAAA AAGCTACATT TTTATTTCTC 600
 CTTTCACGAA GGGTTATGCC CTTACAGATC CNCTTACATC CGTTCCTAGA NGCATGAAAN 660
 40 TCTTTAATTG AACTATGGCC AATCGCTTCC TGACGNACAA CTCGTGATA CTGCCANINT 720
 TANCTTTTGT TCATTAGAA ATGTTTCAAT TCTGTCTCTG CACGCCGCC GGANGAAATC 780
 45 CTGGTCNCCN ATTAGTTGGA ACCATTCTAG GNNAAAAGAC TCTTATCTA ACN 833

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1281UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

5 GATCTGAACG TATGAGAGCG GGTITTTTACT AATTATAGAA CCATATGAGA TAGAAAATGC 60
 GGCAGTTCCA AATCCAATAA TGCGATTAC GTGCGTTGAT GOCTCCATTG CAATCAAACC 120
 AGTGTGTTGAG AAGTTTTGCT CAGTTATTAT TACATGGGG ACCATTTCTC CGCTTGACAT 180
 GTACCGTCCA ATGCTGAATT TTGAGACAGT TCTTCAAAA TCTTACTCCA TGACGCTGGC 240
 10 GCAGAAGTCC TTCTCCCAA TGATTATAAC CAAGGGGTCA GACCAGGTAG CCATCTCTTC 300
 TCGGTTTGAG ATCAGGAATG ATCCCTCAAT TGTCAGGAAT TATGGTTCCA TATTGGTTGA 360
 ATTTGCCAAG ATTACTCCTG ATGGTATGGT AGTGTCTCTC CCTCATATT TATATATGGA 420
 15 ATCCATTATT TCAACTTGGC AGACAATGGG GATCTAGACG AGGTTTGGA ATACAAGCTC 480
 ATCCCTCGTG GAAACACCAG ACGCCACAGG AAACCTCTC TACCTTTAAA AACTNACNA 540
 AGGCCNGCC NNAAATGGGNC GGGCCANITA ATTCNGTGG CCGNGGAAA ATTCINAGGA 600
 20 ATGGATTGNG ACNCCCTCGG NGGGAGTGT TGAAAATGGA TCCCTCCCTT NACOGANAAC 660
 GTTINTTTAG GGAGGGTINT NCCNINANA AAANATCCA ACCGGGAATA CTTTTCTCTT 720
 NNAGCATGAA NCCCCCCCCT TTTGGGAAA TTCAGGGGTG AGGAANATAT GGTTAATGIN 780
 25 CCCCCANCN GNNNCCNNA AAAAANCACT CCAATGTCC CAGGNCCTTN NGNACCACTT 840
 CTNNNAITG GAT 853

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1282RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

45 GATCCGGAAT TATAGAATCG ATGAGCATTT CATTTAGCAA CCTTCTTCCA ATTGTTAATG 60
 GTTCATATAT AAACCTCCCTA GCTTCTCTTT GATAAATCCT TTCAAGAACA GCACCGTOGC 120
 AGTCTGGGTT TATCTTTATA TTATTTCTTG TTATGCAACT CGCATGGTCT ATGAGGTCCC 180
 TACATACATT TAGGTGCGCC ATCAGTACCA CCTCTTCCC CAGATTCTCT ATGTTCTCTA 240
 50 CACGTTTGAA TAGAGTTTTT AGGAAACGCA GCTTAAAAC TTCACCTTCC TCAGTGTTC 300
 TAGAATTAGC AGGCAGTAT ACGGAAATGA CCACCACTT ACAGGCAAT TCGACTAGAA 360
 55 GGCATCTCCC CTCCTGTCT AGTTCCTGTG CATTAGCATC ACTCCCATAG GGCAAGCCAT 420

CATAACCACC AATACCAATG GTCGGGTCTT CGCAATATGC TACCAAGGCG CCATCCTTTT 480
 TTAATTTTTT AGTCTGCCTG TAATACCTCC TCCCGCCTTC AATACTTGTA ATGATTATOG 540
 CAACGATCGG CTGCTTCAGG GATTCTGTTC CACNCCACN CCNATACCTT TCTCCTGN 598

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1282UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GATCTGGCA AACACCCCA CTCGTGTAC CTCTCGATG CTGTCAATG AGTCTTGTG 60
 CATGCTTCTA TCCTTCAGCA GGAACGGGC TAGGTACGGG ATGTTCCGCC GCAGCAGCC 120
 GCAGATAGCT TCGATGACCG CGGGGTGTA CACGGTCACC GACTTGTAGT ACCCGGGAA 180
 GAGCGCCCGG TTGCTCATCG GTAGCACCAT CAGCTCCTCG TACTTGGCG GCACCTCGCC 240
 CTGGCTGGC GGGTTGACC GGGCGCGCC GCGCGCGAA GACGCGAAC CGCGCTGCC 300
 CCGGAAGAA CTAGCCTCG AGACCGATT CGCTGCTCT TCCGTGGCT GCGCTCGC 360
 CTCTCGTGG CGCACCGCTT CCTCGTGGG CCGCTCCTCC GCGCGGGG GCACTTTT 420
 GTCTGCTC TGTCCGGCT CCGGCTCTT GCTTCAGTAT GCACTGCCC GCGCGTGTA 480
 TCCCGACTG CTGCGCAAG GCACTCTTT TTGGGGGGG GGGGGGNNN NNNNCCCN 540
 CCGCGCGCG GCGCGTTCN CCGCGCGCG CCGTTTGTG TTTTCAGCC GCGGNTTGG 600
 CCATCCCCC CTNNTTTTT CT 622

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 798 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1283RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

GATCAGGAAA TCGACGGGAC TGGCTGATTG TCTTTATAGT CAAGCATATT AAACACAGT 60
 GACTTAACT AGATTTACAC GTGACATGCA ATTGTGTGTT TTTTTTT TTTGAAAAC 120

CTGCATCGAG CTATTAGATG CTCATCGACA CTAGTGTACA AACAGTCAA GGCTTAAAAG 180
 CTCTGCAGCA TGGACCAGTC GAATAAGGAG CATCGTCTTA AAAAGGAGAA GCGACAGCT 240
 AAAAAGAAGC TGCCTCCCA GGGCCACAAT GCGAAGGCAT TCGGGGTGGC CGCTCCGGGA 300
 AAGATGGCCA AGCAGATGCA GCGCAGCAGC GATAAGCGGG AGGCGCGCT GCAOGTTCCG 360
 ATGGTGGACC GGACGCGGA CGACGACCG CGGCCACTCA TTGTGCGGT TGTAGGTCC 420
 CCGGGGACGG GTAAGACAAC NCTGATCAAT CGCTGGTGG GGGGTGACC AAGACGACCC 480
 TCGCGGAGAT TAACGGTCCG ATCACGGTG TCTCCGGCAA GCGCGCGGT CTGACGTTCA 540
 TTGAGACGCC CGCGACGAT CTGAATCCG ATGTGGACAT TGCGAAGGTT GCAGATTGG 600
 TGCTGCTGCT GATGGACGGT ACTTTGGTTC GAGATGAGAC ATGAGTTCC TGACCTGGCN 660
 CACNCCACGG ATNCCCTTTT NCTGGATTAC AANNCNCAT TTTTCATNC NAGGCCNCTC 720
 CNGCTCNAAA ACTTTTNACC TCGTCTGAC NATTTTNCN GGGGNNCNT CCCCTCGTN 780
 TTTTTTATGN NGNNCNT 798

(2) INFORMATION FOR SEQ ID NO:371:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1283UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GATCCGCTGG CCATCGCG AGAGCTATGT GCATCGCCTC ATAGTGGCCT TGATAOGTGT 60
 CTCAACCAAG ATTGTGGAAG ACACCGTGCA CTCCACGAG TATTTCAGCA AGGTCTGGG 120
 CATATCGAAG AAGCTCTTGA TCGCCTCGA GCTAGCCCTC ATACTGTCC TCCGGGCGA 180
 GGGTTTGATG GTCACGGCTG CAGCTCTAAA CGCTGCCTCA AACGCAGTG CTGGCTTCG 240
 CGAGCAGTCT GCGCTGCCAG CCGCTGCTGC TCAGTGATAA TCGCCACTTC TAGGCCACA 300
 ATTGGGTAT TTAATAAGCA ATAAATACTC CAACACTAAT AGTATACACC GTTTGCGAGA 360
 GTAAGCAOGC AGCAGGAGGT GGCAGCTTTT CTGGTACCAC CTCAAGCCCC TTGCCATTGC 420
 TGCTATCTG GTTTAGGCAT GAGCAACCTT AGTCAGTTTC GAACCGTGA TATATGTTTC 480
 GAACACGTTA CCTTTTCGGT GAAAGAAAA AGCCTAAAGG CGAAATGTTT TCCATGTTAA 540
 CACAGCAGAT TAGAGGTACC TTGTACTGGA TATTCTGTAG GATCAGGGC TACGAGCATT 600
 CATCCAGAAG CTTTGAACCT ANGTTGTTT NGGATGCCAG TINGGACTT ATNCCGTGCN 660
 TNTAAANAA TACTTCGTCC TAGTCTTTGG AACAAACNIG CATTGTGTGT TCTINGTTTG 720

GANNATCGGN AAGACANCTT TTGCCCTGCT AANAAGACNG TTGGGAACNG NNGCCNNTGN 780
 CCCNCTCCGA GNCNNGAACN GGCCCCNTTN CNMTTCNNCN GGGGNNNNC 829

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 817 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1284RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GATCGATCTG GTCAGGTCTA TTTGTGGCAC CGATGACAAA AACATTTTTC TTTCGATTCA 60
 TACCATCCAT TTCAGTTAAC AATTGGTTAA CGACTCTATC AGAGGCGCCA CCAGCATCAC 120
 CCAITGAGCC ACCTCTAGCC TTTGCAATGG AATCTAGTTC ATCCAAAAAG ACAACGGTTG 180
 GCGCTGCGGC TCTAGCTTTA TCAAAAATAT CACGAATGTT GGA CTGAGAC TCACCATAAC 240
 ACATGCTTAG CAACTCTGGA CCTTTCACAG AAATGAAATT AGCAGATACT TCAGTTGCGA 300
 CTGCTTTTGC CAACAACGTC TTACCACTAC CTGGAGGACC GTAAACAAC ACACCTTTTCG 360
 ATGGCGATAG ACCAAACTTA ATGTATTGGT CAGGATGCAA GACGGGATAC TCAACGGTTT 420
 CCTTCAACTC CCGCTTTATG TCATCCAACC CACCAACATC GTCCCAAGTA ACGTTAACC 480
 ATTCAACCAC GGTTTCACGT AGCGGGATG GATTGGAGTT CCAAGTGCG AATCTAAAGT 540
 TATCCATTGT AACTCCTAAG GAATCCAAGC ACTTCAGGTG CGATTTCATC CCTCGTCCCA 600
 ATCAATTAGA CTCATCTTCT CTTAATCTG TTGCAATTGA GCTCTGAAC ACAAAGAGGC 660
 ATATCAGCAC CCACATACCA TGGTTTCAGC AGCTAGCACT TCCAATCAG TCATCAGCCA 720
 TCTCANTTCT TGNVTGGAT GTTTAAATTC CCACCTCCA GTGCTCTGGA NACCANTTTA 780
 TTNNGTCAA TTTACCAACT TTTAGNCGN TNNATGG 817

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 831 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1284UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

5 GATCAAGCTG ATATGTATTC TCGGCTACT GGTGATATCC GTGGTAATCT TCTTGGGCGG 60
 CGCTCCCAAC CACGACCGTA CTGGCTTCGG CTACTGGAAG AACCGGGGC CCTTTGCGAT 120
 GAGCCTCGCG CCAGGAAGCA CGGCGGTTT CTTGAAGTG TGGCGGCGG TGATCAAGTC 180
 GGCTTCGCC TTCACTCTAT CACCAGAACT TATAGGCATT GCATGCGTCG AGGCGCAGGA 240
 10 CACCGGGCGG AACACTGAGA AGGCATCGAG ACGTTTCATA TACCGTATTA TCTTTTCTA 300
 TGTGAGCTGC GCGTCATGA TCGGCGTCAT CTTATCAAGA ACTGATCGGA AACTCATAGA 360
 GCGCTGGAG ACAGGGGCGC CAGGCGCTGC CTCCTCTCGG TTGCTGCAGG GGATTGCCAA 420
 15 CCGAGGGATT CCGGTGCTCG ACCAAGTCAT CAACGTGCGG ATCTTGTCCTT CTGCGTGGTC 480
 GGCAGGCAAC TCCTTCATGT ATGCATCCAC GCGCATGGTG CTAGCGCTTG CGGCGAGGG 540
 AAATGCGCCA AAGTTCTCA CCAAGATCAA CAGATATGTG TGCCCTACAA CGGGTCATC 600
 20 GTCTGCACGC TCGTCGCTG TCTTGCTAC CTGAACGTCA AGACGACTCC GCAATGTGTT 660
 CCAGTGGCTG TCGAACATAT GCACCATCTC CGCTTCATCC GCTTGTTGCG CATGGCTCCC 720
 TTATATCCGT TCCNGGCGT TCTTTTCACA CTCNANOCN TNCCTNCCA GTTCCCTGCA 780
 25 CCNTTTCNCC ACTATTCNT TMTAATGINT CTTTTINGAC AATGTTCCCT C 831

(2) INFORMATION FOR SEQ ID NO:374:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 817 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1285RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

40 GATCCGGGTC CGCCACAAGC TGCTGGTCCA CATGCTGCTG CTGCGCGGCC CCCCCGACGC 60
 GCGCGGAAAG AAAACCGAAA TCAAGGCCAG CATTCGGTT ATGCTCTACA TATCGCGCT 120
 45 CGTACCTGTG CAGGGCGCA CGTCTGGT TGATAACGCT GCGCGCTTC ACATCGTCC 180
 CCGGTGCTG ACAGACCTAT TCCGACCGG GAGCGGGAC TCACTTCGA GCTGGGACG 240
 GCGCGCTCC TACGAGTGC GGTGCACGA TCGCTGTAC GATGGGACG TAGGCTGCT 300
 50 TGCTTCGGC AGGGGGGCC CGCCGATTC GCGCGGCC CGCCCCCGC CCGAGATTG 360
 GCCACTGGGT CTCCTTCGG CCCTTCACG CTTGTGTTG GATGATCTAA GCAGGGTCCC 420
 CACGTACCAA CAGCAGCAG ATGGACACTC CCTGCCATTG CATCACTCT CCCCCGGTA 480
 55 TGCGGCCACC GCGCCACNG CCGGGGGCA ACAGGCACN TGACAATCAC TTNTGGGTG 540

EP 0 866 129 A2

CGTCGGGGCC CCCCAGACCC CCTTGGGCCC TTATCTGACC CCCCCCAAAC CNACCNITGCN 600
 CCCAATAGGG TCAAACCGCG GNGTTGNA TTTNCTTGMT CNGNNNNNG NNNNGGTTTT 660
 GGGCCCCCCC GGTNNCCCC CNANTTNGC CCAANCGGA NCCGGGGAGG GTNNNGTGN 720
 NNNNGTAAAA ACTTNTACCC CCCCNTTTG GGTNCCNGG CCGNGGGTTT TTTTTTTOCC 780
 CCGGGNGCCC CCCCNGGG ACCNTTNGG NACNATT 817

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 831 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1285UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

GATCTTCTTC ATGACGCTAC TGTAGACAGT TTCACAACCG ATAGCCTGAA GACACAGTAC 60
 AACCAGAGCA AAAGATATCA ACTGTTTCGG ATTCCGTAAT CCGAGCAATC CAGCTTTAAG 120
 GACCTAAGTA TTTTGCAAC CACGATCCAG ATGAACGCCA TTCGATCTAC AGTGAACCTG 180
 GCTCTTTTGG AGATGCATCG CATGTGGTTC GACACTTGGT CTGTATTAG AAACGAAAAA 240
 TACCTGGGTA AATTATGATT ACATGTTATA TATAGTAAAA GATAACAGC CACTCAGTGT 300
 TAAATGGTCC ATCATGCTC TAGGACTCGT TGTGTGTGCT CGACAGAACT GCAGTCCCCA 360
 TTTGCCTGCT AGGTTTTTGT GAGGCTTTTT TCTAATTGTC TAATTTAAAG TCCTGAATAT 420
 TATCTCCAA TTGTGGAATG AAAGACACAT GTACCACTAG AGGTTCAGCC CGATGGCTGC 480
 AAAACGGCAT ATTTGTCATC CAAATCATGC CGCTGGTCCA ACAGTTTAAT AATGTCTCTG 540
 GAACTTCGAC TACGTCGGA ACTGCTCTAT CATCTGGAAT ACCNCTCCT GTTATGCNTT 600
 ACCATANTCC CTTCCCTTGG TGGCCNAATT CTTAANCAAT TTTTGNITAA ATNCCCCNT 660
 GCTNNCTAA GGTNAATTCC NNTTGGCCCC CCCCCTGGG TTNTCCGTT CTTTGGAAATG 720
 GAGGAAGGCC AGGCTTGACC CCAATACNC GGCCTCCGGG AAGNTCCTC CTINGCCTTN 780
 CCCANIGGEN TNCCTGGGTT NGNNGCAAN CNACNNNGG CCTCCTTNCN C 831

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 802 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1286RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

GATCGCACCT ATAATGAAGA CCGTTTITTT TTTATGAGAA ATAGCAGCCC TCCAGGGGTT	60
ACTTATTAAA TAGCTACAGT AAGATTAGGT TATTGGTTTG CAAATTCATT GGTAGATCAA	120
CTTGTAACCT TCAAATAATG CTTCGCTGGC ACGTCATAA AACATGTTAT GCGCGGTGTT	180
GACAACTACT CTGAAGCTAT AGTCAGGTA GTGGGTGCA TTAGCTGGAC ACACCTTATC	240
TTCCTGCGG ACCAAGACAT GCGCTGTGCA CCGCTGTG AGCAAAGGTG GCGCGTTAAT	300
TAGGTCITGC CAGCCTAGAA GATACTAGT GATGGATTG GTGAAACTG CTACACCGTC	360
GTAGAAGTGA TTTAGCTTCC TGTACTTGT CCGCATGTTG GAGAAAAGA ACTTAATTCC	420
GGAGCTGTC AACCTTCAT CTGGTCGAAA TTGGTCTTA TGAATTTGAG AAGCATGATC	480
AAGAAGGGCT TGAAGAATGT TAGTGAAAGG TTTAGATATG GCTCGACGAT ATCCAACTTT	540
GATTTGAGAG TTCTAGGTG CCGCGCGCC AATAGAATGA TCTTTCTGG TTCAATTGTT	600
GACCGCGTAT CCTGAAGGCT AATGCCAAGC CAAATGCACC CCATCNATTG CCAAAACTC	660
CCACNGACAT TATTATGGTT GGCNCGTAGA CCATGAATCT AAACCCCTA TCACNCACCC	720
CCCCACANG GTTACCATOG CCGATGTCC TTCCCANCC TGAGNTCNAC CCGATTNTCC	780
CCCTATTINC CACATATCNT CC	802

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1286UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GATCTTCGCA GCCAGCGCGT AGTCCACCG CGTCAGTCC TCGCAGAAG CCGCGCGTG	60
CACGTACAGC ACCACCGGGT CGTCGGGTG CCGCTGTG GCGCGGACA CATACACCG	120
GCGCGCAGTC CGCTCGCGG CCGCAGCGC CGGCCCCCG AGCTGGAACA GGTGCTATC	180
CTGCACAACG TACGTCTCT CCAGCACTC GCGCGCGG TCGAACGAC GCGCGCGTG	240
CCACCAAGGC ACGCAGTCC CGACGAGCG CCGCAGCGG GCGCGCGG CCGGTTCCG	300
GTGCGCGCG GCTCTACGC CCAGCAGTCC CAGCAGCGT CCGCGCCCC CCGCGCGAC	360
CACCGAGTAT ACCAGCGCG CCGCAGCTG CCGCAGCGG AACCCATAGA ACTTCAGCAG	420

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AAACGGGAGT ACGCTCCACG TTTTGTITGG AGATCCCATG ATGCGCGGCC GAGGGACGTC 480
 GACGCCCCGC ACCTGACGGG GCGGCTACTT ATACACCACA AGATTCTATA GAAAAGGAAT 540
 5 GCGACCAACG ACGAACGGTG TATCGTTTGG GAAAAAAGG AGTCCCCCAA CTAAAGCTTG 600
 CTGCTGGCT ACGAGTTTGT GTTTCAGGTT TCTTCATAGC ATCCAGTTG TTTTGTITGT 660
 TTGGCAAATC GCATATGAAC CATAAANAT CAAANNITGT ACAATTGCTG CGACCGTTG 720
 10 CCCATCCNC CGCGGAAANA TCCAGAAATC GAGANAATT CAGACGCGG GTTTGCCAAA 780
 NTCCGAAAC CCCAAANTOC CAACATTOCT GNCACATTG ATTCTGNNC NNCA 835

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 799 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1287RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

GATCCCACTG GTATTAGGTG TCTGAACACG GCCAAATAAA ATACGCAAAA TGAAGGSCAT 60
 30 TAATAATCTT TCATCAGTGT TGACAATAAC CCTTGACTCA TTCTGAGCAA ATAACITTTG 120
 TACTTCGTG TTGAATAACG TGTATCTAA TAAGTTCITC AGATTGTCCC TATAITTCAC 180
 AGCTACTGGA TCCTTGTATG CTAACAACGC ATCTAGGGCC AGTTTCTGCA CTTCAGCGT 240
 35 TCGACTACCC AATAATTCCA TCAACCTTTG GCGGACATCT TOGGATTTGT AAATAGCTTT 300
 GATATTTCTG AACTTGCCCA ATAATTTCAA AATTAGATTG CTATCGTCT CAGACCATGT 360
 ATCCGCAGAG TGCCTGCTA ACTCACCCAG ATGGTCTTCA TCTTGGTTGG CATCGAATTG 420
 40 ATCATTCGGT TTAAAGACAA AAGGTACAAT GAATCTGCTA TTTTGCTCCC GCGAGCTGTN 480
 GCAGCGGAT TAATATCTTC AATGCTTGTT TCTAATCATA CGGATATCC GAGTGAACCG 540
 CGANCCCTT TAAGGTTTTC CAACCAAGGA TTTTTCGAAA NCAACATNCN TTNGAACNT 600
 45 TCCNAANNCA AATAATTNAT CCTAAAAAAT TINTGCCNA NTCCAAAAAN TCCCNAGGG 660
 GTNNAAGAG TGGCCCCAAA TTCNAAATNA GNGVTTTTIN GGNVTTINCC NAAAAAAAT 720
 CCCNCCNAC CNGNNTTTA ANAATTTTGG GGAANCCCAT TCCCCCCCCA AGGGGAAAAA 780
 50 AGNGTGNNCC CNATTTTNA 799

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 817 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1287UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

GATCAGGTGG TGTGGCCGA TACCGTGACG GAAATGGATG TCCTGGCCAT GCCCGAGATA	60
GATTTCTCTG ACACAACGTC CTCCTCGAAG GGCTGATGC GCGAGAGCG CTCAATGGAG	120
AGGCACGTAC AGGCGCGGAA CACCGTCACA GACCATGGG ACATGTCTTT GGAAGTGGGG	180
AGAAGATACG CCGCTGACGA CGACCTGGAG CAACAGACGT CGCTACTGGA CCTCAACTTT	240
GAACTCAGTG ACATGCAGAA CTCCAAATCT TGGGTGAAG GGACGCACAA TTCCGAAGAG	300
ATCAGTGOCA ATGTGCTTGC AGAGTGGCAA CGCCAGGAGC TGCCCGGGAA CGAGGCATT	360
GAGCGTGAAG AGGATCTTGA TTGGAATCTG GGATTCACGG AACCAGCAAT TGTAAGTCCCT	420
TCAAGCGATT TTGAACACGA TAACAGCATA GAAGTGGGCC GGAGAGCAGT CCGGAATGC	480
GGACCTTCAG GAACTGTGG ATTTGGGATT CGACTTGGAT ATTGCCAGGG TTGACATTGA	540
GGCTACAGCC GCGAGCAGA TGCTGGCAGT TTGCATCTGA GCTTTCCGA AGTATAGTAC	600
GTCTTCCTGG AACACTGTTC ACANCAAAA CAAGAAAGGC AACTGGTTAT CAATCTACA	660
TTCAACCCCA CCGATTACT GAAAGGTGNT CNAACCCCC CCNACANTG CTCNTGANT	720
ACCCATCCCN NCCCATTCN NCCNAAAAC GGNVNTGAC CCTTTNAAAT GATCCINCAA	780
TTTTGCNTGA CATCTGCTC NITTCACAG AGNCCCA	817

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 787 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1289RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

GATCGGGATT GACCGTAATA TTTCAGCTTT TTGATGTGAA TTGCCAAGAG GAACAGCGAT	60
TTGAATCTCG CTGACTCTGT TGTGAGTAAT TAGTACAAGA AACTGTGGCC TGTCAAAATT	120
AAGCCCTGGG AATAGGACTT CAACTTCAGA AGCCACGAT CGTCAAGCGA TGATACAAGT	180
GCCTACCAAC ATTGACTTAA CATGAAAATT GATAGCATTT TTATAACAAT GGAAGCAAAG	240

GACTAAGTCC TTCAAGTGGT GCGCAATGCA GCGTGTTAGC AGGTTTGGC ATATTCCTGG 300
 AAGATGTCAA CCTTCCAAAA ATATTCCTCA GAGCATTAA TATCATTACA CAAGCCCTTG 360
 5 GGTGAGACA GAATCTTGAG AGGTGCTGCG ATAAACTCA AAATCGCAGT GCTTGGAATTA 420
 TAGGGCTTAT ATACTGATTT AAGTGGTGGT GGTTATCTAT TCAGGGTTGT ATAAATTAAA 480
 ATATCACAGT CCGTATACTC TTACACACTA ATTATAATCA CGTGATATTT GACTATTTAT 540
 10 TACACCAGGA CACCTCGCTA TGAAAATAGC AACAGGCTGA TGGTATTAAC ATCTGAAGAT 600
 ATCGCCAACA TTAGAACACA CTACTGACAC AACGGCCAGC CATTGAGAC TATGGCTCGT 660
 ACTACTGCAN TACTGTCATG CTTATCTGAC NOCTGACCNC TGATGTGTGC GGAAATCCNT 720
 15 TTGATCNGCA AAATCATNTC GNTGACCNCA ANTTCTACTN TATTAACCCC CCCACCGCCA 780
 ACCTTTG 787

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 788 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1289UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GATCCAGGC TGCCCCAGGA TGACGGAAAG TTGCATGTC TTTCGGGCGC TACAGGCTCG 60
 35 CTTTCGGTAC TGAAGATTAA ATCGATGATC AAAAACTCG AAGAGATTTA TGGTTGGGAC 120
 CATATATCCA TTCAAGTCAT ATTAAC TCAA GCGCTGCGC AATTCCTTTC TAATAAAAAC 180
 CCAAGAAGA AGAACCTTTA CGTGCTAGC GAAACAACT CATTCTCAA CTCCGTGGCT 240
 40 CACCAGGGGA AACTTGCAAC AGAACAACTC AGACGCATCC TACACTGCGG TAAATAGCGT 300
 CTCCAATACC CCTGCACTTG GGGGGCGCAC ACCAACGCCA GCAGATCTTC TCAGGGGCGC 360
 AGCGCCGCAA GCGCGGGGCT CCGGTCTAAG CCAGGGCGCA GCTGCGGCGA AGATTGAGCT 420
 45 CCTCCACAC ATACAAGTCT GGACGGATCA AGACGAGTGG GACGTGTGGA AGCAAAGAAC 480
 AGATCCGTAC TGCATATTGA ATTACGCAGG TGGGCGATAT CCTTGTCGTC GCGCCACTTA 540
 CGCGAATACA CTTCCAAATT GCGCTGGGCG TTGTTAAAC CGCGAACAT GTTCNTCGGG 600
 50 NVTGNAACCA NTTTTCCAAT TCTNCNCCCA NCGNGTTTN GNGNINTNA ACCCCCCCCC 660
 TACCCCCCNA AAAANAANAA NAAAAACCCC GTTNTCTGTG TTTCACCNCC CANAAAAAG 720
 GGTNCCCCCG GAAAACGAAC TGGGGGAGAG GAGAGGNANN AAATTNCNAN AATCCTTTTA 780
 55 NCCNCGG 788

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1290RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

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GATCGCTAGA TGCCAGGAT GAGACTGTTT AGGTTAGGCA GGTGTTGTAT GCGCGGCAG      60
AGGGAAACCC AATGACTTTG CATAGAACAA ACCCGCATC ACCCATGTCT TGCGCTGTAT      120
AGAGACTAAG GTATCTGACG ATCCCTTAGC GACTCTCTCC ACCGCTGAC GAGGCATTTG      180
AGCTCTTAGC AACTGCACAA ACCTACTCGA ACTCTGTTTC CAGACTTCTT TCTGTTGTTC      240
TTCAACTGCT TTGCGATGAA GTACCCCGCA GGCTATTMTT CTACCCGCC TGGTGTGTGT      300
CTATATACCC GGTGTATTTT TTGATAAAAA ACTCAGCTCT TCTCTACCG CAGAAATATA      360
TATCCAGTCC TTAGGCGCAT GCGAAAATCT GCGTTTTTAC CGCTGTTTCT OCCAGTCTTA      420
GCACTGGCAG AAAAAAGATG TATGGGTAT AGGCGCTGGC CCGCGGAAA AAAAAAAAAA      480
ATAGAAAAAT AGAAAAATAA AAAGAAGTGG GCGGCCCCGC GGGCAGACGA AGAAAAATA      540
GGGCGCCACC CCTCCAAGCA GACGACAGGC GAGACATAAT AAATCCACA CCAAGGGAAG      600
AAGTCTTGTC CAAGCTCCCG GCTCATACGC CTGCAATCTT GTTCCATCC GCTTGCAACC      660
CAGTATGCAT GTCAAGCATG NTCGAGCTC CGCTGCTTGG AGTGAATCT CTTCCTACCC      720
AGCCGAATCC CATACTTGCC TTCACATACA TACCTTTCAT T                                761

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(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1290UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

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GATCAGACAT GGTGTTTTTC GGCCTCGCT CCTTGTGGGT GGGTCACCG CAGTTCACTG      60
GGCCAGCATC AGTTTTGGTG GCAGCAGAAA CCTTAGGAA TGTGACTTTC TCTTGGAGG      120
AAGTGTATTA GCCTAAGGTT ATACTGCCAA CCGGACTGA GGACTGGGC TTGGCCAG      180

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GATGCTGGCA TAATGGTTAA ATGCCGCCCC TCTTGAAACA CGGACCAAGG AGTCTAACGT 240
 CTATGCGAGT GTTTGGGIGT AAAACCOGTA CGGTAATGA AAGTGAACT AGGTGAGGGC 300
 5 CTCTTTAGAG GTGCATCATC GACCGATCCT GATGCTCTCG GATGGATTIG AGTAAGAGCA 360
 TAGCTGTITG GACCCGAAAG ATGGTGAAGT ATGCGTGAAT AGGGTGAAGC CCNANGAAC 420
 TCTGGTGGAG GCTCGTAGCG GTTCTGACGT GCAAATCGAT CGTCGAATTT GGGTATAGGG 480
 10 GCGAAAGACT AATCGAACCA TCTAGTAGCT GGTCTGCGG AAGTTCCTC CAGATACAGA 540
 ACTCCTATCA TTTTATGAGT TAAACNAATG ATAAGTTACC GGGTTGAAAT GACCTGACTA 600
 TCCCCACTTT AATAGTTAGA ATCCCTGTTG CTTATTGAC 639

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1291UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

GATCGTGCAC GGCAAGACGT CGGAGCTGCG TCACGACGGG CGCGGGCTCT TCACGGGGGT 60
 ACCCCAGGCC GTGGCAGTGA CACGGTACCA CTCGCTGGCT GGACTGGGCT CAACGTTGOC 120
 GCGCGAGCTG GAGGTGACCG CGCGCACGGA GACAGGCGTG GTTATGGGCG TGCGGCACCG 180
 35 CAAGTACACC GTGGAGGGTG TGCAGTTCCA CCGGAGTCC ATTCTGACCG ACCACGGGCA 240
 GCTAATGGTG CGCAACATGC TAGCGCTGGA AGGCGGTACG TGGGCTGAGA ACGACAAGCT 300
 CCAGCTGCGG GCAGCGCGCG GCTCTGTGCT GAGCGAGATA TACGCTCAAC GACAGGAGGA 360
 40 CATGGCAGCG CAGATGGCTA TGCCGGGAAC TGGTATGGCG GACCTGGAGG CGAGCTTTTCG 420
 APTGGGGGTT CTGCCGGCGG TGGTGGACTT CCATGAGCGG CTGGCGCGGG ACGCCCGCGG 480
 CTGGCTGTGG TAGCCGAGAT AAAAGTGGT CTCCGTGCGG TGGCAATATT AGCGAGGCGC 540
 45 TTGGCNCAN AANANGCGCT TNCNINTGCG CGAAGGCGGA ATTTTCGGCC ATCTCCGGTG 600
 CTTTACCGAA CCCACTGTTT TAAAGGGACC CGCNAGANCN NAATTATTNC CCGACCCNCC 660
 CTTTGANAAA AACNANACTG CCCAANACC GCGCGTTTG CTNCTTTANG ANATCTTTAT 720
 50 TNCNNTTCC AATNTTTGAA GCGCGNTTNC GCGCNACAAT TTCCCTTATT TINAAATTTT 780
 NAACCACCCC CCCCAGACC NTTTTTTTTIN CCC 813

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 773 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1292RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GATCCGTGTA TTTTATTATT ACATTATTTA ATTAAAAATA ATGATTTAAA TAAATATTTT	60
TTATAAAAAA TAATTAGTGC ATTGTACAT GTTCATTAAA GAATGATTAT TATCAAAACC	120
ATCAACTAAT TGTATATAT TTATTAAATA TTAATTTCAC TTAATTAGA ATTAGGAAC	180
TTATCTATTA GTCGGGCTG TTTCCTTTT GATTATTAAC CTATCGCTA ATAATCTGAA	240
ATATTTAATT TTAGATTAAT AATATATTCT GAGATTTAAT ATTTTAAATA AAATAAATAA	300
TTATTCCTTA AATAATATTA ATAACIATAC CATATATATC TAATATTTAA ATAATCATA	360
TAACATATGT TTCGTAGAAA ACCAGCTATT TGCAAATCAG ATTGACTTT CTCTACTTAC	420
CATTATTCAT CAGATAATAT TGCTACATTA ACCTGTTCAA TCGTTTTTAT ATTTTATTAT	480
ATTTTAAATA TAATAAATAT ATATTTTAAT CATTTGATAA TAGTAAGATC ATCTGCTTTC	540
GGTTTAATTA ATATTAACTA AATTTAATTT ATTTTAATTA ATTTTACATN GTTAAANATT	600
TAAATTAATT TTAAACCAN TTTTATTTIN AAATTTTGN AAATTAATAC TGGGGGNCCC	660
CTTCCAAGG GGCTNNNNIN NATTTTINA AAAAAATAA AAAGGGCNN ANAAACCTTT	720
TAAANTTCC CCNGGGCCCC NNAANANINA AANATTINAC CCNAAAGGTC CCN	773

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1292UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

GATCCAGTTA CTTAGTAGAA TGATAAAATT AATAAATATT ATTTATTAAT ATTTGGTTAA	60
CAATAAAATT CAATAATTTA TTAAATAAT GATTAAATAA TCTCAATATA AAATTATTAA	120
TATAATGAGA TATATATTTT TAAAAAGAAT ATATAATTAA ATAATCCCAA CCAAATTTG	180
TGCCAGCAGC TGCGGTAAGA CAAAGGGGGT TAGCGTTAAT CGTAATGGCT TAAAGGGTTC	240

GTAGAATGAT TATTTAAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA 300
 GTAAAGATGA AATAATAATT ATATGAATAA GACTTATAAA GTGAAAATTT AAATTATATA 360
 5 TTAATTGACA TTGAGGAACG AAGGCTAAAG TAGCAAATCG GATTGATAC CCGAGTAGTT 420
 TTAGCAGTAA ACAATGAATA CCTATTTATT TTTTATTAAT TAAAGAATAA ATTAAATGAA 480
 AATTAAAGTA TTCCCOCTGA TGACTIONT TGCAATAATA AAAATCAAAA CAATAGACGG 540
 10 TTCCGACTTA AGCAGTGGAA CATGTTTTTT AATTGATAA CCNCCANAA ACCTTACCAN 600
 TTTTNGAATA TTTAATTATA ATAATTINIA ATTATTACGG NGTGCATATT NTCTTCCCTC 660
 CGGCCGCNA GTTTTTINAAT TATCNINAAC GAACAAACNC CCATTTTTTT TTINANAAAA 720
 15 ATTATTTATT TTTTGAATAT TNAAAAAAA TAAANATCCT TTNTCCTTTT TAATGGNGA 780
 GTNTTTTTTT TTNTCN 798

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1293RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

GATCACCGAG CAGCTGGTTC GCTCGGCAT AAGCGGCTT GGTCTCTGCC CACTGTTCTC 60
 CAAGACCAAG CTGCTGTGCC TGGAACAACA GGTTTGTGAG CTGACCACCA GGAATTTTAT 120
 35 GTTGTACAC CTCTGGGTGG GGGCCCTTGA GTTCGCTTC GAAGCATGAG TACAACAGTC 180
 TCATCTCCGC CCAGTATGCG TCTAGTTTGA TCGCATGATC GGGGTCTACA CCGTCCGGA 240
 TATCGCCACC CAATGAGGCC TGCAAGGCG TAATGGAGGG CTGGGACGTT AAGCCAGACA 300
 40 TCGAGTTGGT GGCGACGTCC ACAACATCGG CGCCAGAGAT GGCGATTGG ACCATTGATG 360
 CGACACCTGT GCCTGCAGAA TCATGTGTAT GCACATGAAT TGGGAGGTCT GGATACTTTG 420
 CCCTGATCGA GCCAATCAGT AGCTTTGCTG CACCGGCTT CATGGTGGCG GCCATATCTT 480
 45 TAATACCCAA GATATGTGTG CCCCATGGCA ACAATCTTTT CAGTCAATCC AGTAGTAATC 540
 AAGGTTGTAC TTCTTGCTG CTGTAGCATA TCACCTGAGT TACAGATAGT GCTCAACCAC 600
 CCTCCGCTT TCTTCACGGG TNAAACCCA CTTCAGTGT CTAGTCTICA CCNTCNAN 660
 50 CTCTGAAATN TCANNCATCC CTTGCTGTT TGACAAATGT CATCCNTTT CCGCNAAAGA 720
 ATTAACACCC GTGGCCCCAA CNOCTGAAN GATTTTGCCC NG 762

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1293UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

GATCTTACAT CTGACAACAA TACGCTGGCG GCAGATGAGC TGCATTGATG GAAATTTTAA 60
 CACAGCTCGG GCAACCAGCT ACACGGGATA TATAAACTCA ATGCACGCG CTCCTTACTG 120
 ACACAGTCCA TCAGCATCAG CACCACCCCC AAAAATGAAG ACTACACACA TCCTATCCCT 180
 AGCAACACTT GCGCGCTGCG CACCTGTTC A GCGCACCT GTTCAGCCCA CGGACCTCGC 240
 CGCAGCGGCA AACGTCCCCG AGAAAGCTGT TCTCGGCTTC TTCCAAGTGT ACAATGTGGG 300
 CGATGTGGAG CTGCTCCAG TGGACGACGG CGCACACTCC GGGATCCTTT TCGTGAACCG 360
 CACACTAGCG GACGTGGACT ACTCCTCCGA GCATGTGGTT CAAAAATGGT TCCGTCTGTC 420
 TCTCCACCAT GGGCAAAGTA TGTAAGGCCG GACCAGAGAC AGTTTGGGTT GAGATATGTA 480
 AGTTTACTTG GTGTCTTACA CCATGCATTA TGACACGGGC TTACGTACCT GCTTCTATAA 540
 GCTAGTTTAA ATGTTTTCTA TGGTATTTAT ATGGTTTTACC CGCGCGATA GTTCGCAGAG 600
 GCTGCTGINT TAAGGCCNAA CTTTATTCCT AANANGGTGG ATTACCCGGT NGAAANAATG 660
 AATCTGAATT GCGGAAATTC CGCTGGNCT ATTANCTCC CNCCCGTCC NAATAAATGG 720
 AANATGGTGG GGTTTAATAC AAAANGNCC GVTGCGGCA ATGNACTGGA TTAATTTCAA 780
 AAACCTCCAA NTACCCCCAA NTGGN 805

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1294RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

GATCCGAAT GTGCTCAAG CTCGCTGCT TTCGGCTGGC CTCGCTGTC TCTGTGGAAT 60
 CGTTTCTGGT GGTCTCCTTC TCCATGTTG ACCTTGGGT CAGCGTCTTC AGCTGGTACA 120
 CCTCGAGAAG CTTGAGTTA TCGAATGCAA ATGGGTTTAG CATCTCGACC ATATTCGCTG 180

CGCCACCTGC CTGCCCCCTTT GGCCCTACAT CGGGAGTCCA ACTTCAAAGT AATGCTATAG 240
 AAAACGCCAT TGGCCTGGCC GTCTTATCAC GTGACTGTTC ATTGAGCTCG ACAGCTACTC 300
 5 GACTAGCACT GCTGCTGCTT TAACTGGGCT ATACACTTTA TATCGTTACA TTACTTTCTC 360
 CGTGGTCCGC GGATGGGTGG TGGTGGCTTG TGTGCAGACT CACTCTTGAA CAGAGGAGCG 420
 TTCTTAAACA TGCTGTGTAC GACAAAGAAC CTTACGTGG AGCTCGGCA CGAATACATG 480
 10 GTCCATATGT GTCACCTGGC CGTTCGGTGC CGTGGCTGTC ACGTCTCTTA GCTGGCAGTC 540
 ATGTGTGCTT CGCTGCCAC CAACTTGCCC CGATAGTTTC GCGGGTGGTT ACTCCAGCAN 600
 ACCGTGTGTC TINGGCTTC TTCACACTTA CAGGAATCG GAANTGCCAG ATCNTACTTT 660
 15 TTGGTTTGGC CGTTTCCTTT CCGTACANAA ANTGGTTTAT ATTTTGGCGG AAAAGNITTA 720
 ATTTTACATT TTCNAAACAA CATANGTTGC NTTTTTACNN AACC 764

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1294UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GATCTGGAAC TCCAAGTTC TGATGTCTTG CTTACGCTTC TCTGGCTGCT CATGAATCGA 60
 CTGCTGCTTC CACCGAATGA ACGACCGCTT GTCCACATTA GGATGTACCT CGATGTCCGA 120
 35 GTCATCCGAG ATTCTATCTT TGTCCACTT TGAGTAATCG ATTGCCATTG CACTACCTTG 180
 TTTGTTCTG GCTTCACTAC TGTGTCTCTT AGATCTTCTG GATCCACCAA TAACTGATAT 240
 CAAAGATTCA TATATGCAAA CGTCCAATA AATAATGTTA CACATAAGGA AGGACCAAGG 300
 CAACGCTGC CCAGTCTAG CAACTTCTGT GTGTACTCT CAACGATAGA AGTCTGGTCT 360
 CGAGATGTTG AGACGTAAT CGGCCACAGC GCTGCTGAGG TGGTGTACGG TCAAGGTGAC 420
 CTGTGTGCA TTGGTCTTTT CGTTTGTGTG GTGCTGCTGC TGGCTGATCT GCTGTGTGCC 480
 45 GGGCTGCTGC TGACCGAGCA TCAGTTGTG GGGCGGGGC TGGCGTTGT TGGAGTTATG 540
 GACGCGAATG AGGAGCGAT ACGGAATACT CGTAGGCGTT CGGCCGNAT GTCGCTAAGC 600
 AACTCTGTTT GCCAACGCGA AGAAGGCTT GACCGANAT CNGTGCACNC CGAACCGTCC 660
 50 TGTTCANITA TTATCCATCA CACNTCGGA AAAAGGGGG GGTTCCTCCT AAGTCNAAAA 720
 CNCTTGANGT CTGTCTTGC GGTGAATCG ATTTCCAAAA CTCTTTTCT NCGGTTTGGC 780
 CCNGCGGCC CCNGGGGGA 800
 55

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1295RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GATCTTTTCT TCAAATTTGGG ACGAGGTGCT TAAGTCATCC TGATCTGCA CAATCACGTC 60
 CATATTGGCG GAGATCAGTG CCGTTTGGC ACCAGAATCG CTGCCCGGCC AGGTGACTAG 120
 CAATCCGAGC TCGTTGACAG TTTCACCTT TAGCTTACAC CAAACCAGAG GAAAGTCCCG 180
 CGACAGCTGC TCGTGCAACC GTTGAAGTG CTTGTATGTC TCCGTGTGG ACTTCACCGC 240
 TGTGCAGCAG TCCGCTGCAT CCACCAACCA TGCCGAGGGG ATCTGCACTG CACGCTGTAG 300
 CTTCTGACA GTGAGATTGC TGAGCGTCGA GTTGTGCAGA ATTTGCTGGA GGTGGTCTCC 360
 AAAGCCCCCC TGAGGTTTGG ACACGTCCCA GCACGATGGC AGTGACGCC CAGTCACTC 420
 CGAAGAAACA ACAGCACTCC GCGCTGTCTG AGCAGAAAAG CAGGCCAGCA ACGCCAGGCG 480
 CGTTGCAAAG GATATCGGTT GCCCCAAAG CCAAGCTGCA AACATCATTC TGGTGGTCAG 540
 CGACTGCTTT TCCACGAGA TCCGTGGGGA CCATGCGCCA GATGGGGGCC TTAATATAAG 600
 CCCCTCTCG CCAGCATGAC TTCTGCCAAC TCCGAACAT TCTAAATGGC CAGCTGCTGC 660
 TTTGATGGTA CCTNCCGCG CTNGCGCAA AATTNATATA CCATAATCCC CNTCCTAAAT 720
 ATNCTTACAT ACCACGCCCC AAAGCGCTCC CGNAGCNEN CCGAGCCCC CACTTTCCNC 780
 NNAAGNANCC GNTGNG 796

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1295UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GATCAACTTC AGTTCTGCGC GTTGTGCGA TGGAGGCCCG CCAACGGCAG ATAGCTTCTC 60

AACTGTGGCG GTACCCCTGCA CGGGCTCCAC GACCGCTGTG CAGTGGAAAC GCTCGTAATT 120
 GTTCTGTGGTG TAGTGTCTGA AGTACTCCAA AGAACCACAG AATGCGAGGC CTGCGAGGAT 180
 5 ATAGAAAACC AGCGTCCCGT ACCTACCGAT TGCCATGGTT GAAGCAAGGA TTCCACTGOC 240
 GTAAGTACTC AATTATTGAG TGCTAGCAAG CTGATGTTGA TTGTGTGATA TCAACGGTAA 300
 TCGGTGCTTA AGGAACCTTT TCAAGAAACG CAAAGAAAT GCGTGGTAG GTGCGAGCAGG 360
 10 TGACAACCTC ATATTACTCA TAACAGTTAT CTATCTAAGA AGCGGCACTA TCGATATACT 420
 ATCAGCTTCG TATACACATA TATATCGGAG GTTTATAATC GCAAGTTAGC TATAATTGCC 480
 ATCGAGGTGT AATACATCGA AGATTGTCTA CGAACTACT CTGTACCAA CACATCAGCG 540
 15 TATGAACAAT AACAGCAATA TTATGACAGG CAATTGCATA AAGTATTCA AAGAGGGTTA 600
 AACAGTTAAA TTCGTAAAG GTTCAGNGAN TATTCOCTGA CACCCATAC CGAATCGCCC 660
 TGCACCAATT GTTCACATGT TCANAGATTC TCGGGACTT CATATGNACC ATGTTGCGGC 720
 20 CCGNAACTCN CATTATGTNA ATGCTTGINT TCTGACTCC CCGCTTGTG CCAAATGCCA 780
 TCCAGGGTG ANAGGTGCTC GTGATCTC 808

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 779 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1296RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GATCATTGT GCGTTTGAG GTACGCCAC GGACGTGGAC ATGTACGTGA TGAGCTTCGA 60
 40 CGGGCAGCTC TTCAATTGTG CGGCACGCA GAAGCTTGAG TTCCCGAGCT CTCCGCGGGA 120
 GAGTTGGGCG TACCTTGCGT ATTACAGGG ATACAAATTC GAGCGCATGG CGCTCCTGGA 180
 CCGTCCGGTG GCCGAACTC CGCGCGAGGT TCTGGAGAGC CGCGGCAAC AGGTGCTCCG 240
 45 CAACGGTCCG CAATACAGGA CTGTGATGAG AACCGGCGTC GGGGAGCACA AGCTGGTGCT 300
 CGGAGCTGAG ATCGACGGCA TCATTGACTT CCGGAGGCT ACGGGGACA AACTGAAGCA 360
 CTACGTGGAG CTGAAGGTGT GTCAGAAGAA CCGGAATTC TCAGAGAAAC TTTTCTCTTC 420
 50 TTGGCTGCAA TGCTTTCTGG TGGGCATAAA CAGGTTTATT ATTGGATTCC GGGATGAGAA 480
 ATTCTCTCTG AAGAGCGTCG AGGAGTTTCA TACGTGAGAG ATCCACACC TGTTTAAAGG 540
 GCACGGAATA TTCCATGTAT GTTGTGGACG CCATAGATTG TATGGTGCTC CTTACAAATT 600
 55 GCTATNTGAC TCCCCCGGGC CCTGAAAANA NTTCAACTGT TACAGTCTCC TGCNNCATGG 660

TGCTTACTTT TGCCCCACTG CCCAACAAAA ACCCOCAATG GGANAAATTN TCCCTNGTTG 720
 GTCCCAATT GGNNGNCCC CCANATANAA AATTCGNAT TATTCCTTG TTCTCTAN 779

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 815 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1296UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GATCGTACGG TTGCTGCTG CGGTTTACCG ATATGGATCG GTTGTTTGCA GTTGGCGAGA 60
 GCACGGTGGT CGGIGTCTCT GCGACGTCT CGGACATGCA ATACCTACAG CGCCTGCTCC 120
 AGGACATGGA GATGAGAAC AACTACGACA ACAGCCACGC AGACGGCGCG GAAGCGCTCA 180
 AGCGGAGCTA TATTTTGTAG TACCTTGCTT CGCTCATGTA CCAGCGCCGC TCAAAGCTGA 240
 ACCCGCTCTG GAACGCCATC ATCGTCGCG GGTGCGAGGA CGGCCAGGCG TTCTTGCGTT 300
 ATGTGGACCT CAAGGGCGTC AAGTACTCCG CCCCAAGCTT GGCTACTGGC TTGCGCGCCC 360
 ATATGGCCAT TCCTCTCATG CGTAAAGTGG CAGATGCCGA AAAAGACTGG CCGCGGTGGA 420
 CCTCTCAATT GCGGAGGGA CTATCTGGA GTCCATGAAG GTGTTATTCT ACCGCGATGC 480
 GCGTAGTTCC CGTGCTTCT CGCTTGCCAT CATGACAAT GATGCGGTG TTCAGCATGG 540
 AGCAACTGGA AGTGGAAGAC ATGACCTGGG GTTTCGCCCA AGGATATTCC GGGCTATGGC 600
 NCCCAAATNT TTTGAATTAC CNGGGCGCA ACGCGCACC CTGTTTACTA TCTTGTTGCG 660
 GGNVTGNC CCACCGCTNG GNEATCCCAT ACNTTCAAAA NGCNTAATCA TCTGCGCTGA 720
 ACCCNCCTGT TTTINGINGAN ACCTTCNCCC CTTTTCNGA TTTCGCCGAT TGNCAAAAAC 780
 CCTTTGAAAA AACATTNCCC NITGGNAAAT CGATG 815

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 766 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1297RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

EP 0 866 129 A2

GATCTOCTCG ACGCTGGTGA CCTTGCOCGC CTTCACAAGA CGGCCCAACT TGGTCACTGG 60
 CACCCAGCCC TTCTOCTCGA CCTCTCTTCT .GOCCTTGGG CCGTGAAGGC CCTTGTITCT 120
 5 GGGCCCGAAG CCGCCTCTTC TTTGTTCTGG AGCTGACATC TTGCTATCGT CGGAATGGAA 180
 CACCGAAAGC TGGGGGAGTA ACTTTGATC GAGCTGCTG ATGTAGTTAC GATACAGCTC 240
 CGGCCGGGCG CTTCGGTGCT GAAAACTGC CCAOGGTCTG CGTACCCAGA AAGGAGGTCT 300
 10 GGGTGCTACC GCTGTTTCCG GCTCAAGAC GTGTCTGGT TTCACACTGA AACCCACACA 360
 TCAGACAAAC GCAGTCCCGG ACGGCTOGAA AGCAAAACC GGTGAAGGA GCAACGGGA 420
 AGCTGGGGG TCGGTCCGA ATCTGTCAA AACAGGGGT CACAAAGGA TTGGCGCTGG 480
 15 CGCCAGGACT GCTACGGGG CATTTGGCCCC GGGGCAGCC CCGAGCAATG GAGCAACCCC 540
 CTTCGGGAGG TACGGCTCAC ACTGCGGTAT AAAGCGGGC AGAGCGGTGG AAGCAGACAG 600
 TGACACACAG GAGAGGACAG ATGTGGACN NCAAAATGAC AATCTATCA ANAGNGCGT 660
 20 CGGGGCCAAA CTATCAANAG NITOGAAGTT CCAAACTNGC CAGATCAAAA GGGCCCAAAG 720
 GGAAAAACT TCCCCCCCAC GACCCTTTGN CATTTTTAAC CGCNG 766

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 795 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1297UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GATCCAAAA CAATGAAGT TTTACAATGT GGAAGCOGTG ACACAAGTGA ATGGCGCTCA 60
 40 GGACCGCTAG GAAGGAAGTC TATGTGCAAT GCATGCGGTA TCTGGTACAT GAAATTAAAG 120
 CAGCGGTTTG GGGAGGAGGA TGCTGCGGTG ATTATGGAAT ACCGGAGATT AACTAATAGG 180
 CACGATGATC GCAGGGTGCC CAAGAAATTT GAGGTCCAT TGCTGAGGT CGAAAAAGTG 240
 45 AAGAGAGCCA TAAGAGCTCG TGTGTGGAG TATTTGAATG ATGTTGAAAT CCGGTTAAA 300
 ACGAGGAGGC GGGCGTTATT ACATAAAGGC AAGCGGGCA GTGCGTTAAA AACAGAGATG 360
 AAAACCCCTG CCGCATGAAG CACTGGAAGG ATGAAACCAG TTTGTCAGCC GGAAGGACAA 420
 TACCGGGGG TAGGAAGTA GAGACTATGC TGTGGCATGT AAGGAACGTA CTTTATTTA 480
 50 TCTAACATAA CTAGGGTTCT TTTGACCTGN TACCTTTGTA TTATCCTTTG AANAAGTAA 540
 CCCCCNCTT TTAAAAANTT TTCNNNTGN AAATAAATCC CCTTTAAGA ACCCCCCCN 600
 55 NAANCAAAAC CTIVINCCCT TNGCCAAAC CCACCCAGAA ATTTTCCNC CNITNCOGAN 660

ACANNGTITN CGAGATTCCC CCMTTTNGGC CNAAAAAANC TCCCCCGAN TMTVINOAN 720
 5 AGNGCCCTTT TNCNCTCCCC NCCNANAATC CCCAAATTAG AAGGGGINTT CNCCCNGCT 780
 CCCCAGATC CAAAA 795

(2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1298UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GATCTTCTTA CTGGACTGGC TGCTAGAAGA TAAACGATTA TGGCTACGTC AACTGCGGAA 60
 CTGTGGGCC GCGTTGGAGG AAGGCGAGGT GGCACCTTT CCAGGTGGCG CTGTGGTGGT 120
 25 GGTCCTCAAC CCGAGTCACG TGACACAAC TGGAGGAAAC ACGATGGTTT GGAATCCCG
 CCGTCTGGAC CTGGTACACC AGACACTGGC AGCTGCATGC CTCAACACCG GCTCGGCGCT 240
 AGTTACACTT GATCCTAATA CTGGCGGCGA AGACGTCATG CACATATGTG CGCTGCTTGC 300
 30 GGGGCTGCTT ACATCCCGTC CCGTCGGGAT GCTAAGCCTG CAAAGTCTAT TCATCCCCCA
 CCGTGCAGAT TCCATCGGCA AGATCTGCAC CATCGGCCC GAGTTCCCTG TTTGCTAAGG 420
 TGTTGACAA CGATTTTGTG GAGCTOGACA TTGAGGCGG CAATTGCTCC AGAACTTACT 480
 35 CCAAGAACAC TTGTGCCATC TGACCACCCC ATGGCTAACA GACCTAOCOA CCCCCCTTCN
 GAAGCAACCG CTGTGATTTT NATCTCCNAG GTCTCTCCCT ACCTATAACG CTCTTGTGAN 600
 A 601

(2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 753 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1299RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GATCTCCAC ATTGAGACGG TAGCAGCCA CATATTGGC TTGAACGCC TTAACGGCG 60

CCATTGCTCC CATAGAGCTT TCAGATTTCG TGTTAGGCTC CAACTCAACG TCATACTGGA 120
 GTTTAAATCG AGTGGGTGCT GTTGATATCC AACTTGGAGG CGTCTTTTTT GTCCTGTAT 180
 5 CGCTTGAATA GCGGCCAGG TCCCGTGGCG AAAATCCATA TATATCCATA TTGGCCACCC 240
 AGCTTGTAC ACATAGAGGC AATAGTGCCA GTAATGCC TCAGCGAAAC CATGCAGCTC 300
 CCCGCGGAGG AGGCGCCCCG CAGCGTCGGG TTCCATAGAC GCGAAGCCCG GCGAGTGGG 360
 10 CGCAAGCTCA GCACGCAGTT CCTCCCTGTC ACGGTATGTC CCCAGCCCGC GGTGCGCACA 420
 CCCAGATACT AACACAGCAC AGACGCTGTA TCAGCTGATT GTCCAACCGG CGTACTATTT 480
 CACGTTTCTG GCGAATGTGC TAGTGCAAGC GTTGGGCGAG GCGCGGCGAG TCGCCATAGC 540
 15 AGTGGCGTTC TGGATGTGGA CGGTGGGCTT GGGCAITCCG GCGCGGCTG CCATTGTGTC 600
 TCGCGCACGC GGTGTGGCAG GGTGTCTGG TGGGTGGGT GTGCTGGGC AACTACCACC 660
 TGGAGTACAT GGAGACCTAC ATTGGAGCC TCGCTGTGAC GCGAGAGGGG GAGTCTGT 720
 20 TTCNCGATG GGTCCCGGC GGTGGGGGT TCC 753

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1299UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

ACGCTTTTGG TTTTGGGCT GATGGTGGGT GGTGGTATAG ACGATGTGAT CTCGGCTGC 60
 AATTGTAAGC CTCTCTCTCC GGAGATATCC CGCAGGAGA AGTCGTCTAA ATTTAACATT 120
 ACGTTCATGT AATCACAGG CACCTTTTCA AAGACACAGA CGATCATGCC ATTCTTACGC 180
 40 TTTGCCACA TGGACGCCA AATGAATTTC TGTGTATGCG AGGATGCTGA CGATGCAGCT 240
 GAAGCAGGAG ACGACAGCGA TGTGAGGCT GGTGTATGA CGCTACTAT TTCACCTGTG 300
 AATACTTGTT CTGGCCCTC TGTAGACATA ATCTGTGTTA GGACAAAGCT CCGCTGTGCG 360
 45 GTGTGTATCA GGTCAAGTAA AGTAAGCGC TTAAATGCCA ATTGGAGAT ACGAAGATT 420
 AAGCATGCCN AATCGTTAGC CCGCTAAAC TGCCATGGGT GATGCTGGGA ACAGGTAAAT 480
 ATGGCCTGAG GTGCTGTGTA CTTACCTGAT ATAAAAGTAT GCGATATGCG GCGGCTTCG 540
 50 TACGTTCTGC TGTAGTCTAT CGGATCTGG ATAGATGTTA GTTCATGGT AAATGGTTGG 600
 AGATAATTTT CGTCTGCGA GCGCTGTATA GTAGTTCTG TGTGAATAT TCATGAAATG 660
 GTTGGGCTAA GCTTCAAGC AGCTGCTTCT TTAGTCTTG CTCATTACTG ACTTCTTTCG 720

CAGGATCTAC GCCATCOGCG TTGGTGCTGA C

751

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1300RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GATCTCTCTG CGCGGTGCAC AAATGACGCA GAAACAGGCA TTCAOOGAAT TGAAGAGGCC	60
TCAACTGCOG CGGATCGCTA CAGGCGCAGT GGGACGACAT CCTTTCTTTG GTGGGTATGA	120
GGATACCTAA ATAAGCACAT ACAAACGTT AAATATGCAT AAGGAGATAT ATGCGAAAGT	180
TAAAGTGTTC TTAGTGCCCC TCGCCACAG TTGGGTGTTT CAGCGATAAT GGGAGACCAG	240
CCCGGCAGT GATCAGATAC GGTGTAGTG GCCATAOOGG CTGCGGACG AATCTACGGG	300
GTATGGTGCC TGACGCTCG CGCGCGCGT CTTACGCTGA GTTCCCCACA GCGTTCCTC	360
GTACTGGTTG ACGTCTTGT CGTGACAGC CCTCGTTTG CGTAGOOGG CCGACTGCC	420
CCCCGCCCTC TGCGCCTCGA GATCGTAAGA CTCGTTGCTG CTGCTOGAAA AGCCCTTCCT	480
GCGCTOCTG TAGTACTGT CCTTGCGTA GTACCGOGG GCCTOOGGG TTAATAOOGG	540
CTGGTATACC ACTTGTGGG CGGAGCATAT ACTTGTGCAC GCTGCTTCTC CTGCGGCOG	600
CGCTGGGG TGCGTCTAT AGCAGCAGCA CGGCCAGCAC AAGAGTCGA GATTCGCTC	660
ACCCCCCAT AAACNCGAN TTACACCCC TATCCNATAC CCAATTGACG CTACNCATCC	720
CNCTATACC CATCNTTGA CNOGGTACCT ACTTTTCCN AANTGACCCC CACNTNC	777

(2) INFORMATION FOR SEQ ID NO:401:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 812 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1300UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GATCGAGGAG TTTCCTACTG AGGTGGGCG CTACATGACG CTGCTGCGG AGATAGACG	60
CAAGTGGTG CACACGGTGC CGGAGCTTAA CGCGCAGATA GGGGCTTCC TGGCTGGCTC	120

5 GGGCAGGCG GGAAGCCCGC AGCTGCAGAC CATCAACCGG CTCTTCCAGG ACCTGATGOC 180
 GTGCTGGAG GAGAAGATGC ACGTCTCGTC CATTGCGTTC GAGAGCTCG ACCGGCTOGT 240
 CGGCGCGCTC GAGCTCGGT ACGAGGTGCG GCTCAAGAAC CAGGAGATCC CCGACAAGCT 300
 GCGCTGGGC AACGACAACC AOCCTGCCAT GCACCTGCAC CACGAGCTTA TGAAGAAGAT 360
 CGAGTCCAAG CAGCAGAGCA AGTCGCAGCA GCGCTGCGC TCCGAGTCCC GCGCGAGGC 420
 10 GATGGCGGCC AAGAAAATGC ACGTGGACCC GCGGGGCGG CGCTGCTCT CAAAGGCCCC 480
 CGCTCCCGNT GGGCCCCGGG CGCCCTTGG CGGCAAGCG CCGGCGCAA CTTCCTCCCC 540
 CGCCCGCGC GCNAGCGCA GAAGCCAGG AACAACTACT CGCCCGGCC CCNAAACAAC 600
 15 AATTTGGGA AGGCTCTTA CTGCTACTGC AACCATTCNC CCTACGGGAA AATGTGGTT 660
 GCGAANGGA AAAATGCCNC TCNATGGTCC CTCCTCGGA TCACTCNAAA CCTTACCGAN 720
 GGGAAATGTT CTGCAANAAT GCAAAAAAC OCTACATACA GNCGGTTAC TANNCCCCC 780
 20 CCNCCCTNCN TGCTTNCNA TGGGTTCNC NT 812

(2) INFORMATION FOR SEQ ID NO:402:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 786 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1301RP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GATCCGCGAG ATTATGCTG GACCGCCAC AGGCAATTAC TATAACAACA TCCTGGGGTG 60
 TTAAAGGACC TAACTACGC TCAAGTATTT CAGGATGATA TCCTAGATGA AGAGCTGGC 120
 40 CACAGCTGG TCGGTTACA ATATGCTCT CTTCGCAA AATTTAAACAT GTCTGTACTA 180
 CAGCGAGCTG GTCAAGCACA ACAGATTTTG TCCTGTATTT TTGGCGTAA CTCAGAGTAA 240
 GATCCGTCAC GAAAGATGTG CATAAAGAAG TAGCAACGCT TTTAGGATTC ATCGAAACGT 300
 45 TCCTGCCAG CAGCAAAGAT CTGTGCAAAA CCTCGCACC CTCTGTTTC ACTGCTACAA 360
 CAGGATAGA GTCTGOCAAA CCATGTTTCT CCAGCCATA TACAATCCCA TTATATAACC 420
 CCGCGCCACC TACGCTGAG ACGATACCTT TCACGCTCTC CAATTGCACG CCTTGGAGAT 480
 50 GCAGTCTTC TACTACTTCA TCTACCATG TTGCGTCCC TTCCAGATG AGTGGTTGTC 540
 GAATGGATGT GCATATATCG GACCGACTTT TTCTAATCA CATTCOCAT CAACTCCGA 600
 CCGTAAGTIA TCATGCTCT CTTCATAC ACTTCCATT GANATCAT CNGCCCCGT 660
 55 TGANCGGTC CGTCTACCT CCNCGCCAA TTTTTCNEN CCTACNCGG CAGGINTCCT 720

NTTNNCGTGA CCGTGGTGC TGCACCCNVIG CNTGNCNCGA CTCCCNAAAC NTTTGGNTGC 780
GNGAAG 786

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1301UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GATCATCTGC GTGCGATACT GGCAAAAAAT GAGAGACAGC ATGATGAAAA TATAGTTAAT 60
AAGATATTGC ATGATATAAG CACAGGCGGG TTTCGTGAA GAGGAAAGGG TGCATTGAT 120
CTGAAATGA GTGAAATGA AGACCAAGAG TTACAACAGT TTAGACAGAA AAGACGAGAA 180
CTTTTGAAAC AAAAGATATT GGAAATGGT GATACTAGCA AGCTCGTATC TAACCCCAAG 240
TCATACGCCT TTTTTCAGAC GATGGTGGAC GATGTTACTG AAGCATCATT TGGAAATACA 300
TTTGATGCCA ATATAGATGA AAAACAGAT CCATCTGCTG CAGGTGGGAA AATTGTCATA 360
TCAGAACAAT TTGTAAAGGA AACCTGTCA TTCTTGTCGA GCAAGAGTGG CGACTCAGAA 420
ATCCCTGCAG AAATAAATC TATTTTCATC AGCACAGTTG AACGTGAAGA AATTCAAGAC 480
TTCATACATT GAAGCAAAAT AGTAACATTA ACATTTGAAA GGAGTCTAGA CTTCCTGCTC 540
AGATGGCTGA CTCAGCAGTG AGATAGAGGT GATTACNGCT TTCTTTANAT ANATTCCNEN 600
GCGCNAAAT TTTTATATGA ACTACTTCAC AANANITTTA AAGTTGGGCC CAGGGGGGCN 660
ATCTTAAGGG AATAAANATN GGTCCAAGC CCAATACTTT TIVINGGAAAN NGTINGNGGTC 720
CCCCNAAAG GATTTAATTT CNACCAACTT NTCNCCANN ACCCCCCCCC TTTTITTCNG 780
NG 782

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1302RP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

	GATCGAAGAG CTCTCGCTG ACTTCGAACG GCACAAGGTA CCCAAGCTCC TGTAAAGAGT	60
5	TATGAAACTC CGTAGCGGAA AGCGTGAACG AACCGTTAAT ATCATTGTCC ACATATATCA	120
	TGCGCCACTT CTTCACGGC TTGTATAACG AAGTAACTC AGACAAGTTT ACGGTACCAA	180
	AGCGCGTGGC GCCAAACAGG CTAATTAGCG CGTCCACCGA ACTCATGCAG AACTGCGAAT	240
10	TGTCATCATT CTGTAGCAGA TGCTGTAGCT CCTCTGCTGT GAGACGCTCC ATCTTCGGGA	300
	CGTCGTGATT CATGAATAAT TTCTTTGCTG TTATAGCATC GGGGTCTTCA TTAGGAACGG	360
	TGGCGGGCTT GGCTTGGGTA TGGTTCGGGT GAGGCTGCTG AGCTGGCTGC GGCTTGCAG	420
15	GCAAATTATA GCTCTGTGGC CTCGGTGGTA TTGGCTTCCC GTGGCCCGGC AGGCCAGGGC	480
	GGCTGTGGA ACGCGAGGAG GATTTCCTG AAGCTGCCA ACGCCATGCG CAGGCAACTA	540
	CTATGTGTAC AAAAATTGCC GTGNTCTGCG AAAACCTTTG GTCTGTACAG AACCCANCCC	600
20	ATGGGCCATG GAACGGNNTG GNTTTTGGC CCAAATTAAAN CCTGGANAA NITGGNAATT	660
	TTTGGCCATN TTTTCCNATT AAAAANGNG GGTINNAAGT GCNAGGGNGC CCATNNGGG	720
	GGGNAANTC CGCGCCTTTT TTTTTTNCAT AANGNCCNC NTTGANNCC GCCCCNNNC	780
25	CCAC	785

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1302UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

	GATCAACAAC ATACTTCTAA AGACATCAAT ATACGCGCG ATGTCTCCGG ATGAAAACA	60
	TGAATTGGTT GAGAGGTTG AGTCCATGG ATACCAGGTT GGCTTCTGCG GCGATGGTGC	120
45	GAATGACTGT GGTGCCCTTA AAGCGGCGA CATTGGTATA TCTCTATCCG AAGCGGAGGC	180
	ATCTGTGCT GCGCCATTTA CATCCCGCTT GTTTGAAATC AGCTGTGTTT TGGACGTAAT	240
	GAAAGAAGGC CGTGCGCGT TGGTACGTC CTTCGCCGT TTCCAATACA TGAGCTTATA	300
50	TTCTGCCACA CAGTTTGTTA CAATATTGAT CTGTACAGC CGTGGATCTA ACTTAGGGGA	360
	CTTCCAGTTT TTGTACATCG ACCTCTTCTT GATCGTGCCG CTAGCGGTGT TCATGTCTG	420
	GTGGAAGCCC TATGAAGTAT TGGCCAAAA GCGGCCAAG CCAATTTGGT TTCTCGAAG	480
55	ATATTGATTC CTTTGCTCGT GCACATGCTG ATTTGTTGCT GTTTCAGCTT GTCCCGTGGC	540

TCGCAGTCCA GCATATGAAG TGGTACCGGC AGCCAGTGGT CGCGACGACG AACATGTTGC 600
 TTCCCANAGN NACNCAACCC TTCTCTNGTC TCCACTTCCA TAAACCCCTGG TCCCAATCMT 660
 5 GCTTCCGGTN GTCCNCCCN NCNCNAAAC NAANITCGAA AATTTTGGTT TATGGCANIT 720
 CCCCCTTCCC TGNCCCTCCC GGTGGANNAT TTCCCCCCCC CGAAACAACCT TGGCNCCTTT 780
 10 CACTCCCGAA GTTCTCCAT NTC 803

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1303RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

GATCAGGTGG CCTTTATGGC CATACTGTGT GGACTCATAG TATATCTGGG CGACTGCACT 60
 ATTACTGGAC TGCTTGICAA GATCTTGGGC ACCATCAGC CCGACTATAC TACATGTCTC 120
 GTTGGGCTTT GCGTGGCTAA CCGGCAGAAA AGATACTTTT ATACTTTATA ATACCAGTGA 180
 30 GCGGGCCATA CCACGTAATC CATCTTTGTT GOCAAATAAT TACAATATTC CTTTTAGCTA 240
 CTGGAATTGG GCTTATCCTT ACAGTGTGAC ATCAATTTTC TATCGTAATT CGCTATCTCC 300
 GCTCGCAATC ACTGCACTGC AAACCATATAT CGTCTGATA GATAAAGATT ATAGGGTAGC 360
 35 GATCAATAGT ACCGGTAAAG GCGTGACAA TATCTGTCTG GCGGTGTTTA GATGGCCGAG 420
 ACGCTAGAAT GTGGGAGCAT GCTGGTTTAG CGATATGGGA AGCCTTCACT AGAACCCCTGC 480
 CACTAGTAGA GCACAGAACG TTGAGACTTA CAGCTGTTGG AAGTATAAGT TGTAAATTTT 540
 40 CAAGGGTGGC AAGTAATATC AATTGATTCT AAATGACTTA CCCTACGTT GAACTGCTTA 600
 CTTTAANITG GGTGGGGCCC ATCAAGCCCT GACACTCTTG ACTTTCCCCC ATGAAAAAAC 660
 TCCCGGGTGG GTTCNANCCC CATTNCCCAA ATACANTCCA TANGTCTGG CCCTTAACCA 720
 45 CTTGNTCCGG AGGATTTTTT TNCANAAG ANNNNACTTT TNAATTTTGC CAC 773

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1303UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

5 GATCTAAGTC CTCTCCCCCA AGCGGTGACG CAAGTGGACT GTCTGTGCT CCGTTAATAA 60
 AGTTATCGAG ATGGTCCACA AGCTCATCCA CCTCGGATAT ATGTGGCTG TGAGTAGGCG 120
 CAGAGTCACG TGGGTGTGCG AACGTGACAT CAGACTTTG GGAAGGGCTT CCTAGCTCAG 180
 10 GGTCCAAATC AATGGACACC TTTTCCAGCT CTGCCAGCGA GCGCAAGAAC TTTTGTCTA 240
 ATATATAGTC GTTAGTTTGG ACCACGCAAG AAACCGGTG TTCGTGGCTT CCTGACGCTC 300
 TCCCGTGTAC CTCGGCTGCG CTGATGACTT TGCCAGTGA TGGGTGAGCG CTCTTGAGA 360
 15 TGACTTGATC GGGGACTGC CACTTTGCCA ATCAGGATC GTCTACAGTT GTAAACGGGC 420
 GCACCTTCTT TCTGTAGGT GCTGGGCTG CTGGTACTGG ACTCCTCTG GACTGTCTGG 480
 GCCTTACTGG ACCTGTCTGT GCTGCTGTTA CTGGAACCGA AAAAGAAAAA TGACTTCCC 540
 20 TCTTTTCATA TGACATTCOC NGTGTGANA CNTACTATTG GCGCCNAGAA AATAANTTAG 600
 GCGAAATAC ACTCNCATG TTTGCTATA TTTCCNTAC CATATACAGC CTGCTGATTC 660
 CCAGTTTAN AANTTTAAGT GCGTACCTT ATATGTGAA NCCGTTATA TGAAGAATAA 720
 25 CCCCCAANT TTGCAANGAA CCGGAGGC ATTGCTCT TCANCANNAT TAAGNACATT 780
 TTGTCTTTC AAGNACTTTA TAAGNC 807

(2) INFORMATION FOR SEQ ID NO:408:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 778 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: DNA (genomic)
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1304RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

40 GATCAATGAG CGTGGCTACT ACTGATGCTT ACTGCAGTGC TGTGTCAATA TTACATATCG 60
 GTGGATAGCT AGATAAAAAT GCTATACATA TATCTGTGCG CATTGTGCGA ATCTATATCT 120
 45 ATTTGTGCGG ACGTTGCGG CAGTAGGAG GTTGTGTGCC GCGGGTGGG CAAATTCCGC 180
 TGAGATCAAG CCATTGCTG TGCTCTTGCC CTCCTTAGA TGGTAGGTGC CACTGTGAAT 240
 50 AAAACCGACG AGATCTTGTA CCGCGGCAG AGGCTGATCG GGTTCATGG TCCGTTTGCC 300
 CGCAGCATTG TATTTCCTGG AAGGACTGC CTGCCAATGG GCGAGATGCT TGACAGGCAC 360
 TGCATACAAG CCGGCATTGT CCTGAAATG GCGCGTTG AGGGCTGTAC AGACAACGGC 420
 55 GATCAGGGA AGTTGGGTGG TCACAACAGC CAGTTGGACG GGCAAGCCTG TGTCATAGG 480

AGGTTTGTGGA AAAAGAGACA ACTGGCTTAT TGTNAAGGTC CCGGGGANCT NCNAAAANAA 540
 TCTTGGTGGC AATACCAACN CCTAAGGATT TCANCGNGTT CCCCAACTTN ATTININITTIN 600
 5 TNGCNCOCGT TTCAAATTCA TATNGGTGGG TTGCGGGCGN GAATNTTCTT TTCNATTTCA 660
 AACCAACGNG GGGGNGCCNT TTGAGATTTG GANACNCCC TCNAAANANA NTGTCCOCT 720
 TTCNCCNNAA AACAAAATTN NGGAGGAAGA GGTTTTANCC CNNTATATNC CCCCNCN 778

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1305RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

25 GATCAATGTA TCCATTATAC CCAGCTTTG CAGGACATA ATATATTGAC TTGATTTTAA 60
 AGCGGTAGAA CTTTACGGGG CTAGGGCCGC TAGGTATCCA AGGTTTAGCA TCAGGATGCA 120
 CGTCTGCAA GCACTTCTGC AAGGCTGGAA TGGGCTGGAG TACTTCGAGC TCACCCGCGA 180
 30 AGTTTGCAAG AGGTGCTTTC ATGGGGTCTT CAATGATAT AGACGCAACT GAGAAAGACA 240
 CGTTGTTATT GTTTTATAGG TTTACTTGTT GTAGTGTGTT GTGACCATC AAAAAAATGG 300
 GCTGGCCGTC ATGCTCTACT CCTCACATC TGTCGGGAGA AATATAGTAC ATTCTAATAC 360
 35 CATATGGAGT ACCGTTTGA TTGATTGTG TCAACTGGAA AGAACTTTG TCTTTAATTA 420
 ATTTCTGAG TTGCACTGCT GCTTGTGTT CCTCTGCGA CGCTTGCGG AAAGCCGAAG 480
 TAACTAGTGC CAAAAACAT GTAACATG AAAAAATCGA CTTCAATTGTT GCTATTGAGT 540
 40 GCCAATAGGC GAGACTCATC CATATGATAT GAAAGCGTTT ATANATCNIT GTTNVGGCTT 600
 GAAAGAATTA TTATACTTTT CNGGCGGTT ACATTATCTT CCAACCAAAT TGTTCCTTT 660
 TNGANAGGNA ATCCCCAAA TTTTINAAAT TAATNGTCN NOGCANCGT TTTTCCCGG 720
 45 GNGGGGAAA NAAAGCNGN NACCCGCCAA ANCCGAATAA AGGATTTCCA TNAAAACCCA 780
 ATTNTCCNAA AC 792

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1305UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

	GATCCCCAAG AAGAACATCA AGATCCACGG GTTCTAGGCG CTATGTACTT TGTGTAACTC	60
10	AATACATATC CTCTCTCTCC TCCACCACCA CCACCTCTC CTCCAGTCC CTCTGGCGCT	120
	CGCATAGTA CCTCACACAG TACGGGAACA GCTCTCGCT GAACAGCTG GCCAGCTCGT	180
	CGCGTTGGC AAACCTCTCG CCCGGCGCT CGCTGTCCA CGGAACAC GCAAAGAAG	240
15	TCCCGTCTGA GCGCTTGGC CACTCCATCT CCACCGCGC GCTCCGACT TCCCGTCT	300
	CCCCACCGT GAACTGCTTC CTCAGCTCT GCGCCCGAG CTGCGCTCC AACTCCCGA	360
	ACTCCACCGT GATCGCAAAG TCCACGCCC CGCGCCCGC CCACTCCAC TCCACCGCC	420
20	GGATCGCTC CACGTACGC CAGTCCGCG CGCGACGTA GTTCGCGAAA ATCCCGTGC	480
	TGCGTCAGCA CGAATCCCC AGAACCCGC GATCCCTCG ATCGCTTGC TCGCGCGCG	540
	GTATACCGC CCCAGCGCG CTGCGCTCC AACTCCAGC CCGGTCTC CCGTCCCGC	600
25	NCCGCTNGA NTCGGGAGN GCTCCACNG CGGCGCTGCN CCGTATGTC CCGTCCCGC	660
	CATTTAGNG GGGNNGGCG TTNNTGTTT NNGAAGNA GNGTCCGNT TCCNGGCGG	720
	GVNNGTITT TGGGNGGAG NACGNGTTT TTGGANCC CANTCNGGA NTCCTGNGC	780
30	GAANGNGT TNCNCCNN TTGAGCCCC CT	812

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 778 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1306RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

45	GATCTGATAT TGGGTAATTG CAACCTTTC ACCGCTTTGA AAAGTACTTT AGGAAGTGGT	60
	ATTTGCAATA TAGTTCATCA TTGTAGTGA AGCAGAGGA TACCTTACAC TTGGTACCGC	120
	AAACCGTGA GCAGAAGTGT TCCTGTCAT ATAGCTTACC AAATGTATTG TAATACCGC	180
50	CGCTCAGTGG CTTATTGCAC ACATAACACA ATAGCTTGT CCGGTGAAA TAATCTGCT	240
	GCGATAGCAG TACCACTTCA GACGTATCC GGAGCTATA AGGAAGAAC TTGGGGCGAC	300
55	ACAAAGCTCC ACAATCGTGA CAAACCAGAC AGTTTTCATG GTAGTAATCA CCAAGCGCT	360

TCAGGGAGTT CTGGGTGATA ACCCCCTTGC ATTGTTTACA GATTTTGGCC GTTTTTTGAG 420
 ATGAGGTGGC GGTITATGCT CCGCAGAGCT TCGCATTACT TGCTCGAGC CACTGTGTCT 480
 5 ATGGTTGATA TGGTCACTAT ACGTCCAGCA ATAGCTGTGC TTCTGTATAT TAGTCATGAA 540
 AAACAGTAGC ACTCCCTATC TTACCCCTGC NGATCGTATT GGTACCGCCA AATNGTTAAC 600
 CCATTTTCCA AGAACATTCT ACCNCTTCOG TTTTGTCCCA AAGAGAGGTN TGCTATATTT 660
 10 GCCAACAAAA GCGCAACTGA AATINAANAA ACCCTTTTTT CCCCCTTTTN TTTCTCCCGA 720
 GGAACCTTTT CGCAANTTT CNOCTAAAT TGTNVTGGGG NTGANANCCN AGAAAANC 778

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 806 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1306UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

GATCATTTCA GTGGATGGCG ACATTCATAT GGATATCAGT TCGACTTTTG TTCCAGTCT 60
 TATTCAGCTG ATTTTCAGGT TACAAGAAAT GGAAGGGGT CTCCATTTTG TAGGGACGAA 120
 30 CAATGTGTAAG ATGTCTCAGG AATTCAAGAC TCAGGTGAA ACGAAACTA TTATCTTATC 180
 CCTTCTGTGA GGGGACGATA CCTACAGAT GATTATCCAA CCCATCTCTT ACGAACTGTC 240
 ACTACATACA GTTTTCACTG ATTTTATTTT CATATCTAAG GTACAAAGCT CGGAACTAG 300
 35 GGATATCGCA ATTATTCGGG AAATTAATAAT TGGATATCAA ACAGCCAAAT TTCAAGTGAA 360
 ATCGTACAAC TTGAAATTGT CGGAGACGCT GCTAACATCA AAGCTACGGG GGAGTTGTTC 420
 TCGAGCGGTT GAACTTTATT GTTCTGATAG TGACATCAAG TTGCTTTTTC ACGAATGTCC 480
 40 CCCCCCGGA AATGAATACC CGCNATNINC ATTCTINAAC CGAATTCCCA AAACCCNTTN 540
 TNAANTAATC CCTTTAAAAA TTNATTTTTC CCNAGNITT ACNCCCGCNA ATTTTTTTC 600
 CAAATGGGCC CCTTANATGA AAAAANACTN CACCCCCCN NCGAAAANAA ATTTCTCTTT 660
 45 GGAAANNNN AAACGAATTA TTCNCCCT TTNCCCCC CCGGAAANAC ANTNITTCCT 720
 CCCCCCTTT AGGAAAANTG TTTTCCCNNA TTINANANIN TCNCCCNOC CCNNAACNA 780
 50 AAATNTAAA NCACCCCNIN TTNING 806

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 753 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1307RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GATCCCTTTA TCTCATATTA TAGTCCATAG TACCCCGTGG ATGCGTACCA CACAGAGGTC	60
CCTCTTCTGG ACCTGAGACC TAGATATCTT GCGATATCAT TGAAAATATC GTTCAATTGC	120
TCCTCGTGA GCGCTTAAC TTCCGCTCG ATATCAGCAT CGGGTGTTTC CGAGATGTGG	180
AAGTTCCAA CTTGCGCTC CAAAACTCC TCAAATCTCT CTGTCTCTCT CAGTGTGGT	240
GGCAACAAC CATAAAATTT CGCAAGCTTA TACAGCTTCA CATTGTCTAG ACTTTGGAAG	300
TGCCCCAAG TGAGAGGGAA TAGCGCTCC TTCAGTCCG GAATCTCACC GTCCCGGTTT	360
GGCAATGGAG CCAAGAAGTC CTCTCTCTCC GACTTCGTGG AATTCATAA GCGCGCACC	420
GACCGCTCTT CCATGTGTG AAGCTGGCCC TGAAGCTCCC CCACTAGCTG CACTAAGTCC	480
TCATTGTGG CGAAATCCGT TGTATCAAAC TTGCGCGGC CCCCTTTAGG AAGGAATTT	540
TGTTCTAAGT TTGCCATGTC ATGCTTTTGC TTGCTGACCT GTAGCTCCAG CACCGACTGT	600
CCTGTCTTGG TGATTAGGAC GCTCTGCCGT TTAAGTAGCG CCTGTAGCTC CTCAACTGTT	660
TCTTCAATGC CTGTCTGAC ATAAGCACT TCAAATTTAG TAGAAGCTT CTGAATATTC	720
CTACACCAA CGCGCAGAG AGAATGGTAA AGA	753

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 811 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1307UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GATCCACCAA AGGGTATTTT ACTATATGGG CCTCCGGGGA CAGGTAAGAC ACTTTGTGCC	60
CGTGGCGTGG CCAACAGGAC CGATGCTACA TTTATCAGAG TCATTGGCTC CGAATTAGTA	120
CAGAAGTACG TCGGTGAAGG TGCTAGAATG GTTAGAGAGT TGTTTGAAAT GGCAGAACA	180
AAAAAGGCAT GTATTATTTT CTTCGACGAA GTGGACGCAA TTGGCGGTGC TCGTTTGTAC	240
GATGGAGCGG GTGGTGACAA TGAGGTCCAA AGAACTATGT TGAAGTCAT TACGCAACTA	300
GACGGATTGG ATCCACGTGG TAATATCAAG GTGATGTTTG CTACCAATAG GCGGAACACC	360

EP 0 866 129 A2

TTAGACCCAG CATTGTTGAG ACCCGGTAGA ATAGACCGTA AGGTTAGAAT TCTCTCTTCC 420
 GGATTITGGAA GCGGTGCGCA ATATTTTCCC GCATTCACAC AAAGTCCATG AGTGTGAGC 480
 GTGGTATTAG ATGGAATTGA TTCCCAATTG GTGTCCAACCT CCACCGGCGC TGACTIONATC 540
 TNGTTTGGCC CGAGGCTGGC ATTTTGTCAA TCCAATTCCC GACCCAGGTT ACCTACAGAA 600
 ANGACTTCCT TAAACCNIGT GATAGGTCCT CCACGGCTAT AAAAATTCAC NCCCCTTCCC 660
 CGTTTITNIGC AAACCCNAAN CNNTCNCCCC CCTTNGGCG TTTTTTAAA GNTTATTTA 720
 TCCAAANNG TMTCTTTT ACNATACTAN TGTTCCAATT TCTATNAAAT NTINTCCCC 780
 CCGTGAAANC CTNCCCCGTT NGCACCCTA T 811

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1308RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GATCTGTCTG CTGTACACC GATGAACGAA ATAATTGTGA CCGTCAOGGA CTTCGAGAAT 60
 GCACTTCGGA AGATAAGCC TTCCGTCAGC GATAAGATA GAATGAAATA CAATAAGCTA 120
 AACAAAAAAA TGGGCTGGAA TGAOGAAGCA GGGTGCAAG TGAAGAAGA AGCATAGAGC 180
 AGCAAGTTAA ATAGGCACAG CTATGTACAA ATAACCAATT TCAACTTGT TCAAAGTCTC 240
 CCGTCTTAC AGATTTCACA CATGGAGACG GCGGAATTTA CTGTATTATA TGCCCTCTCC 300
 TCGAAAGTT TTTTGAATC TTCCAGACAT ATTCOGTATT TCTTCTTTT CGAGAAAGAA 360
 ACATATGGTA TTTCTCTATT CCTGTAACTT GAGCTTAGCA ATTTCTGTGG ATATAGTTCC 420
 GCAAAGAGGT AGATCCGTGG CACCTCTGAC AAGAAGGAG TTATTCTTCA GAGAATGAAC 480
 ACGCCCGGAT ACATGCCAG AATGTATATG TTCATAAACT TCGCTCCAA CATCAATGGA 540
 ATGGATAAGA GCCAGGTAA CAAGTCCCAT ACTAGTATAG TCCAGCGGAA TGCTTCAACA 600
 TTGGAATACC CGCATGTG ATATCCGGAG CTCTTTGATT GATATAACAA CCCCCNCCCT 660
 NTNIGCCNC AAAATTCGCC CTGATGGTAC CCTAANGGT TCTTGCAAAA GCGAACCCT 720
 ATCCCCTGG AGCCNAAACC CTTTACGAGN AACNNATTAT GCGCCGGTNT TTNAOGTCCC 780
 TNNCTGTCTN N 791

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1308UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GATCAAGTGG GCGTAAAGTC GCAGAGAAAC TTGCAACTGA ACTGCCACTG GGGCTCATGC	60
ACCACCAAGA CGGTTAAGOG CGACCATATC ACCTCCACCC TGGGTGTGCA TGTTCCTCTG	120
AAACCCCTTCA GCTGCTCCAC ATGCAGCGGT AAGTTTAAAC GCGGCAAGA CTTGAAGAAA	180
CACCTGAAAG TGCACATGGA GGACACCATG AAAGAGCGTT CCGGTGGGGC GCGGGGCTCG	240
CGTGGTGTTC GCAAGACAGG CGTTAACAAG GGCTCTGGCC TACAAGAGAA GGCGGCAAG	300
TTACCCCAACC TGACTGTGGA GAGCTTTGTC AGCCAGGAGA TGCAAAATTA CTACCCCTAC	360
TACAAAAGCA GACAGCACTT AGACGAAACA CTGTGCACA TTATTTCTCC GCGGCGCAGC	420
CGCTCTAGGT TGGTACTTTG GGTTCGGAAC CGCAAGCTA CACAAGGAAA GCAGTGTCTT	480
CTTCACGACG CTGTGCAGG ACATGTCTCG TGCTTGCTT TCTCTGCTC CTTGCAACAG	540
CCCCCGGCTT GCGGTTAAGA TGGTAATGCT TCCCCCGCC CAGAACAGCA ATATGCACGC	600
CGTGCCCTAG ATATCCAGC GATGCCCGGA CTCCCTCCCT TTGGTGACTC TCCNGGANGC	660
AATCCANCC TTTGCCCCGAG ANACACTTCC GACCCNCTCC ATATCCCTGC TCTANCTGCC	720
CNCCTACCG CTTTCTCATA AAATGGCATT GTTGGCCGAN CCTATCCTCA TCAAGCCCCC	780
TGATANACCC TGNAAAAGAC TGANTCCCCC CCAAACC	817

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1309RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

GATCAATTAT TAGAGGCAAT ATCAAAGAAG TOCCATATTA CTGAGGAGAA CAGGGAACAG	60
CCTGGAGAAA GAATGCCGCA GACGTACAGA TACACGCTGG AAAATCAGCT TGCCAGTGA	120
GTGCTCGAAC AGCGATAAG AGTATTGACA GTGGTAGCGT GCAAGAGTCA ACGACAAAAT	180

5 GAACAGAACA TCATACTTCG GCGCGAGAT GTTGAAGCTC GACTTGGTCC GCGCGTGGAC 240
 CTTTTTTGAA GAAGTTGCGC CAGGATCCCA CGCGGGCCTT GCGCGACGCA GCAGGGACTG 300
 GTCTCCAGCG CGCCAGCAGC AGGGAGCTTG TCACCACGCT CACAGAGCTC ATCGCCATAC 360
 CCGCGCGCGC AGCCATGGGC GGCATTGTGA TGCCCCACGG AATGAGGACG CCCATGCTGA 420
 10 CTTGGGAGCC ATGAGAGAAT TGTACAGGAC TGCCAGAAA ATGTTTCACT TGACGCGGTT 480
 AACGTGGCGC GCGCGAGATT CGATGGCATA CAGAATGCGG TTTAGCGGCG GCGCCCGAGG 540
 AATGTCCCAA ACCACGATTC CCGCGCGTTC CGCAGAGAT CACTGTTGCC GGACAGCGAA 600
 15 ATACCGAGTT CACTTTTACA ATTGCCACAA TTTCTTTTGAN GCGTCTTCC GATAAGGCAC 660
 ATATNGTIN TTTTGGCGC ACTGCGCAA NGTNCACCTT GCGCCCTGG TACTTTCCCT 720
 GAACATTTTG ACGGATNCCC AANCGTGCAA ACTCTCCNC CCGTGTINN CCATACCAT 780
 20 CCATTTTTTG GGCNC 795

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1309UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

35 GATCAGGACC GCGGTNCCTG ATTGATTTGG CCATGAGTTT AAGTATGACC CAGAGGCGCG 60
 CCCTGGTGTG TCTAATCTGA TTAACATCGT AGCTGGCATC CAGAAGAAGA CTATCGGGC 120
 GGTGGAGGCA GATATTTGCTG GATTTAAGGA CCACGCAACT TTTAAAACT ATGTTACAGA 180
 40 CATCTAGTA GCTGAGCTGA GGGGGCCAG AGAGGAGTTT GCGCGTATA TGAATGATAA 240
 ATCATACATA TAGGAGGTTG AGCGCAATGG GCGTGAGCGA GCAGGTGCGA TAGCTGCTAA 300
 AACCTTGGCA GAAGTCAGAG CGATAATGGG TTATTAGTTA TATTGAGATT CCAACTTTGT 360
 45 CTATAGACTA GCAATAATTA TAAAGATACA TCAAGAAGAC CAAGAGCAGA TGCGTAACTG 420
 GTTGTCATC TTTGGACCTG CCGGATATCA GCACATGCAA CCAATATCTG CTTGAGCAGT 480
 CCTCCGCTT CTCGTTAGCT ATTGTGCCAC CTTGTATCTT CCATCGTTA TACAGCCAGC 540
 50 TEAGCACATC ATCCATCTAT TTTGAGCCCA TTCTGCTAGG CTGATGCAAT AGACTTCCAT 600
 ATTTGGTAAT CATTGTCCCN TTATTTTTTA GGTACCACC ATCTNTTTTC CNATGAAAAN 660
 CGTGACAATC CNGGTTTTT TCNACCTCC CTCATNAAA TTTCTTTTAT CGTGGGTTTC 720
 55 GGATCAANCC CTNNGGTCN TCCCTNCGC CTCATCCNG GNATTTACAC CCNTNTTTT 780

CTCCCCCTC ATNAANC

797

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1310UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GATCCAAAAA AATTTTAATA CTGAAAAAGA AATGCCACAA CTAAGCTCAG CTACCTTAAA	60
GAATCGGGAC CAAAGCTGTA AGGCAACAGC TCTTCCAATG TTCGCTGCAG AACCTTGGAC	120
CCGTGGGGT TCATCATAAT CACCGTGAGC TTCTTGGAT CAACGAACTC GCGCAGGACC	180
TGCGGGCAA TCCACACGG GGTACGAGC TOGGACGAGT CCGACTCAA TGCGATGCAG	240
ACCCAATTG TATGCCCCG TGTACCGCC TTACGACCG CTGTGGTTC CCGCAAATA	300
CCGCTGGGT AACTGGCATT CTGACGTTA GCGCGACAA TATACTGCC TGACGCTGTC	360
AAGATGCAGC AGCCACCGG GAACCTGGAG TTATGGGCTG TACGAGAGCT CCTTCGGGC	420
TAGTGCTCGA GCAACCGGC CCTGATATGG CTCTCCCTGT GTGCTTGSCA TTGGCTTCGG	480
TGGGTCGCC TCCTAGGTAT TGGGGTTC CTAAGTACTG GCTGCGAACC CTTATGTTTT	540
TTGCAGGGGA ACGAATTGG CCGAACCGG GTGAATCCG GGAACATNCA ANTACCCNCT	600
TTTGGVINNC GGENAAGGG NNANNTTCN NNCTINGCNC CGCNGGAAN AAANAATGTT	660
AACCATGTGG ANTAAACCTT TAANATGANN CCTATGGCCN GTTTAACTTT ATCCCCCNC	720
CCCCCTTTT AAANGTNNNA NCCCCGCAT TTTAOCCTTA NNCCNGCGG GNGCANNANC	780
CCACAAATNN TMTGTGNGC GCNNGCGTN NCTAATATGG AGCTINGGN	830

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1311RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GATCTTATCG TTCAGGTAC CGTGTCAAG AATCTGAGAC ATAACTTGC GCTGCGACGA	60
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GTTCTTGGA AATTCTTGT AGTACTGTC GTGTCCGCT TCCAAGCTT CCTTCCCCG 120
 CTTGTACAGC AGCTCCACT TTTGGTGA GAGCGCTCT TGCTGGAG AAGCTTGGC 180
 5 GTCTAGCGC ACCTCGTCC AGGCGATGTC CGCAGGCACC AGAAGGTTGC CGCTGGGAAAC 240
 CGAGCGCAGG TCATCGACCA TGCCGCGGCG AGGTTCTCTC CCGGGGACT CGGCATOGAA 300
 CCCCAGATCG GACTGGCCCG CCTCTCCGCG GACTGGGCG GCATCGCTGT CCTCTCGGC 360
 10 TTGCTCTTG GCTTGTCTCT CGGCTTGCTC CTGGGCTTGC TCTCTGCTT GCTCTTGGC 420
 TTGCTCTCC AGCGAATCT CGGCTTGGT GCTCTGCTT GCTGGGCTG CCGCTGCTG 480
 CGCCGCGAGC CCATGTTGC AGCAGCCCGC TGACGTCGTT CTGCGCCCG GCATCGCGT 540
 15 CTCTTCTGTC GCGCTGAAT GCTGTGTC TGAGCTGTC TGCGTGGCT CAGCCCTTCC 600
 ACAGCGCAA GTGTCTCTT CTNAACCCCG CANNGCCAAT NGTTCCGCG CIVCATCCCC 660
 CMTTMTTCC CTGGTTTCC CTTTGGTNGN CCGGCGNAN ACTTTTCCC TGGCTTNCN 720
 20 CAATTCCTTT TCAATTTGGT TTCCCCCA AATTTTAN ANGGGTTAN CTNVCANN 780
 NGCNGNNA GAGAACT 799

(2) INFORMATION FOR SEQ ID NO:421:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 790 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1311UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GATCTTCTGA TGCATATTTC CGCTCTCACC TTGGCGTTA AGTTTTCCTA TGTAGATAGC 60
 40 TCAAAGTCAT CATCCCGTC ATCTTTTCA GGTATAGAT TCTGTGATAC TTCTCTTCT 120
 TCTCTTCTCT CTCTCTCTC TTCTTCTCTG TCTATATGAT CTTCGCTGT CAGTTCATTG 180
 TCTATTCCAT AATTGGGTTT AACTTTGGC TTGGGCTCTT TTGCTGGCT ATGATCTTCC 240
 45 TGGATAAGTT TCTGTCCATC TGCCAATCC GTTTTCTCAT CAGTAGCTTG CGAACCGGGC 300
 ACAGTATGGA TTTGTTTTGA GCTAATTGCA TTAATACCT CAGATCTTC AAGAGTCTT 360
 TTGCCAGCAT GACTTTCCGA AGATTTCGAG CGTTTACCTG CAGGCGCACT CTTACCCCGT 420
 50 TTATCTGCAG GAATGTAGTC CTCATCGTCT TCATCTTCTT GTATCGTCTG TATGCTCTC 480
 CTCACGATGC CGCCCTTACG CTGTCCCTAC ACTCTTCTAT ATCTCTCTCC TCATATCTAC 540
 CTCTTTTCCA GTCTTCTCCA CTCATACTAT CTCTACCACA TATCAGGATA ACGTATAATG 600
 55 GTGTGACTTT TTTGGATAGC ATCCTGCGC CTAGGAAGC TNGGTTCCG AATATAATTT 660

AACATCTTCC CAATCACAAA TTINCTAGTA ACNGTGGTAA ATTNAAACGN AANITTTTAA 720
 CTTTCATAC GGTTTANGNC CCATGGCTCT TGAAANCGGA AAAATCCGGG GCCCCCCTTN 780
 GAACTTGTTT 790

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 788 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1312RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GATCATTCTC ACCAGTACAA ATGTATATTT ATATGTAATT GTCTCTCTCT GCTTTTGGCA 60
 TATTTTTTTA TTTTTTGGG TGACAGGTG CACTGACGT GACGCGCAAG CCGCAGGCGC 120
 GATTCCTTGC AACTTTTGT CAACGCGCA CAGACAGTCA GAAAGTAATA GGAAACAATT 180
 AAATACGTTG TTATGTTATA TGAAGTTATA CATAAGTGGC TGCCATCAGG TTATATATTG 240
 CTTTAAATAA CCCATTGTC TGGAAACCTC CTCTGTGAAT GCTCGCTCA AACCGGGATG 300
 GTTCGTTCG ATCTCGGCA AATATTACTG ATAATTGATC TACAGGCTCT TTTGTCTCTT 360
 GAGTCGTC TCTATCAGG ACGGTGCTA ACTGTAGCGG ATAACATGTT TAAAGAAGTT 420
 TAGTTCCTTC TGTGAAGGAG CAGCAGCTTT GAGTGCCITT TCATCATAT ATTGTCAAG 480
 GTAGGAGAG AGTAATGTT TGTCTCTGGG TTCTTTGAAG GCTGGATAA TAATGACTTG 540
 ATTGTGACTC CTGGTATGG TACATTTAAC ATGCCAATCC CAGTCCCAA GTTAGATTCT 600
 TACCGGTTTT GTTATACCTT GTTTNATAAG GGTACTTTG CCCCCNACT TGCCAAGAAA 660
 TCATCTTATC CTTTGANAG GTCACCTGTC CCTTAATTGT AAACCTACNC CCTTTACAAT 720
 CTATGCTTAT ACCNGCCAT TGTCCCTGAA GGATTTTINT ATTAACCTG CNCACATCCC 780
 TTGGCTGG 788

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 769 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1312UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

5 GATCAGGCAA AGGATTTCTA CTCGTATGTT GGCAAGAACC TGTCACAGAA ATCCGACAGC 60
 AAGTTGCTTC CTCGGAGGAT TCAATTGAA CTTCAGAGGT TTGACTATTT TCACTCTCTA 120
 CTCAGTATG TTGTAGGATG TAACGCTCGT GATTTTGCTG TGTCCTTGC GAGGTTTCAA 180
 TCTTCGATCG ACCCTAATAA TAAAAATACA AACATGCACC TCGTGAAGAA GTATCGTTCC 240
 10 CATTTCCTAC CATTTAACAA GATAAAGAGC CAACAGCGCA TAAGGCTTTC TAAAGTGTC 300
 AACTATTTCTG ACTTGAATGA CTTCTACCAA CTTCATCAG CTACCTCAGA ACCAAATAAG 360
 CCCCCTCAAAG AAGGACTCTT ATGGTCTTAC AGGAATAATG GATGGCATAA ACAGTGGGTG 420
 15 GTACTACAAG GATCAGAGCT CTCAGAATAT TCGATTGGA AGACGAAAGC TAAGGTGCTC 480
 AGCOGACCGG CCATTAATTT GACGTTTGIG TGTGTTAAAC GTTCGGAGAA AAAGCCTAAC 540
 GGATTTGATA TCATAACTAC CGACGGGAG GCTCGTTCTT TCCAAGCAGA GTCAGAGGAT 600
 20 GAAATGAAGC AGTGGCTGTA TGGGCTTAC TCTGCTGTCG GGATAATAGC CATTGAGGAG 660
 ACAGATGAGA ACAAAGATCC ATGTCTATT GTCCGTAATG CGGATCCGTC AAATAGTGCA 720
 25 TGCTGTGACT GTCCGAGCGA TAAGCAAGTG AATGGATATC TCTGAATAT 769

(2) INFORMATION FOR SEQ ID NO:424:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 799 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1313RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

40 GATCGTGTCT TGCTGACTTG CATGTCTAGC TCAGTTCTTT ATTACCCGOC TCATGTTGAA 60
 ATTTTCCAGG AACCATGCA CCAAATGTAC CGATGATATA GATTACATCT ACCCTTCCGC 120
 AAGCCTGGAA GGAAGCTAGA CCTCTAATCT AGTAGCTTGC CATGTACATC CCGOCATCCG 180
 45 ACCCGCGAAG ACCAGCCAAG GTGACGGCCG GCCAGCTCTG CGAGCTGTGC CACGCGCGCA 240
 AGGCGCTGGT AAAGGCCCC AAGAACTTGC AGAAAGTCTG TAAACTGTGC TTCTTCCATG 300
 50 TATTGGAAC CGAAATOCAC AATACCATTA TGGAGAACAA GCTATTCCAG CGCGGGGAGC 360
 GGGTGGCAGT TGGCGCTCC GGTGGGAAAG ACTCCAGGT GCTTGGTAC ATATTGAAGC 420
 TGCTCAACGA AAGACAGAC TATGGTCTCG AGATTGTGCT TCTGAGCAT CGACGAAGGG 480
 55 CATTGTGGCT ACCGAGACGA TTCCGCTAGC TACTGTGAAG CGCAACCCAG AGCAATACGG 540

TTTGCCCCG AGATTGTGTT CCTACAGGAC CTCTACGAAC TGGACGAATG ACGAATAGTG 600
 CCTGCGCCCN GGAATGCNCA ACACTGCNCC TTACTGCGGG TTTTITCGAC CCAGCGCCTG 660
 5 ATTCCCGGGG GGNAAATGCTT GAATCCACCN NNTTGTAAAN GGCCATACCC GAAAAAATGC 720
 CNAAAGNGCC CANAAATCCT GGCGGGGAAA TTTGGCNAAT CNAAATAACN CTTTTCOCCA 780
 AANAGGTCCC GNTAANNIT 799

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1313UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GATCAAAAAA GATACGGATG TTATGCTTGT TAAAATATTA TATGCTATAG TACAACGTAT 60
 CGCGTCAAAC ATAAGCATG AGGACTATAT TTTTAATICA CTAAGTGG CGAAGCATCT 120
 CCGGAAGAAA TAGCCTCTG TATGGGGCTA AGTCCATAGG CGTCGGTTGG GCTCATCTCT 180
 30 GGAGACTTTA AAGAATTAA TCCGAAGGCT AGGCTCCCAT ACCCAAAGG CGAGTGGGCA 240
 CTTTGTTCGA GAGATCCTTC TGACATAGCC TTCTTAGTG ACAGTGGGG AACATGGGG 300
 CGGAAGGAA TACTTTGTCC GTGCAATGAA CCTCGGATA AAGGCTACT TAGCCGTTT 360
 35 TTGAAAAATG TGACAGTCTT GTCTTGATA TCTAGCTTGT ACCTGGTTGG AGTGGGTTCC 420
 TTTGCAAGAC CAGTGGGTTT TTCGGAAGG CTTCGGTCT TCCCGGAATG AATTCTGAGT 480
 CCTGGTAGGG AACATCCGAG ACTTCCAAA AACNNITCN CTNCCATTT TCNAAAAAT 540
 40 GGAAATCNC CCGGCATTA TNGATCTCTT CCCAAATTAC NNCCNCCC TCACITTING 600
 ACTTGGGNAT ANAGANCCCC NTCNNACCCC TCCAAANAAA AAAAATTCCTC NINGTGCCCC 660
 NINATTCOCC CCGGGGCCN NNTTTTAATT CNGGGGAATT AAATTTTGTA TCCNNGCNGG 720
 45 TNGAAGCANG TTATNGCCCC CCTTGACCC ATNPTTINACT TMTAATTTT TCCCNNGG 780
 GNTGGAAACT TTGCNAAAG GCANGCTTTT TGAACCACT 819

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1314RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

	GATCCATAAA CTATCTTCTC ACTGCGCGGA TGCAAAGTAT CAAGGAATAG GCGACAATOG	60
10	GTAATGATTG GCTGAGCTC ACGCAGATAT TGGGCACTT CTGATATCGG TGGGTGTGTC	120
	GATGCATGAT GCACATGAAT AAAAGGAAGA AGCTTGGAAA GAGGTACAG GCGCGGTAG	180
	CGTGTGATGA GAGCTGTTAG TTGGCTTCA ACATCAGCAA GTTCTCTAT AGGGGAOGCA	240
15	GGGTGCTCAA CATCATTTAT TAGACACTCC AGCAGTTTGT CTGAAAAAA GGTGTGCATG	300
	GACAAGTGCA CCTCATCTT TGAGATGCG CGGATAACGT CCTCAGOGA CGCCAGTCTC	360
	ATCGTGCAAC TGCGTCAGAA AACTCTTGAT TGATAGGTA ATGCAGTCAG AAGAAGTGT	420
20	TAAAGCACT TTCGATGCCC CAGTGAAAC TAATCTCTGT CCGATATAAA ATGGAACGTG	480
	TTAGCAACAA TCTTCCATAT CCGGAAAGTG TTTTACAAGC TTCTTACGAT TTTCCACTCC	540
	TCGATTGAAT ACTCGGCGCN AATTCTTTTA CCATATACAC CCGNINCGG GCTTTTGAC	600
25	GAATCTNTA TTTGTGTAAG AACTGGACAC TTTGAACTT TGACATTGC NGANTCCGAA	660
	ACNCTTTTCN CNGCGAATA ATNINAACCC CAATCTGAC CCAATACACT CCCCCCAAA	720
	CATGACCCCG CACANGATTN TTTTTCGCCN AGAATTNTT NAACINTTTG CCCCCINANA	780
30	CATTNTAAAT C	791

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1314UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

45	GATCTTGCTG CAGACAGATG CCGGGAGCT ACCCTTTGGA ATCTTTATAT AAACCTTTT	60
	CCAGCTGTAC CGCAGTAAAC TCCCTTGCT TCAGGAGCTC CAGGCTGCA CGCACACTOG	120
	AGGCTACAC GGTGACTGC ATTGGCTTCT GTGGGCACAC GGAAGTCTTA AACGAACCTC	180
50	AATCCCATCC AACCAGTTCT GCTAACGTAG CTACTTCTGG CCAATGCTC AGCCCCATAC	240
	CGTGGAGCA ATCTTTCCAA GCCACATAAA CGAAACCTAC ACAGTTACTG CGCAAGGCAA	300
	GTGCCAAAG AACACAGGTT CCGCAGTACC AGAGCAAAA GCTTACCTGT CAACACTTOG	360
55	AACATTCGGG TGGCCTTAAC CATATGCCAC ATGAAGCAAT AGACCCCTAA AATAGAAAGC	420

GATTGGCCCG GAACAGACAT TCCTGGTGT GTACTTGGAA CTCACATAGG GGCTGCACAC 480
 TGCTTAAAGT CCTCGCTTGC AGCTGAGGCC ATGTGCCCCCT CATTAGTGAC CCACGTTGAT 540
 5 CTCGAGCCCCG CAAATGATCG TCAGCGTGCA TCCGACTGG CATTGCAAGG GATGTTGATC 600
 CCTGANGGG AGGCTTGCAA CAGCGCCNCC CTTGTTTCNC ATCCATAGGC TGTGAGGCC 660
 GGAATGATCC NCTCTCCAGG GGAACNCCCT CCCCACGCC CCATAGGGCC CNCCCTGGGN 720
 10 TTTGCCCCGG AACTCCDA ACONGGTTTA AANNTTTTTT TAAANONCC CAGTGGTNTC 780
 AAGGCCCCCN NGCCTTTTTC CANCCCGCAN TTTCTNAATT TTTGNCNGCG GNA 833

(2) INFORMATION FOR SEQ ID NO:428:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1315RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

GCGGCGCTC NNCCAACTAG TGGATCTCA TTTGTGCCC GCGGACAGG TTACCACCOC 60
 TTTTCTCTCC CGTCAGCATC TCACTAGCT GCTGTAGCTG GTACTCCCTG TCGCCGCGGA 120
 30 ACAGTTGCA CTTGTCTATT GCTGTGCATG AAAGATCGTG CAGCTGAAT ACATTACCGT 180
 AAGTGATCAG CCCAACAGC GCGTTGGGG GCACCAACGA CAGAGAGGTG ATGATCGAAT 240
 CCTTCAGCGC CTGGAGGTTT TCCTCTCCG CGGTACGTC CACGACGTAG AAGAAGATCG 300
 35 GCGCCACCTG CACCGGCCGA TTTGTGATGT ACTCAACCGT CGTGAGGTC AGTTCCGCGG 360
 GCATCGCCTC CTGAGACATG TTCGCATAGT GCTGCGGAAG ATGTTCCGC GTCCCCGCAC 420
 AGAGGGCAGC CCCACACGTT CGACCGCAGG TCGATCTCGC AGTACGGCTT CAGCACCOCG 480
 40 CTTACAGTGT TGGCCCCACC CACACCCAC CCGGTTTGT ACGAAAACCA CCGCCAGCT 540
 CCCTCCAATC TCCTTCCACC GCGTTGTTAC AGCATCCCN CCGCCNCCAC GTTCCTTGT 600
 45 CACGTTCCCG TCCGGGAAGC CCGGAAAAC ATTCCACGA HAACCGCAC CCNTTTAGTT 660
 CTTCTTCCT NTTTCGAAC CACCTTGAA CCGGANCCA CTTTANNC CTTTACCC 720
 CTTTGATCCC CACCGAACCC CCAAAATGA ACCAANNAGC CCAACNND TGCNAAAACC 780
 50 GANTTGCCCN TTTCAAGGTC CCATCCTTG CCCCCGNGA ANAAANTNC NCCGCCNA 839

(2) INFORMATION FOR SEQ ID NO:429:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1315UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

GATCTTGGCG AATATCGGCT CCCAATCCGT ACCCATCCAC TTGACACTA CCGACTGCAC	60
CGCCAGCGTG TTCATCGGCA CAAGCTGCTC TCCTAGGCTC AGCAACGGCG GCACCACAAA	120
GTAGAACCGC CGGTGGTCT CCAGCTGCTC CCGCTGGTTG CGGAACGACA CGTAGTAGCA	180
ATAAGAGCCC GGTACGTACA CATCCACATC CAAGCAGCTG TCCTCCAAGA AACCTGGCT	240
CAGCAGATGC TTGTAAACT TGTTCGGCTG GAACCTGGTA TTCCTTTCCG GCGGGCAGTT	300
GGTCCACACT AGCCCGTCCC GTGTACAGG CGATCGGCG GCTACCACCA ACCGCACCCG	360
CAGCCCGCTG TCCTCCCCAG CGTCTGGCC AACAGGTAAA CATGGCAAAG TGAGCACACC	420
CTTTCCAACC TCTCTCTCA CCGCTCCCC GTGTGGTCT AATCTCAACA GCACGGTTTT	480
CATGGCTGTT TGCGCCCTTT GCTGGATCT AAAGGAAGCT TGGCTTGTC TGCAGCTGCT	540
AGCCTTGGGA ACTGCCATAG TCCTTTGACC TTGACCGGT GTTAAATAGT GCATTTCACT	600
ATACACAATT TGAATTACG NCTCCNCNG TGCTAACTGA GGGANATTAC CCNAAACCCG	660
GANGOGANNA TAACNGVINA NAATTNCCC GGTGCGACNC NTGCCNTATG NTTCNTTTT	720
TGGAAANAAA CCTTNGGNN GGTNGGTGN NAAAAATTGA AAACCCNGN TNAATCTNC	780
NTTNACTTN TCGGAAAACA AAANINGGC CCCCCCN	818

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1316RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GATCAATAT ATGCGATGGT CTGAAGGTT GTCCAAGTGA GTAGCTTAGC GAATACTTTG	60
CCAAGGCGTC TCGACATCA AGAAGAGTCT CAAGATAATA ATAGTCTTT TTGGGCAGTA	120
AGCGAAGATT GTTCTCGCC TTGTCAATT CTGCGCGTC OCTGGACCA TTTGGTGGC	180
TGTTGAAAAA GCGCCAAAAG TACTTCAAAA TGACCGATTT TTGACCTGG AAACCTGOCT	240

EP 0 866 129 A2

GGAGAGAGAA GTCTGTCAGC AACGTAAATT CACTGAGAGA CAGCAGTGTT TCGATAATTG 300
 CAGATTCTTG ATTCTCTTC GTTAATTTTG GGTACAATTT AGATGAGCTT AATAAAAATT 360
 5 GTAGTGCTG GACAGATGGC GATTGAGCCA ATAAATAATG GCTGATGGAT TAAATGATGC 420
 CAGCTGCGCC AACTCATCTG CATTCGCTAA GGAAAGCATT GATTTCAGAC TATAGTTATT 480
 GGCAGCATCC ATGTACTTTG TTGTACTCGA TCAGGTCTT CACTGAGACA CCGTCAGAAA 540
 10 GCGTCACCGT CTCTGCAATG AGTTAGAGCC ATCCATAGAT TTCCCGAGG CAGTTCCCGC 600
 CATGAATTTT CACCCACTTC CCCCCCGTC CATACCGCAA TTGAACATT CCGGTCAAT 660
 ACCTCTTCC TCCCCCGNT NTTCNCAAN AGGGAAGTTA NATTCCTGNC CTTTTTTTIN 720
 15 AAAACCCAAT TCNCACTTT TCNGGGAANT TTTCGGGTT GAGNAAAANT CCNACNCCG 780
 GINGCCGGTT TAATTNCC 798

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 820 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1316UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTGT GACTGGCAAC 60
 35 CATACATCGG CACCATGCA CCCACATGAT GGTTTTCTTG GGGGTGGGC CGTGCTGGC 120
 GGGCTCCCG GTCTACGCTG GCGGTGTAG GGGCCGGCT GGGCGGOCAG GCGGAGCAAT 180
 GGGCGGAGGA ACAGCGAGCG CGCCAGCAGC GGTGCGCAGC TGGAGGTCC GGCATGTGTG 240
 40 GAAAATTTGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCTGT 300
 AGGTTTGAAC ATACTATACA AGCTCCAAT CATCGACGAT GGCTGTTGGT AAGAACAAGA 360
 GATTGTCAAA GGGCAAGAAG GGTTTGAAGA AGAAGGTGT TGACCCATTC ACCAGAAAG 420
 45 AATGTTACGA CATTAGGCC CATCCACTT CGAGAACAGA AACGTGGTA AGACCTTGT 480
 AACAGTCCAC CGTTTGAAGA ACGCAGCTNA CTCTTTGAA GGCNNTTT TCACAGGTT 540
 NGCNITGGCC AACCANCNGG TTONTAGGAT TNNCNTTCC NAAAGGTTC AATTANAATT 600
 50 TACAGGTCC NGGGCAAAAC CTTTNGACA CTTTCCCGG TTTGGGATTC CCCCCCNA 660
 CATTTTAATT CAAAGNCCA AAATTTGGCN ACCTTAATTA NGGNATNTCC TMTNAAACC 720
 NGNAAAAANN TMTNAAATTN TTTNNOCTTG CNINCCCAA AAAATTINCC CATTNAAAA 780
 55 ACNITTTTNC CNCCCCCTCN NTINAACNCC NAAGTTTTN 820

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1317RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GATCTTTATC TTTCGATGAT ATCTTTCTCG AAGAATCGAC AAACACCTGG TCAGCAAAT 60
 TGGAAGCTAA GTCTCTCCAA TCGGATGCAA AATAGTTGAC ATACCGGCA TTAACTTCA 120
 CTAACGGGC GGCACCAATA TCTCCAGAA CTGTATTAT TCGCTACG TGAACGATT 180
 GTTCAATCAG CGTAATATTC GTCAATACAA AGAACCCAAT TCTCTGCATC TGAGGTATC 240
 TTTTATGTGG AGCTCCGACT TCGGCTCTA AGTTTGGATT TAGAATCTTT TGGGCTTGC 300
 GCTCTAGAGA TATGGTTAAG TAATCTATAG CATCGCTGAA GAAGCAAGAG AGCAATTGCT 360
 GTGCATTCTT CGGTGTCATA GATATCGTCC AAACATTTTT TGATTCAITG GGCAGCATG 420
 ATTCGGGAGT CATCGATTGT ATAGTAGCAA GGCAACCAGA CTTGTATTCA CTAACTTGC 480
 GTAGTCTGGA CATAACATCA ACTGTGGCCT CAGTTACAC CATTATCAGT GGTAAGTGA 540
 CCCAGAGAAG CGGTTTTTGA CGATGTACT TGTNTCNATC TTTTGAACA NGGACNCGGA 600
 AATTTCAATT CANGTCNGGC TNCNCTOC CAAAACNGTT CCGTGTCT NGTAAAGGTT 660
 TNNCCCTAAA AATNGGGVIT CCGNGTINAG NTCCCCCCC AATTNNAACN NAANACCCNA 720
 TTTTNTAAT TCCCCNCCA AAATTCATTT ATACCCCCCN TTTTNGGTAT TNDAAATTIN 780
 GGGGNNNN NTTCAAAAA GGGGNG 807

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1317UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

GATCGTTCAT ATATTGTGA AAGAAGAGTT TTCTCAAGC ACTTTGAGCT GAATAATCTT 60
 GTCAAACATA TTGTCAGGTC TCCGCTGGTC GTTAACCGCG CGAAACCTCT TGAGGAACCC 120

ATCTAAGATC ATAATTGCOCT TTCTGGCTC CGATAAAGCT TTAATAGATT GATGGTTGTC 180
 GCOCTTTTCT GCAACGCGG ATTTAGTTAT TTCTCTAAG GATTCACAT CCTGTAGT 240
 5 CAAAAATGAT AAACACACGA CTTTGACTGC ACTGTTGTAC GGAATATAAT TCTCCTTCAT 300
 CTTTTCOAAC CATTGAAAA GTTGTTCGG CTGAAACGGC ATATGATTGT TTCTGTCCAC 360
 AATTACAGCT CTGAAGTAT CCTTTTGTAG AAACCTAGC GGTACCGCA TCAATTTGCT 420
 10 CTTATCCTTA GTAACAATAT TATCATCTG TATGTGGCC CAGGACTCTC CAAAAATATT 480
 CTTCAATGCC AGCGGACTG TGTCTTTCC ACAACCAACC GTGGCCACAG GGAATGAAAA 540
 TGAACCTGGT ATCTCGTCT ACCTTATCGA GCTCCAGATG CATACTGGTC CCCCCNAGCT 600
 15 CCTTTATATC CTCGAATTT CCATAATATC CAATCCAAA ATCCCCAAAT CNITCCTAGG 660
 AANATTTTCC NNNACTINGAA ATCCCTTAC CTGTINTATA CCCCCTGNAA ATTTNGGATN 720
 TTGATTCNG CCAGGGANTA CNATTCCNA TTTTINTTIG TGANNAACAA NGCTTTTGAA 780
 20 TTTTGTGCC CNCCNCTGT GNANLCCCN CCTCCTCCC CCCCINTPTN TTACN 835

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 748 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1318RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

GATCGCCTCG TCGTTGCCC GGCTGTCAG GCTCTGGCA AGGAACTGCC CGAACCGACC 60
 AACCAAATCT GGCATGTCCT TCGGTAGAT GAAACCTGC TGCTTGCTGT CCACCGCATC 120
 40 CCACAGTTG TTCAGAATAC CCTCTGCTC CGTCATGACT CTTGAGCGGT GAGTGCAGTT 180
 CCCAAGGCTT TTGTTGTGCT TGGCAGTTGA AACGAAGCTC GCAGCGGCAA AACACACCG 240
 GCCCCGCGC AATTGCTCAC GTGCTCTC GGGCCACATA AGCAAGCACA CCTGACCGC 300
 45 ACACGCACCC TGCAAGTAG GTCAATACCA AAGGGGCACC CCGCTGACC GTTGCTGCG 360
 TCGAGCAGC GCGCGCCAG CGCAACGGC CACGAGCATG CCGTTCTCC GTAGCGCGC 420
 GCGCGTTGG CCATGCGGA AAATACCTG GTTTGGCCA CTGATGCGT CTGCGTCCG 480
 50 CCGCGCCGC CCGCGGCCA GGCACCGTG CTTGGTCAGG GCGCCGGGC GGGCGGGTC 540
 GGTACAGTT GCGTTACCC GGGGTGCTT TAGATGGAAG GTTCTAGGTC TGTGCGTGC 600
 TGCCCCCTGT TGTCTACCG CCAACAGTGG GCGCGGGTA CCGGCAGGC ACCAGTGGC 660
 55 AGTGGCTATC ACGTGAAAAG AGGCGGGTA ACGGTGGTC GCGCTGAGA CACATGCAA 720

CTATTTACAG GGCACCTTAGG NGITGACC

748

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 758 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1318UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

GCAAAAAATG AGGTCCGCCA TGCGCGCGCG CTGCGCGCCG TCGCGACCA AGCTCGCGCG 60
 CCCGTCCGCG CCCACAGGC ACCAGCTGCG GCGTGGCGGG TAGCTGGCGC CCATCGCGCA 120
 GTGCGGCACC GCGCCCGCGC GCGGCAACGT CCACATGTGG CGCACCACT TCTGTGTGAG 180
 CACACCGGCC CGCACGTGG CCGGCGCTGG CGCGCCCGC GGCACCTGGC GCTGTGTGGC 240
 AGCCAACTGG CCTGTTCATGA ACAACGCTGT AGGAATGCCC ATCTTTGCCC TTTCGGCTGG 300
 CTGCGGCTGT GTGTGTGCTA TACGCTGCCT TATATACCTG CCAGGAGAAA TGTCTGCTAC 360
 TATCCCCGCG AAAATATCCA TCGATGCGA ACGGCGGAAC TCGCGGAAA CCTGGAGCCC 420
 CGCCTCTGTC GATCGTATGG AGAAACAGCT AAAATCGCTC AGCTACTCAT CTCTGGGCT 480
 GTGGTTCAAG GTGCGCGCAA TGCGGCGCAT GCGCAAGTCC GTTTTTCCTC TGTGGCGGGG 540
 CCAGGGAGAG CGGGCGCGAG ACGGCGAGAT TTTGTGCAAG GCAGACCGCG TTGGCTGTGG 600
 TAACCGGTAT GAAATACGGG GAAGCGCGA TTACAGTGG GTTTGCTGT CAGGGGTGCC 660
 TGGGCGCGG GAACCGGGTT ATGGTCTATA TTACAGAATG TGTACAAAGG AGTCACTGG 720
 GGGGGTCCG GGGCGGACA GCTGCTCTG TTTCTTCC 758

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 801 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1319RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

GATCTTCCTG CCTTTTGACC TCTTCATTAA TCTTCTCCTT TAACTTCTTT TCGTGTCAA 60

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GAATGTCGTG TAGCAGTTCC TCTTCCTGTT TCGGTTTCTT CCTGTTCCTC CTGCAAGAT 120
 GCAGCATCGA GTTTTGCTGG ATGGGCAAGA AATTAGAATT GATATGCGCG ATCOCTACGA 180
 5 AGAAATCGTA CGGCACAACC TTAATGAGAT TCTCGCACCA GTTCCAGACA TCACCTCTAT 240
 CGTCAATGAC TACGACCATC GACTGGTCCA TCGGGAACAG ACGCTOGAGT GATTTTGTGG 300
 TCAGCGAACC GTTTTCATCG CGTGACAAA TTCTATOGCC AAAGAGCTTC CCATCOGGGT 360
 10 CAATTATCTT GGCAATCTCT AGCGCATAGG CTGAGTAGC CATGGTGTAT ATATGCAGCT 420
 CGAAATGCGG CGGATCTTC GCAAGAATT CCTTCAGGCC TGGCOGTAAT TTCACGTTAG 480
 TACCAACACT TGGCGCGTTG GTTGGCTTTT GGGCCCCATA TAGAACGGCG GCAGCACAGC 540
 15 TCTCCATCC GANAGANAAA AACTGCNCAT CCTTAGCGCC CGGTATTGGG GTTTGTGTTG 600
 GTTCCCTTTG ACCACTCCCC CATGGTGGGT TCACACCGCG NATNGATTGN CGTCTGGTT 660
 CAATTTTACC CCCAGCATNG CTGCGCNCN TCCNNCAAC TTGACTGCN CCNCTGACCA 720
 20 AAATCCAAT TGCNITGGAC CCGATTGTIT TTTTNTTIG AAAGNNANT TCTNGTGN CNCTGACCA 780
 CTGGGNOCC CNCTTCCCN A 801

(2) INFORMATION FOR SEQ ID NO:437:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1319UP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

GATCATGGC ATGCTGGAGA ACCCAATTTT CAGTCTCAG ATGAACGAAA TGCTCAACAA 60
 CCGCAGATG ATGACTTCT TGATACAGCA GCACCGCAC CTGCAGGCAA TGGGCGCGC 120
 40 GGGGCGGAA ATGCTOCAGA GCGGCTTTT CCGCAGATG CTCACCAACC CCGACATCAT 180
 TCGCAGATG TCTCGCTGC AGATGGCAT GGGCGGTGC GCGCGGAGC AGGGCAOOGA 240
 CTTTCCAGCC CCGGCTCG CCGCCACACC CGAGCGCGCC GCGGCTGCG CGAACCGTT 300
 45 GGCTGCCATC CTAGGCTTGC AGCGCGGCG TGCTAACCG CTGGGCGCTG CGCCCGCAGA 360
 CCGCGGCTT GCAATGCCCC CTCTAGACCC GGTATGCTC TCTTCCCTCT TCGGCGCTG 420
 GCGCTGCCAG CCTTGGCGCC GCGAATAAC AGGCTNCCC AAGNANGN TANCAACAA 480
 50 ANATTCGCC ANGCTNAATN AATNGGGCN TCTCAACTT GAANAANAT TTCCGGGCTT 540
 NAAGCGCNG AAGATGTTCT NTCNNGGCG CCTTNTAT CTNTNTAAA GGNAAANTIN 600
 55 TAGGTGNGA NTNTCTGCT NCGNGGGCG NGTTCGCGT TTTNTTTAT TCCCNNTNT 660

TTGINTTCTC CNINCTGNIT TGCNACCCCA CNCAATTTTT TTINGGTGGG GGCTNCCNIN 720
 TTTTCATNNN TTNCNANNAC GNOGNTAATT ATANTTGINT ATCAAGTCCT NTTINTTTTT 780
 5 NNCCNACNGN TTGGGTGGCC CCTTINANNI GAGGNTGGTG TAGGGAAAGA AAAT 834

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1320RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

GATCTTTTCA AGAAGTTTAA CAATGACTTT AAAGCTAGCA TTGATAAAGT ACTCAAGAAA 60
 OCTAACAGAG CGGAGATGTA TGATGCTCTT TTGTCAATTA ACGTCATTC TAACAATATC 120
 25 ACCTGGGGAT TGAATAGAGC TATCTOACT GTTAATTGGT CGTTAAAGAG ATTTAAGATG 180
 GAACGTGCTG GTGTACCCA TGCTGTGAGT AGGCTTTCTT ATATTTCTGC TCTGGGTATG 240
 ATGACAAGAA TTCTTCGCA GTTCGAAAAA TCTAGAAAGG TTCTGGTCC TAGAGCTTTG 300
 30 CAACCTCGC AGTTCGGTAT GTTGTGTACA TCCGATACG CGGAAGGTGA GGCCTGTGGT 360
 TGGTTAAGAA CTTAGCATTG ATGACACATA TTACCAOGGA TGATGAAGAG GAGCCCAATA 420
 AGAATCTTTG CTACTTACTG GCGTGGAG AACATTACAT TGGCTAAANA ANGGCNCCT 480
 35 TCCTTTTAAA TNNNGGGGGT TTTATTGGA AAGGGTACTA CCCCCGGTNC ACAAATCCC 540
 CCCCNGTTT TTGTCCCCC TTTTAACTN TANAAAAAC GNGTAAATTT CCNNATTTCT 600
 TTTCCNNIN TCCCAANNIC CTCAAACTT NTTCTTTTGC AAGGAGGGGG GAAATTININ 660
 40 ACCCTTTINT TTININGGAA GAGAATTTTT GTCCCGNGG CCCCCAAAAA TTTTAAAGG 720
 GAANTCNITA NATTCNNAN NGGGGNINT AATTTTIGEN TTTTANAAA AAANCCCCC 780
 CNCCGNAA A 791

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1320UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

	GATCATGAGG GAATCCTTGG AAGAGGATGA CAAGAAGTCC GACGATGAAG GTGACCTGTC	60
5	TATTCCAGAT GCGCCTTCCT CTGAGGAGGA TTAGGCATAT AATGGGTCTG TTATATGTAC	120
	ATTAAATTAAC ATTCCGCTTT AGCTTTTTTA CTCCTATCCT TACGGTAGCT CACCCATATC	180
	TGTAGCCCTG CTCAGTTATC ACTAAAACGA GTGCCAGGCC CTAGTACTAT ATAATCCCGA	240
10	GTTCGAGCTG AGAAACAATG TCTGATTCCG CTGGTTTGCA TGGGAGTACC GCGATGCAAG	300
	ATCCAGATAG CACTTTAGTC GAGGAAAGGT TGGCGGCTAC GCCAAAAGTT ATCAACAAGG	360
	TCAGCAAGAA AGGTTCAAGC CCCCTTTCAG TGTTTAAGTT TAAAGAGGGG AGCCTATCCT	420
15	GCCNAAANTG CGCCAGGGTN CNTGAATTIN GGAGAAAAA NTGGTTTTTT TCCGGAAAAG	480
	CGCCCCNTGA NNCCAAAATT TATTNGGGAC CCNCNACACC NCGAGAAATT TNNITNAAGN	540
	GCGCCCTTTA AAATNCCCAA TNICTTCNAA ANNATTTGAG GNGGAAAGAC ANTTTNTTIN	600
20	AATTNCGGGG GGGGNTTTTT TTGCGCCCC GNGNVCNVC CCNCTCCAC NANTTTNAAA	660
	NATAGGAGGA ANGGNGGNG GCCANATTTT CACCTTTCNN AGTNGANNG CCNGNAAANA	720
	GNNITGATGN CCACCAATNC GGGTGVINGA AAANANINCN NACTGCTTGT ACACAAATTT	780
25	TTTTGTGCCG CNGGTGACAG AAAAAAGAN GGATTTTTTN ACAACCNAA AAANAAAAAA	840
	AAAA	844

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1321RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

	GATCACTGCG TTCTGGACT TTCTATCGTC GACGGTGCTG TTCTTCAGCC GGGAGGCGAT	60
45	ACGGCTGGCG ACGCTGGCGA TCAAGACGGG CGGGGACGGC GGGCGGGGG GCGAGATGTC	120
	TGCGGAGCTG CAGACGGCGG TGAATTTTGC AAACATACCG ATGTGCATCG GGGGCGCGCT	180
	GCGGGTGGTG CTGGCGGTGT GGCAGTACTC GAACCTCAAC AGCTACTTCA CGCAGCTGCC	240
50	GTTCTTCTCG TGGTGCATCT ACCTTGIGCT GCTGTGATC CTGGCGGAGC TCGCGAGCGA	300
	GCGCTGTAC GTGGTGAACC AGTTCATGCT GAACTACCGC AAGCGGTGCG AGTTCGAGGG	360
	TGCGCGGGTA GCAGGCTCCT GCCTGGTGAA CTTCGCGGTG ATCTACTGGT ACGAGAACTG	420
55	GTTGAATGGG CGCGGCAGAC GTGCACGACA GCTACAGCCA GGAGGCATCG CGGTGCTTGC	480

TTTTNCCCCG GGAAGGTTG CCCCCNCAA AACTTTNCTT GGGCCGNTCT ACTTGAANAA 540
 CTTGCGNCTC TGGGCCCCCA AAAACTTTTTT TCCTTTTNTT TNACAAGTTC CTTTTCGGN 600
 5 NATTTTTTAC GGGNTTNTTC CCCCCGNAAT TTNTTGCCCC TTCCNAAGGT TTTTTCOCCC 660
 TMTTNTTTTA NCCNCTTIN NCAAGGGGGA AANNITTTTN CTTCOCCNC CCGGGAGAA 720
 ANNGGGGANT TTCCTTTTTT TTAAANGEN NCCCCCCGN ANGNITTTIN CCCCCAGAA 780
 10 NATTTTTT 788

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1321UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GATCGAATTC GATTTCCTTT CGGTGCAAGG AAACAGAGCC TTGTTAAAG TGGGATACGA 60
 AGACCGTGCC CAATTTTGGT CGGCCCTTTC TACATACATC TCAAGGAGG AACTTATCGG 120
 30 CGTGCCATTA GTGGTCCATA TATTGCAAGA ATGTACAAAG TTAGAGAGGA TGAAGGTTGG 180
 GGAGGACGAT GAGCTATGGT TCAAAAGGAG TTTGGAGGAA NAAGTANOGG ATTCCAGTTG 240
 TAATTAGCTA CAAAAGCGGA ACGGGTCACA CTAAAATTCC ATGCGCTAAC TTTTCCACTG 300
 35 AAAGAAGCCA CATGAAGCTT TTATATCTTC TGGGGCTCCT CTGGGACGCT TACACGTCCA 360
 GAACTGTTTC CCAAATTCC TCGACGTTTT CGAGGTTTTA AGAACCGATC GGTCCTCGTG 420
 CTTGCAGAGA GGTGCATTTG ATGGGGCGAA AAATGGTTTT TCAACCGCG AGGGTGGTTG 480
 40 TTCAGGAGCT TTGTTAGTTC GAAGTTGGAG CGCCATTCCA TTGATTGCC CTGTCTCTTC 540
 CTCCTNGCA CTTGCGCTT GCTGCTATGT TTAATTACTA NAAGCACGA NCCACACTTA 600
 TCTGGTTTTT TTTTCTATC CTGANACTOC CTTGAATTAT TGCTCTCTT TGAATTCCC 660
 45 CCTGTCCAC GTTNGTTACA CTTTGTCTT GAATATCTT CTTTCCGAA GCACCATNT 720
 TTATAATTAG TCCTATTGAC CCCCCCACC TGGTTTTTGT TTTCTTCCA ACANGTCTC 780
 TTCTCACTN AGNTTGTAT ACNGAATGTC NACCC 815

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1322RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

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10  GATCCAGGAA ATAGTACAAC GCCCTGGAT AATGCCAGG ATTCTGACT CCTAACGAAA      60
    AGCCTCTCCT CTTCTAATTT CTTATTAAAG TAGTTAGCTG CAAACTGTAA CAAATCCCCC      120
    GGCCGTCCTT GCTCCACTTC TTCTGGAAT GGTCCAGTA GGTCAGGTG TTCCTGTGAT      180
15  AAAACCATCG AGTAGTTTGT TGTGTGATG AGAAAACCTG CCTATAGCGG AACCAAAATG      240
    CTCTAGTAGT GTGACGACAC CGTTTATCC AGTTTGCTAA GCAGCTGCC TAGGTTAGGG      300
    AGAGTAGAAA GGTTCATTGG ACCCGAATTT CCTTCTGCGC GCGCGAAGC ACGTTAAATG      360
20  TGATTACAGT GATCAGCTA CTGGGGCTAA CTACCAATTG AGACAGGCTA GTTGTGAAG      420
    CCTGAGGAGG TCTCCGAAAA GCTTGATGTG AGGATACTCG TGTTCAGTTA TCTTGTATGC      480
    CTGTATTGAT CTGTCCGTGA GACCTCGAGC TCTTCGTCCG TCAATGCCCC GCGCCTAGAG      540
25  AGCTAGGTG ACTCCGAGTT CTACAAAATT TCNAAACNCC TTGAAAATTC NCAACATTGT      600
    TMTGGACCAT CNANTTCCCC NCCCTGGGAA NNAAGCCCTC CANCCTTTTT TNACGTTGCT      660
    NACTTNCNCT CTGAAAAAAC GTTCNATTTA CCTTNTTNTA CNOGGCAGGA AACCCCCCAN      720
30  TTCTTTTCC ATNACCGGT ANCTNAAAGA ATTTTCTNGC CATGNGGTTT ANG          773

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(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1322UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

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45  GATCTTCACA ATCGACGCCA CGTCCATGCG GATGTTCCGC CGCACTGCGG TCACTGTGAG      60
    ATATTCTGAC GGAGAGAGCC GGTACGTGTT GATCATGAAG TTGCGCACAT CCTTGTACGC      120
    TTTGGCCGTC TTGAACCGCA CGAGTCGTT GAAAAAGTCG GGCAACGCGC GACGCTOCAG      180
50  CTCATGGATC TGGTTGAAT GGAACCAAGA GGCAACGAC GGCAOGATCA CCGGGTGCGC      240
    CTGCTTCGCT AAGAAGCGCG CCGCCTTGTC CTCCAATTTT TCGCGCTCCT GCTCGTAATC      300
55  GATCTTGGGT TGTCTCTGCT GCTGCTGCTG CTGTTGCAGA TGTGGCAGCA CAGGTACAGA      360

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TGGATTCAAG CTGCCCCGTG TGCCCGACGA AAGCGTTCCA TCGCCAGCGT TGTCAATATT 420
 GCCATCCTGG ACATCCATG GCTCGCTCAT CGTTATAAG AGTATGCCAC GCTACTTTCC 480
 5 CGGTTTAATA GCTTTCAAAC GGGTCTTGGC TCTGCTACCC CGCTTAANTC CACACTGGTT 540
 TWIGTTTTCC NCCATACCCA AANTTTTAAA ACCCATTTTT CCACATCAGC CCCATATCCT 600
 CCGTTTGGTN GNGGAAATTT GAAACCCANC OCTCGCTGG CGGAAAANNC TNCCTATGGA 660
 10 CCCCCCTCCC NTCCTTCAAT CGGTCCCCCT NACCAAGNNT TTAGCCCCCC GGNANANGAC 720
 CAATTTGGTC CTTCGGTCNC TTTCCTTNT TAAATTGAAA AAGGTINCCC TTTGAAAATT 780
 AACCNGCCC NCTCCCCC GANAATGGT TTTTTGT 817

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1323RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

GATCAGTTTG CAGGGACCAT GAGCAGGGCG GCGACGAAA GCAGCTCTCC TTGTACACC 60
 TCCGTGCAGG GGCTCAACAC GGCCTGCAG GCGACGACG ACGAGGAAGA GGAAGATGCG 120
 GCACCGTTTT ACATCCATCC AGATTTGAGG ACATCAGC TCTACTTTGA GAAGATGATC 180
 35 GATGAAGAGC CCTCCCGGC GCGTGTAAAG CGGGTGTCT ACATTAATCC GTATGGAGAG 240
 GAAATTTTCC CTGTGCGAA CTCTGGTCT ATCCACCAGC TGAAGCGATG CGATATGCTT 300
 GTGTATCCA TCGGGTCTT AATTACCACC TATTGCCATG GTGATCCTCC GGTACTTGCG 360
 40 AGGTGGTCTT CCAAGGAAG ATGAAAAAAT GCTACTGGTC NCTCCAATCA ATNNCAACC 420
 TCCGATTAGG GGGGGGGGNT TTTTTTTTAA ATTTTAACCC CCTTTGGGG TGACCCGNNC 480
 NAAAAAAG GGGGCTTGN NNTTTTTTTT TNGNCCCCC CACTNTTTC GNAGTTTTTT 540
 45 TTTTCTGGNG GGGGGCCCC CANNCGGA AATNTTNNC AAAAGGAAGN ATTTNCCCCN 600
 NANGGGGANT TTTTNTTAA NNAATNNAA AAAAAATNN TTCCATTCCT NNAATTTNN 660
 NTTTTNNNN CTNTTNGGN TTGNAANTT NACCCCCNC NANAANTTN TTTTTTTCC 720
 50 CCCCCCCCC CCGGGNNNN TNCNTTTTTT TNNNGATN 759

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1323UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

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10  GATCCGTTTT TCCAATATTT CACCGTCTTG TAAATCAACA GTTGAAAAAC AATGGCGTGC      60
    TTAATCGACG AACGCAGCAC AACCAGCAAT AGGCTTCGAA GCGTTCCAG AGGTGATATC      120
    GCAAAGTTGC TCGAGCACTA GAAOGGACTG GGTCAATTATA TAGGTGGTAG TAAGAAGTGG      180
15  GTAGAAGGAA GGGGACTATG GTACAGGCGG GCGTGGAGG CAGGGACGGC GCAGTGGGTG      240
    CCGCTCATGG GCATGGGCAT ATGCGGCAGT TGTACGAGTT GGTTTACAAC CGGGGGGGGG      300
    TGGGGACGTA GACGTTTACT GCGGGAOCTG CCGCGGCACG GGAOGCTTGA CCGGAGCAAT      360
20  GTTGTGTGCA CGCTAGTGGG GCTGTACCAC TCGATTCCGG GCGACATCCC GCTGATTAAAG      420
    ACGCATTGNA TCGCCCGTGG GTGINTCTGA NCNAAGTTGG ACCCNGGAAC CTGATTGTTT      480
    TGTGGCNAGA ACACATNCCC TTGTGGTGG ACCCACCGA NAATTAAACC GCCCCNOCOA      540
25  GACNAGCCGC CCTCCCCCN GNGCGTTTGG GTTNNNGCCA TTINGTCGGA CNTCCAAGAA      600
    NITTACTINGC ACCGCGGNG GCACCGCGN CCGGGCACTT NITTCAACNC CNTTCCCCC      660
    CNTGGGGGGG NCCCCCCCCT TGAAAAANNG TGGGGGGGAC CCGTTGGGT CCCNTTCCCC      720
30  CCATTGNATT TTNTTTANA NANNACCAAC CCGCTCCCT TNNCCCCACN CAAANNNGT      780
    TNGTTAANCT NCCCCNTAT TCINCCCCC CGNCCNTAT TCNACCGN CNGT      834

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(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 785 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1324RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

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    GATCCTACCG GGATGCACGA CGCATACAAG TATATCAGG ACCTTGCCGA GGAAATGGGA      60
50  CATAAAATTG AAGGAOCAGA TCACAATTGG TCGTTCTTA TCATAGCCAA GATATATATA      120
    TATATCTGGG ATAATTACAG CGCTTGGTAT GTATACCTOC TACATACAAA TACTTACATA      180
    CACATAAATA TAATACAGCT ACTTGTAAAG CGAGAAAGGT TACTTCTGGA GAGCCATTAG      240
55  AGACGCAACG AATGTCAAAA TCAACCTUGG GCGGACTTCA TTGATATCTT CAGGAACCAA      300

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CCAGATTAAA GCACCAAGTT TTCTCGGAT AGAAATTGCC AATTTAGCGT TTGCATACTT 360
 CTCCTCTCTT GTTACGGGCG GGAGTAACCA AGTCATAATC CACATATCCT GGAGCTAATC 420
 5 CGTTCAATAC ATCCAATAGG AAATGGGCAT TGCTCAACGA AGCATCCCTG GAAAGACATA 480
 TCCTGCTCGA TTGTCACCC TTGGCACTTG CCTTGCGCCC ACTTTAGATC TGACATCTGA 540
 ATNCTCTACC AAACAACTIN TGAGGANATN TGTTTGACAA GTTTTCTGCN CCTCACTGCC 600
 10 AACTAAACT AAGGTCACAC CTNTTTGCTT CCCCAATTCT AACCCCTTNN GCCCCOCAA 660
 AAAAATTINA ATTCCAAAT TCANNCCCTN TTTGGTTTCC CCCCCAATNA NCNINAATTT 720
 CNNCCCTNN CTGGNCCCGG NNGAAACCN TGAAATAACC CCCCGAATAC CTNCTTTGCC 780
 15 CGAAC 785

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1324UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

GATCTTAAAG AGGCTCAGTA TGCAGAGGCA GTTTCAGAA GAAGACAGGC TGGGCTTGA 60
 AATCCCTCAG CTCCCGCGGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGGCCA 120
 35 GCAAACGCGG CTGCGGGGCG CGCGCTGCAT CCTGGGTGCC CTTATGAAC CGAGCAGGGC 180
 GTGTCCACT GGTGCAGGCC AAAAGCGGGA CTAAGACTAC TCGTGTGTC ATGAGAGCAG 240
 GCTCTCACT GAGAGCAAGA TAGAOCAGTA CTTGAAGAGC GAGGCGCAA CGCACAAAG 300
 40 CGTATTCCAC CGGACCGTC CCAAGACGA CAGCTACCGC CCGACTTGC AGCCGCTCTG 360
 CTGGACAGC TGGACGAAG GAAGGGAGAG CCGCGCGCG CGCAGAGCGC GCGTTGAGA 420
 AGCCCCGTT TGGTGGGTGN AGCATCCCC GGANATNCT CCCAGAAAA ANNTTTTGA 480
 45 ACAAGCGGCC CGCCCGCCCC CCNCAGAAC TCCNTTAGC GAACNTTNA AGAAGATNT 540
 TNCCANTTIG CGNCCCTNCT TGGANAATGG TGGCCNGCT TNACNAAAG CTAGGTGNC 600
 GCGCCGAAAA NCACTTTGCT TNACCGCATN CTCCCCGAA AGANAGANAG NTCCCCNCAC 660
 50 TTTTNGCAA TTTTNTCCCC CGGANAAG GTTCCCGTNN ANCGANGGG NGGCGANNA 720
 ANAAACCTAC NCANTTINAA CATTCCCCC CNTTTTTNC AAAAAAGANA ATGNNTTTTT 780
 CACNTGACA ANTGATNCT TTTNTGAAG GNGNVAGTAC CCCCCGCTTG CTTNTCTTC 840
 55 CCTAGANCT NCNATTTTGT TTTNT 866

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1325RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```

GATCAATGCG GGAGTGGCAA AAAGCGACTC AAGGTGAACG TGTTTCAGCA CTGTTTCATGA      60
TGGGGGGTGG TCATTTTGCC GCAGCCATCG TATCTCACCA ACGCATAGAT ATCAGTGGCA      120
ATGCCAAGAG GCATGGAGAA TCGTTACAGG AACAGGCGGT GCACTTTCTT GAGCACAAAA      180
CGTTTCACAG ATACACCACG AGGCGGAAAC AAGGAGGTTC ACAATGGGTT ATGGATAAOC      240
CCAAGGGGAA AGCAAATTCC GCAGGCTCTA CGCTACGTAG ATACAATGAG GCGGCATTAC      300
GGAATGACGT TCAGGACCTG TTAAAGAAAT GGAGGOCATA CTTGGAACGC TGCGAACACA      360
TATTTATTAG GGCAAAAAAT GTTGGCGACA GGAGGTATT CTTTACGGAA AATACCCCAT      420
TGACCAAGGT TAGACCCGAG GATTGGGACA TTCCCATTC AACCOCGTAG ACCTACCACA      480
AATGAGCTAA GGCGAGCATG GTGCGAGATA ACATACTTGA AGAAGACATT GAAGCCCAGC      540
CATCACATCG GAGCGGCATA CTCCTAAAGC GACAATGATC CACTGCCAAT AAGCGACGTT      600
GTACGCAACT TAACCCCGNG GNAAACCTTA NCAGGAACGG CTTCTTTCTT TGGATTGNAG      660
GCCCCNNNT ATTCCCTNVT CNAANNCNT NNTTCCCCAA CCTCTTTTTA AACCCCCGGA      720
AAAANNVTIN AAACCCNCNC CCCCCCCA                                     749

```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1325UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```

GATCGTGGCA TGTCGTATGT GGTATTTTGA TGGGGGGCGG GGTGGGAGTG CCAGCTGGAC      60
TACGAAATCA AGGACGAACG TGAATTTTCA GCGGCCCTAG ATACTGTCAA GGTGGGCTA      120

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GCGCCCGAAA AGAAGTGGCC CTGCCGCACG ACCGTGCAGC CTGGGCGTGG AGCAGGGGGG 180
 AACCAACACGC CGACACGCGT ACCTCTGTCC AAGCTCTTTG TAGGTGOGAA AAACACCAAG 240
 5 TTCAAGCCAG TGATGCGCTC TGCGGATGCC GCTATGCGGG CAGGCAGTGC CGCTTCGGGC 300
 CGCCACTGTG CGCTATTGCA TAAGACACAG ATAGATGACC CACTGGTCAT GAACAAAGCC 360
 GGTGACGACG AAGTGAAGT TGTAGTCGAT CCTATTTTGT CAAAAAGCT ACGCCAGCAT 420
 10 CAGAGAACAG GTGTGAATT CATGTATGAC TGCGTCGGG GGCTCGCAAG GTCCGAGAAG 480
 GACGATGATA GAACAGTGAT GATCTTGAA TATGATAGTG ATGTCAAGGG TTGTCTGTTG 540
 GCGGACGAGA TGGGATTAGG GAAACATGC ATGACGATTG CTCTGATCTG GACGCTACTG 600
 15 AAGCAGCATC CCCAGGCCAT CGTCTGTTC DATGCTCCGC AATTGGGGGG TTGTTTTC 660
 AGGGTTTTTT GCCANAAATT CTCNIGGTAT GCGCGGTGA CTCTGATTGG CACTGGGAA 720
 AANGATTTCN CCNATNGNN GCGANGAAT AAATTGGANC CTNGAANCN ATTGCNAANT 780
 20 ACCCCCCAAA ANAAAAAATG N 801

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 774 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1326RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

35 GATCGAATTG AGTCAGATTG GATTGOGATG GCTACTAAGC AACGTGCATT GTCAGACGGA 60
 CCGAATCAGG TACACATTGA AACTCGTGAG TGGCTAGTGC AGACAATCAT AAATGAAAGT 120
 TGTGGCTGGA GCAAGGGAAC TGCGATGCGT TAACTTTCTC AAAACACTCA TGGGTGGTCA 180
 40 AAAATCAATC TATTCAATAT ATAGTATATC AAAACATTAA ACCAAACTAG GCGCCAGAA 240
 TATTGCCAAA ACATTGCACT GGAGTATTAG TATGCAGAGA AGTAGCAATG GCGGCTAGC 300
 TGGTTACGTG GCATTCAAGG ATGACTTATA GAAGCCCATT AATCATCTTT TAGTGACAGT 360
 45 AAGATCAGAC ATTAAATAAC GTATCGAATT TTAGGGGAGA AGTCATCACA CTTGCATTAG 420
 TATACCGCAA TAATTGCGG ACCACATCAG TTAATACTGG GCATGGTTTC TAAAAAGCGA 480
 AACTGGGTTC ACATTCAAGT TGTPTTGCAA CATAGATGTC TCTCTCATG CTGCTTCTCG 540
 50 GTTGAATAAC CATGCTTCAG TAGGCACCGT TCCAGTATT TGGTAATTAG TTGCCAGACT 600
 CCTTTATAAA GGATGACCCG AATATGANCT TCATTAACA TTGCGNGAA AANANATTTG 660
 GCANCCGTAN ATATTTTCCT GCCAATTGAN ACGTTCINT GAACCCCTNC TTGGGNGOON 720
 55

GCTTCCCAAA AACGAANTTC CCCGTINGNT NTTTTATAGG TNCNAAGAAA AANA

774

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 779 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1326UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

GATCAACAAG CGTTTCGGGC AGCTGCGCGA GAACCTGCGC CTCACCGGG TGACGCGGAG	60
CGGCAAGCGG CGGCTGTTTG TGTGCCACAC GTGCAAGCGC GCGTTTGGC GGCAGGAGCA	120
CCTGATCGGC CACAAGCGGT CGCACACGAA CGAGAAGCGG TATATCTGG GATCTGCGA	180
CCGGCGGTTC AGCGGGCGGG ACCTGCTGCT GCGCAAGCG CACAAGCTGC ACCGGGGGAG	240
CTCGGGGAC GCGCTGCTGA AGAAGGGCTC GCGCGCGGG CAGCGGCTGA GCGGGCGGT	300
GCGGGCGGC AAGAGCGCGG AGGGGCTGG GCGGGCGGC AAGCCAGGC GCGGCTGTC	360
GTCTCTGGC CAGTCCGGG AGAGCTACGC GTGGTGCGG CCGGCAGCG CCGGGGGGG	420
CGAAGAAGGT GCAGTTCTCG ACGCGCAGC TGCTGCGGT GGAACGACG CAGGAGCGGT	480
CGACGTTTAC GCGCTGGAG GCGAAGGTT GTTGCAAGAC GTGAACAGC TGTCGCGCT	540
GGACGGACG CCGAGGAGG GAGCTGCAGC CCGGTGGC GCTGTGTGG CAGGCCAGC	600
ACACGCGTC GCTGTTTGG CACCTTCCC NGTTGGCGT CCTTACGGG ACCTGCTTGN	660
CGCTTTTGG CCGAATTGCA GGTGGAAGG GCTTNCOCG CGNGGONCN CCGCCCCCC	720
CGCATCCCC CCGTNNCCC AAAATTTCAA GTTAACCAA NAACATCCC TTCTGCGT	779

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 763 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1327RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GATCCAAGCG TCTGGAGTAT GCTAAACGAG CGTCTCATGC CAGGAACAAC GTATTATCTC	60
GTGTAACGCT GTCTCGAGC CTCGAGCCAA ATCTGACCGT TTTTGTGCTA GAGCATACCC	120

AAAAAGAAAC ATCTTGATGC GCTAAACAAC ATGACAATGA TTAGOGOGAG GATGOCCTTTC 180
 5 ATGTTCTTAAA TTCATGCCTC GAGGTCCAG TCGGTGCGC ATGTAGTCCT GCGGCGGAT 240
 TATATTGGG CGTAGCTGTG GTGAAACATC GCGCTAATT GACGGATAAG CAGCTGTGTA 300
 CCTTATTTTC ACTATTTCTT TTCACATACC AACGACTAAG GTTGATTCCA AGAGGTACTG 360
 10 ACTGACCCAG TGGACAGCGT AGTTATOGGA GTAACCTGGC AATGTCTGAC GGGTCTCGG 420
 GGAGCGGAGG AATGGGCTGC TCAAGGCGA CGACGCGGA GCTGACGAAG GAGCTCAACA 480
 TCCCCAAGGA CGTGGCGAGC GGCATGAGGA AGTCCTGTG GTACGACTTC CTTAATGTGC 540
 15 CTGGCGGGGA CGACGAGCG AGCCATCGG GACGCGAGC ACAGGACAG CTGAGGACGG 600
 CGCGACGGA ACTGAAAAC CAAACGGCG AANGGCGCN AGGGGNGG ANCAANGNG 660
 GAAAGGGGA ANTTTGGCGA NTACNCITGT TGGCCNCCC CCGCGTTCC GANTTTGGGT 720
 20 TGNCAAATC CCTCTCTAC TTNCAACCT NCTGAGTNA AGT 763

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1327UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

35 GATCGGAGG GTGCTGGAG CGTGTCTTG TTCTGTCTCT GCTTGGCTAC GCGGACTTG 60
 GCAGCGCGG CGCTCTGAG CGTCTCATAC TTGCTGCTG CTACTTCAT GGTTCCTATC 120
 GTCAAGGTG AGCAACTGG ACAACAGCAC CCAGCAAGG TTGCATTTAT ATAGTGCTA 180
 40 CCTGTACGAT AGGGGACTGA TGGCTCTGG ATGCGTATCT ATCTCATTC GGAAGTTCT 240
 CGAAACGAA AGCGCCAGT GCTGTGAGC GACAATAGG AACCAATG ACACAATAGT 300
 GCGGTGGC GACCGATCC CTGCATGAAG ACCGAATGCT CGAGCAGATT CTTGTGCGG 360
 45 CGTCAGCGG TAGCGCGCT CGTGTGTGG CGGAGCGCG ATATGCGATG GCACCGGATG 420
 GCGATGTGCT CGGCGCTGG GATTAATCTA GCTCTTGGG GATATGCTTC TGTAGGAGGA 480
 AGAGGGGTA GGGAGAAGC CTGGACGCG GCTTGGGAG CTCTGCAAG TTGCGGGGC 540
 50 GTGCGCGGT AGGCGCGGC ACACCGGNA AATNCGNGN GANCTNGTN CCTCCNTTC 600
 CCCCCCAA ACTTGGGGC NTNCCNCC CGAATNNCA GNGNCCOC NAAATCTNA 660
 ACCCCCGNA GGAAAGNNTT GCGCTNTGA NCAANNACN CGGTINAAA NTCCCGGGG 720
 55 TTTGNGGCC CCGAAAANG GATAAACCN GGNACNACC TTTTGAAATC GCGTTTNTT 780

TTNCCCCCAN ACNT

794

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1328RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GATCTCTTCT	GCAAGTTTCT	TTATCGGAAG	CCCAGGCTCT	GGATTTCCTT	TCTCAACACC	60
AATGGTATTG	TCTTCGATAT	CAGAGAAGGA	GCGCTTCGAA	TTTTGGGCAC	CACCATATGG	120
ACTCTCTTCA	TTATTTTTCG	TATTTTCTCC	ATCATTTCG	CTTGCCAAAG	AAGAATCCAT	180
CGCACCCATT	ACATCGAATT	CTTCATTATC	AGCTTCTCCA	CCTGTGTAG	TATTTGTTTC	240
ACCATTTATTA	TCTGTGTGCT	TATGTATTGC	ATCAGGGGCC	ACACGGCTCA	TTTGTATCAT	300
GCTAGATGTA	TATGGGACAT	AATCCACCTT	TTCCAACAGA	GGACCGAATC	GCTCAACCAA	360
GTATTGATTT	AAAACCAGGA	AGTTCTTTGT	ACTGACCTCG	GCATATTTCCT	GATCTTGCCC	420
GAAACGTGCC	GAAATTACCT	TAAATAAGTC	GAGCAAGCAT	GAGTTGGCCA	TGTTATCAAA	480
GTAAAGATTT	TCTGTAGCA	GCTGACAAAT	TGGATCAAAA	AGATCTTAGA	TATGAGATAG	540
TTGTGATAAA	ATTCATCATT	TACAGCCAAG	ATACCTTGA	TACCCGAATC	GCAGCCAGCC	600
TTAACTGTAT	AATATGGATG	GTTCATTAG	TTTCAATAG	TCAATAGATG	CCATTTTCCA	660
ATATNAACCC	CCCTTGACAG	CATAATATCA	GTTCNIGTT	NINATAATCC	CCCCATTTTA	720
CCAAACCCNC	NCNGTTGATT	NCCCNCTC	CACCCCT			757

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1328UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

GATCGGAGGT	ACATAAGTGC	TCTACCGACC	AACCCCGCTC	TCCATGCATC	AACCAATGGA	60
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GTTGAAACAG TTGACTGGCG AGCAGGCGGC CGCACTAGAT GGGGAAGTCA TGGGCCCAGA 120
 CGTTGGCTAC TGGCTGCATC AATTGATGGA GCTAGCAGGT CTGCGCGTGG CCGAAGTGGT 180
 5 CGTGCGGCAT TGGGGGCGCG CACAGGCGAA GAAAAAGGTG CTGTGCTTAT GTGGGCGCTGG 240
 CAATAACGGC GCGGATGGCT TGGTTGCTGC ACGGCACTTG CGGCTCTTGG GCTATGACCC 300
 TGTTGGTCTAC TTGCGCGGGC TGTOGGCCAA ACAGCCCTTC TAGGCACAGC TTGCCAAGCA 360
 10 GCTACACTTC GTGGGTGTCC CAGTGCTCTC CGAGGGCGAT GACTGGCGTG CGCATCTTGA 420
 GCCACGTGAC ACGCTCTGGG TTGTGGATGC GCTCTTTGGC TTTTCTTTTC GTCCGCGGCT 480
 GCGCGAGCCC TTGCTAGCA TTGTGCAGA GCTCAAACGC CATGAGGATG ACATCCCAAT 540
 15 TGTCGCTGTC GACATTCCCA GTGGTTGGGA CGTTTGACGC AGGACGCTCA CCGCTTCAGA 600
 CTTATGCACG TGTGCTGATN TCTCNIGAAC GCGCGCCAAA AGCTGCTCCC NNCACATTG 660
 AAACTGGTTT TTTACCNCCC ATTANTTTGG GNGNGTTTC ATCCCNAAAC CCGCGCCGN 720
 20 CCTCCNTGTT TTTANTCNCT CCGGATATCC TGNCCCATC CANANTGGGT TTTTGANITG 780
 CCATTCNNIN ATCT 794

(2) INFORMATION FOR SEQ ID NO:456:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: DNA (genomic)
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1329RP
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:
 GATCCGGTAC GCGGTGCTGC ACTTCGGGTT CTTCGGCTG GGCTTCTGGT TCGCGTTGGT 60
 GCGGTGTAC GTGCAGTTCA AGAAGGCCCG CTGTGTAGTT AAGTAGAATA TAGTCTAATG 120
 40 CTATGCAGGG CCGCGGGCGG CGCGCGGCGC GCGCGGCGG TCACTGACG CGGATC 176

(2) INFORMATION FOR SEQ ID NO:457:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 50 (ii) MOLECULE TYPE: DNA (genomic)
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1329UP
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GATCCCCGTC ACGTGCCCGC GCGCGCGCGC GCGCGCGCGC CCGCGGCCCT GCATAGCATT 60
 5 AGACTATATT CTACTTAACT CACAAGCCGG CCTTCTTGAA CTGCACTAC ACCGCCACGA 120
 ACCGCCACGA GAAGCCCAGC GCGAAGAACC CGAAGTGCAG CACCGGTAC GGGATC 176

(2) INFORMATION FOR SEQ ID NO:458:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 767 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1330RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

GATCTTGAT TTGACATTGT CAATGGTGT AGAGGACTCG ACCTCAAGCG TAATAGTTT 60
 25 CCTGTCAAA GTCTTCACAA AAATCTGCAT ACCTCCCTC AAGCGCAACA CCAAGTGCAA 120
 CGTAGACTCC TTCTGGATAT TATAGTGGGA CAAGTGCGG CCATCCTCTA GTTGCTTACC 180
 CGCAAAGATC AAGCGTGTCT GGTCTGGGG AATGCCCTCC TTGTCTGGA TCTTGAATTT 240
 30 GACGTTGTCA ATGGTGTGAG AGGACTGAC CTCAAGGTG ATAGTTTTC CTGTCAAAGT 300
 CTTCACAAAA ATCTGCATAC CTCCTCTCAA GCGCAACACC AAGTGCAACG TAGACTCCTT 360
 CTGGATATTA TAGTGGACA ACGTGCGGC ATCCTCTAGT TGCTTACCTG CAAAAATCAA 420
 35 GCGCTGCTGG TCTGGGGGAA TGCCCTCCTT GTCTGGATC TTGGACTTGA CGTTGTGAT 480
 GGTGTGAGAG GACTGACTT CGAGTGTGAT TGTCTTTCC GTCAAGGTCT TGACGAAAT 540
 CTGCATACCA CCTCTCAAAC GCAACACCAA GTGTAAAGTA GACTCCTTCT GGATATTATA 600
 40 GTGGACACG TTGGGGCAT CTCTNNNTTG CTTACCTGC AAAAAATCAA CGTGTCTGT 660
 CCTGGGGGAA TGCCCTCCTT GTCCCTGATT CTTCTNNNTT GACATTGTCT ATGGGTNCCN 720
 AAGANTCCNC TCAATTNTG ANTTCTTCC CGNCAGGTN TTGAANN 767

(2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 794 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1330UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

5 GATCAGATGT TTTGTGCTAG TACGTGCGA TAGTACTAAA ATTACCATAT GGCATCAGC 60
 ATTATACTAA CTAGTGTGT TTTGCAGTAA GGGTAAACC ACCCATTACG CCTGTTGTAT 120
 CACCAGAATC CAAATGCGTT TTTGAAAAGA GGTTAATTGA GCAGTATATC GATGAGCATG 180
 GGGTAGACCC AATCTCCAAG ACAAGCTTGA CTAAGGATGC GCTAATTGTC ATTGCCCAGA 240
 10 CACCCCAGCA GTACGCGCTC GCAAAGCAG TTAAGTGGC TACGCTCAAC GCGAATTACA 300
 GCATCCCCAA CCTTCTGTCA ACACTACAAA ACGAATGGGA TGGCGTGATG CTGGAGACAT 360
 TTGAGCTGCG GAGTCAGCTG GATATGTGCA AAAAGGAGCT ATGTCAGCG CTGTACAAGT 420
 15 GCGAGCGCGC TATCCGCGTC GGGCAGCGG CGAAACAGGA GAATGATGAA CTCAGACACA 480
 CGTTGACGGA GCCTGACGGA GGCAGTGGC GGGCAGGCTG CCGATGCCCC GCGGCTTCCA 540
 GCGGAATTGA TTACCGCGAT GGCAGAAACG CACAAGAATA TGTGCAGCAA ACGAAAGAAA 600
 20 GAAGGAAATG AAAGCCAGGT AGTGACGGCA TTTGCTCTCG GAACAGCGCG TCCAAACGGG 660
 NTGCGAGGTC AACCGGTTTT TTGGTTACCC GTTNNVTGG TTCCGGAAAA ANAATTANCT 720
 NNCTTTTAA CCAAAGGCA GGGCCNNTT GCTGAACAAA AAGGGTTTTT GCTNCTNNAA 780
 25 AATINGCCNC TNAC 794

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1331RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

40 GGATCATTTCT CAGGTATTAG AGATTGCTGA TGGCACCGG CTTTTTCTTC AAGGAATTGG 60
 ATCGGAGGCG CCTCTAGAGT TGAAACGAGT TTATTATACT CAGCCATTGC TACAAGCATA 120
 45 TAATCAATAG CCGCAGCGCA ACTCTGAAGA TGATCTAAAG AAGGAGCATC TGCTTTTCT 180
 CGTAGAACAT TGAGAGCGGT TGCTCTATA ACTTCATGCT TATAAGTGA AGCACTCGAA 240
 ATAACATGTG ATAAAGGTGG AGAGTTGGCC AATGTGTCA AAGCTTCTAA TTCTGAAACG 300
 50 GAAATTAGTG CATACCCAGC AGCTGCAGCT TTATTCTTCA AATGATCGAG AGAAGGTGAT 360
 TCGGCTACTG TTCTCAAATC CAGAAGAAG TTGGAATCAA GGATTTCOA GTTCTTTTCA 420
 GATGCATGTT TCTTGAGGAA GCCTTCATCT GGGCTCTCG TATATCTGCT TCAACTCATC 480
 55 CATAGTAATC AGCAGAAATG ACAATCCATA TATGGTCTT GGCTTTGTT TGTAGTTAGT 540

CGATGGCTGG ATTTTCCCAT GGTAGAAAGA AGAATATCGT GCTCTTTCTT TTCAAACAAC 600
 AAATATCATA TGCCCTTGGC TTCTCCTGC CAAAATTOCA AAATTAGANA TTTCINATCC 660
 CCTTTAATAN TTCCACATGT TOCCAATTOC TOCCATNANA TNACTGTCTA ACTGTTTGTT 720
 GCNNACCCAA AAANAATTOCT TOCTNTCCCT TTTOCCANA TGCTOCTTIN CCAGTC 776

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1331UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

GATGTGGCG CTGCTCCAG AGCGCTGCC CAAGGCCAG CGCTGGAGC TGGCTGCAT 60
 CAAGAGCTAC GTCTACGGG ACGGCTGGA CGAAACCCCC TGGTGGGCT CCATGCAGC 120
 CCCCCCGAC TGCCCCGGC AGTCGAGGA AGCCAGGGC AGTGGGGC CGGGGACGA 180
 CGAGCTGGC ATCTTCAGC TCTGCAGCT GCTGGAGGAC CAGTCCGGT CCGAAGATGT 240
 CATCCCGAT AGCATGGATG CGGGCGAGC GGTGAGCTG GGCTCCCCG AGCCCCAGGC 300
 AGGCTCTCG CAGCACAGT TCTGCCAGA TTCCAGCAC GGTGCCCCC TTGGGCCCCG 360
 CCGTTAACC CCGTTGAGC GCGCGCCGC CTCCTACTC CCGTCCGGG TGTACACCGC 420
 GCGCGCTCC CCGCTTGA CTATTCCGA CAGCAAGGA TGAACCCCTA CGTCTCCAG 480
 GCGCCAGCC AGGCGCCAG CCGCCCTCC CTGNTTGAAG GTNNGAANG CACCCINCCA 540
 AANITTAGG GGTNGGCG CNGGGCGCT CAACGNITG GGTCCGNAA AANCCNITG 600
 CGGGTNNCC CCNCTTTAA GCGGCGNTG AACNCGNT NTTGGGNA GGGTTTCAN 660
 ACNCAACNG TNNNCCCC CTTTTTTCT TCAANAAG GCTNTTGT GTCNITCCG 720
 CCNGNNGN AATTTNTT TGIGGGCTG NNCCINAGA AAACNCCNC NGGNCNNG 780
 GGGAAAAAA AANTTTTTT CCNNGGT 808

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1332RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

5 GATCTTTTAT GTTCCTTTAG AGCAAGGTCA ATTTTCACAC CACTTCTATC ATCTTATATC 60
 CAGAATAATT TGAACAAGAA GGTACCGTCT AGTGAACGAC GTGATTTTCAT GCCGGCGTCC 120
 AAGGTTCATG AGTCATTACT GAAAATGAAG CAGCACTATA TCGAAAATAG GTTGCTCGAA 180
 10 CTACAAAAC TTCATCAGTT ATTCTGTAAA GATAACGTGA ATTTTTCCAA AAAAATGATA 240
 AATGTGAAG AAAGAAGAAT CGTAAATCTT CTAAATGACC TAGATGATGA TGCTAACTTT 300
 ACTTTTGAGA CTGTCCATAC TAATTTTGIG AATAATGAAC TATTCATGGA ACTACATGAT 360
 15 CACAAGTCAG TGATATGCG CGTTTGACA TTAGATACTG CGGAGGATTG CAATGCGATG 420
 AAGAAAAGGT TACGACCATA TACACTCAGC TCCTCGACTA TTTCAGGCTC AAGTTGTCCA 480
 ATATTGATGT AGATCCAACC GCCACTATGA ATTTNAGTTC CGAAACTCCN TTGANCAGTG 540
 20 TTACCTCCTT ATTGIGTTTG TTACNCAAT TGATCCCTCC ANTTTCOGAT TCTGGAAAAT 600
 GNGGAAAAC CNNGAAANT GCNGAAAAC CTAAAANAAG GAANACCGTT AACNGGGTTN 660
 GGAATGTCTA TTGGGGGGG GCCNNANCTT TTAAAGNNC TTTGNGGGG AANANNCCNN 720
 25 NCTCCCNINA AANTTTTTTC CCCNGGNNAA AAANTINTCT GG 762

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 798 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: PAG1332UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

40 GATCTTTTTC AGACGCAGTG TACTATCGAT GAAGCATATG ATTATTATAC AAAACTTCTG 60
 TCCGATACTA TTGCATTAAA CCGCTTAAT AGAAACGAAT TTTTGGAAG TTGCGACACA 120
 45 TTAGAGATGT ATGGAGTGC TTCTATTGAA AATGGCAAGC ATGGCAAAAA GCCAAACAA 180
 TTGGTAAAC TGATCAAGAG TACAGTTGAT GAAAAGCAGT TCCATGATGA AATATGTAAG 240
 ATGGACTTGC TTAAGAAATT GATAATATAA AAGGCTACGA GCTTCAATAT TATAATACGC 300
 50 ATTGCATAAT TTATTACATT AAATTGATAT AGGTATATTT TTCTTCGAAG AATTAATTCT 360
 AATCATTTCC ATGTGAAGAT ATCGCCCTCT GTGTTACCTG CGGATATTTT GACTCTTAGT 420
 ATATCTACAT ATTTTGGGGA GCCATTATTT AAACGCGCA GCTTGACTCT GGACCCAAGA 480
 55 GCCGTAAATG CAGCAGCTCT TCCTGAGGCG AATTTCTTCC AGCAATTGAG GCACCATGTG 540

CCGTCCTTTA ATTCCAGCAC ATATAACAGA CCGTCCCGTC CAATAACCOCT AACACAATTA 600
 TTCCCTTTCT TTTCCATCAT GTTTCOGATA CTGGACATTC OCTGAAATGC AANTTTAACA 660
 AGCCTTATAC CAGTGAAATC NTGCGTTTTG AAANATGCOO TGCCAATTTC AACCCGTGAG 720
 GTGCGTAACC TGAACTTTTT TTGAAATTTT AACCCCCCA ATNANINTTC NTTTTTGNA 780
 CCCCATGCCT TGTTCNCT 798

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1333RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GATCACCGGG TGAATATGCT GCTTGGCATA GTTGATATAC ATTGTGAGAA AGTGACCGG 60
 AAGGATGTCC GACTCGGACA CATGGGCGGG CTTGTCTCT AGGTAGAGGC TGGTCAGGTG 120
 CTTGGCTAAT TCTCGATC 138

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1333UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GATCGAGAAT AGCCAAGCAC CTGACCAGCC TCTACCTAGA GGACAAGCCC GCCCATGTGT 60
 CCGAGTCGGA CATCCTTCOG GTGCACTTTC TCACAATGTA TATCAACTAT GCCAAGCAGC 120
 ATATTCAACC GGIGATC 137

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1334RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

```

10  GATCATAATC CAGTCGCTGT CGAGATACTC GACAGGAATG GACGTCAGCG ATTTGCTCGA      60
    AGAGCGCGCG AAAACCTTGT CCGTTGGCTC CGGCGTTGCG GTGAGCGTCC CGGCGGCGGT      120
    GCCACCGCTC GACTGCAGCC GGCACGCTT CCGCATTATC TGGTTCATGG AGAATAGCGA      180
15  CGATACTGGA CGCTTCATGA TGCATTAA GGCACAACC TGGGCGTAT CATGCTGGCC      240
    CCGCCGGCAC CGGCCCACC GTGCCCCCG CAGGACAGTC CCGAAACGGC CTCGTCTTAA      300
    CCGACCTCC AGCATATACT GGTTCACCTG CACGCTTCC CGCCCCCTA TCAGCGGTGT      360
20  CGTCTTTTGC AGCAGAAOCA TCTCCACAG CTGTGTATAC TCCTCAAATA ACGCTGGTGA      420
    TGTACTGCG TCCCCGCGC AACCGCTCT CCCAACACC GTGTGCTCA AACGAGAGCT      480
    GCTACGGCTG GAGATGCTG GCASCAAGAG AGAGTGCTC CCTTCATTGA ATTGCACGAT      540
25  AGTAGGGTAC GAACTCATGC NCCCTATGCC CTACACCATG NANTGGTTT CTATTGTINN      600
    TNGGCCCCC NATNCTGTT CCAACININ TTANCTGGC CACNTTTTTT TNGGTTGCC      660
    CCGGAACCT CCTTCCCTTA ACCAATCTG GGCNCTTTC NCAACAGGAA ACCTTINIGAA      720
30  CACTTCCCC NAAANGTNGC GAANAAAAAN TTTTTTINAT TNCCTT      766

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(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 796 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1334UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

```

45  GATCTGCGC GGCTCGGCG AGCCGACAG CGCGCGCTG GCATTCTGG AAAGCGCGTC      60
    CGCCGCGCGG CGCGCGGTG GCGGCTAGT CCGGCTGTA CAAGTCGCC CGAACAAAC      120
    GCTTTTGAC ATCACTCTCA ACGGCTGCC CGGCGCTGCG CAGTACTAG CCTGATCCG      180
50  CGGTCGTGT GATGTGTCC GCGCGCGGC GTCCACGGG CCGGCTGCG ACGTGTGGA      240
    AGACGCGCTC GGTGCGAGC GCGCCAGCC GCTCGGCGT GACCTCTGCG CGGCTCCGC      300
    CCGTGTGTC GCGCGCTCG CCGTCAGGC GCTGATGCG CGCGCTTCC TCGTGGGCG      360
55  CGACCGCGGC CACGCGCTG CCGCGCGCG CGCGTGGCG GTGCTGGCG GTAGCGCGG      420

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CGCGTGGCAG AACGACAAGG TCGTCTGCGC GTGCTCCGGC GACACGCTGT GGCAGGAGCG 480
 CGGCTCCGCG CGCTCCGCGA ACATCGCATG AACTGTATAC TACATACCTG CTACGTTGTG 540
 5 CTGCGGCCCC CGGCCAAGCG CTNCTCCAN CGGGGGGGGC CCGGGGGGOC TTCCAACCTCA 600
 CCGCCGGGGG GCGCGCGCTG GCGCGAAAAC CCGCTTCGCG AACGNCCAAN AANNCCANN 660
 CCNTACNACN CCCANTTANC CAACACNTTC NTCAACGGGT TNVINGCCCC CCCCCGNVNC 720
 10 TTCTCCGGNG TTTTTTTTTT CCGGANNATT NCTGNTCCCN CGGNTCCCN CCTTATTTTG 780
 NNINGCCCCC CCCCC 796

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1335RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

GAGGCAACGG AGGTGGCGGT GGTATCAAAG GTCTGGTAGT CGCTATGTCC TTTCGGAGCT 60
 30 TTITGGGTTT TGTGGTCTTG CTITTTGTGG AGCTAAGGT TGGGCGGGC GAAATCACAT 120
 GCAGTGGGCG CGATTCCAGG TCCGCCAAGT TAATGGGANA CACCGGCGCG CTCAGCATAG 180
 TGCTGTGGGT CCTCCTATGT GATTGCGACC CAAACGTATG GTCCGCCCTT GGGTGTGCAT 240
 35 TTCTGAGCT TGTATATCC TCCGGGCCAC TAAACTGCG CCTACTCTGA TTCTCTGTCA 300
 GTAACGCAGA GTAAGACACA CGCTTGCTTC GTGTGAGCGA TAGTGTGCGA CATAAATTAC 360
 TATGCGGGGA NCCNINCCAA NPTTAACCTN TGNAANAAA ANACCCAAAC TINTTCAAAA 420
 40 CCAAANITC NATTTNGGN NNGAAAATN CGNTTGGN AACCCCCCGT NNINGGGGTTT 480
 AAATGGGGTT TCCAAAAAAA ACCCNCCANT TTTCCCCCC CCCCCNAAAT TINTAAAAAN 540
 NCTTTTAAA AANNINNTT NTGTGGNVC CCCCCCCCC CCGNAAAAA AATCCCCCN 600
 45 AAAAAANCNG GINTTTTCC CNINGGGGGG AAACCCCCC NAAAANNNN ACNINCNNN 660
 NNGGGNCC CCCCCCN ANCNNTGG TNCCTCTT TNANAAAANG GNCCTCAAN 720
 CNTTTTTTN NNNNNNNAA AACNCCCTT TCNNCCCCC CCGNAAAAA AATTTTNNN 780
 50 NNNNTTTN G 791

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1335UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

```

GATCAGATAA GAATTGAAGC TCAGCGGCTG ATGAGCGCAC TGCTTCGAT ACGGTGGTCC 60
TGTACCAGGC TGATAAAATG TGACACTATC ACCATAATGG GGTGTAGCT GGATACGATG 120
TCCGGATGCG GATGGACTGT TCTGAACAAG ACGTCCAAOG TGGAGGGGCC ATAGTGGGAA 180
ATCTAATTAA CGTATTTTACA TATCAGTGGC GATGTGTCTA GGTGCCGGCC ACGTCGATTT 240
CCTGTCACTG GACAGCGCCG TCATATAAAC ATTATGTGTT AGGGTTTAAA GTTGCTTTGT 300
GCGGTGGAAA ACAACGTCAC AACTAATAA AATCTAATC GAGCCAGCAA GCAACTATGT 360
TAAATAAGCC GAACAGTTTA CGATTCCAAG GGCAAGGTGG AACCCCCCAA GGCCCCGCTC 420
CNANTCNFTC CCTTACAAAA AGGGAGGGGG GOCCTACCAC TACCGAAACC ATACNGGTTN 480
NAAACAACCC NAANCCCGTT TTTCCCCCCC CCAAAATTAA ANANTGGGCG CCCCCTGNNC 540
NCNATTTGTT NNININANGG GGANAGGACC CCCCCCGGG GNNNGGNTCC CCCCNNTCNA 600
AAACCANNAC CCCCACCCCN ANAAAAANGG GGGGGGGGNN GGAACNCCC GATTTCATAA 660
AAATTTAAAA ATINNNGGAA ACCGNAAAAC GNGTGNNCN TNCCNNING AAAAANGTTT 720
TTGTNGNNA CANCCCCAA CNNTTNINAG MNCCCGNNC CCCCAAACNN AAAANTTTNC 780
TNGNANGGGG AACCAATCCC CCCCCNT 807

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(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 782 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1336RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

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GATCATGTTT AACCCAGATA CGAAACTGA GAAGCTAGAG TGGATAGAAA AGCTGGGAAA 60
AGTAATAGAG CTGAACAGGT TTCACCAACC ATGGGTAAA AAGTTCTTGA ATAGCAGTGA 120
GAATATCTC TGAAGAAAAG CATGACCACA GGATTACATA GAGTAACTTT TGTGCAAAGT 180
TTATCTGTAT GTACAATTC ACGTTATAAA TTTTAAAAGT ACTCGGGCAA AATCGGCACT 240

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TGGTAGCGAT AACGCACACT CGAGTGAAGT CCATCCAGTA CATAAACATT ATGTCAACTA 300
 CTTACCATT A TTGCCATTGC CAGATGAAGT ACCCATGTTC TGGTGATTGC CTGACCCATT 360
 5 GTTACCACCTT GCAGCGCCCA GGTTTGGGGG AATCATGCCA GGAAAGGGAA AGGGCGGGAA 420
 ACCCCGAACA TGGGTGGCAT ACCCATGGGA AACGCCAGGC GGCTGGCGCA GAGAACCGTT 480
 GTTTTGTGTC CGCCAAATTG AAGTTCCTTG GTTTNCCNNN CCCCCCGCA AAAANCTTAA 540
 10 CCCCCTCCCC CNGCCCCCN TCCCCAANC TTTCNNNIG NNGTTGGAGC CCCCAAACCC 600
 CCCCATATNT TNNCTGGGCC GGGGTTTNNN CCCCCGGGA GACCCCCCCC CGCNTTGTGN 660
 NTNTTACCCC CACCCNCCCC CCCCCCGGAA ANCCNGTNTT AAAAAATNCN AANAANNNT 720
 15 GGGCCCCGNG CTCCCCGGGG CTCCNTATA CCCCCCGNN GTAAATNNC NAAGNGGNC 780
 CN 782

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1336UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

ATCGGCATTT TAGGGATGAT CCGATCACC ACAGCTCGA GGCCTTGTA GAAAGCCAGC 60
 AAGCCCTGCC CGCTGTAGAT GTTGGCCCCC GTGGCAGAAA ACCCAGGGG CTTCGTGCC 120
 35 TCGTTGCGC GCCTGTAGAT CTGCATGCGC ACCTTGATCG TGTCCAATGG GTGGCAGCAG 180
 AGCGGCTCAA ACAGGCCCCG GGTCCCCGCC GCAACTAGGT TCACGGCCGG GTTGGTAGAT 240
 TTCTTAGACG ACATGTGGTT ATCAGGGTAT GGCTGCTGGC AACTTGCGCT GCACGGATCC 300
 40 GCTACGCTTC TCGTGGCGC ACCTATATAT ACAACGGGCA CGACGGGGG GCGGCCGCA 360
 CCTGTCTCC GACGCAGGC CAATAGGAGC TCGGCATAC CCCCCGGGA ACGGGGTGAG 420
 TCAACCCGGC CGAAGCGCG GGCCAATGGA ACCGTCAGT GAAAAGCAA GACTTAAAGT 480
 45 ACTATGTAGC TACACACTTA GGCTCGGCC ATCTGGGCA GTCTGGGAT CGTGGAGGC 540
 ACGTCGGGC GGCAGCCGTG GAGACGTGTT ACGCACCACC GGCCACAGT NTCCTTTGCA 600
 CNAACTTGCA NTCCCAAAN NCCGNAGCG CCGCGCTCN CGCCTTCTT TGCCGCAAAA 660
 50 AGAACATCCT TACCAACTTC TTGTGGCCT NCCACTTCTT NAACCTGTT CCNNACGAA 720
 NAANOCTACC CCCCCCNVT TTNCCGNAA TCNACCTTN TNCNINCTTT TACCATTNT 780
 55 NTNAAAGGG TGN 793

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1337RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

GATCTTAATT TAAATTTTAA ATTAAGTATT TATAATTTAG AAATATATAA TCTAGAGATA 60
 TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120
 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTGG TGGCATCTTA 180
 ATTTTATTAT TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240
 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTAA TTTAATATT 300
 AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA 360
 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420
 TTTCATAATA TTTATTTTAA TTAGTCTAGT AATATTTCTA TTTAATAGTC TCCCTTTAAT 480
 TGGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAT ACTTAAATCT 540
 AATAATTAT TATCTAAAGG TATATAAATT AATTAAATCC TTTTATTATA TTATTTAAAT 600
 TATTATTAAT AGTAAATTAT ATTATTTAAT TTATTCACCA TAATTTTTTT GATNATAATA 660
 TATCCTTTNN TAAATGGGGA ATTTATNAAT AATTANCITC NANGAATTTT AATGAANAAC 720
 CCCNTTANN ATAAAATTAG TTAANNNTGN NCTCAAAANN CCNATCA 767

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1337UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GATCAATTAA TAAATGGTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA 60
 CTACCTGATT TTATTGAATC AAATAATAAT TTCTTAATGA ATACTACTAA ATCATCATCT 120
 ATTGAGTTTA TATTAAATTC ACCACCTCTT ATTCAATTCAT TTAATACTOC TCTAATTCAA 180

TCTTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAAATG 240
 GTAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATTAT 300
 5 ATCATTAAATA TAATAACTCT TTAATTAGAG TGGTACCACA AGAATGCTGA AAGCATTAGG 360
 GGTGTGTACC TTAGCTCTCT AATTAAAGTT ATAAAATTAT CTTAACATAA AAAAATAATT 420
 AATTAAATAA ATAAATAATT AATTAAATTT AAAATGTTTA AAAAAAGAAA TAAATAATAT 480
 10 GTTATATTTA AATAGATCAA AATTTCAACA ATTTTCATTT CATTTAGTAC TACATCACCA 540
 TGACCAATGT TACATCATTT AGTTTAATAG GGTTTACTAA TAACCTTTAN CCTTTTACCA 600
 AANNANNGGT ANTANINGGA AAAATTATNC CCTTAATAAT AACCTTNATN AANNATINT 660
 15 ATATACCAAA ANNTTNIGAN ATTTNAAAAA ATATNGGCOG AANNNCNTA TTTTNGTAN 720
 CCCCCNCNTA CNGCNGAAAA AANGNTTACC CGTGTTCGCC CNTATNNTGN NINCCCNAAA 780
 ATAAAAAATG NGCCCCCAC 799

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1338RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

35 GATCAACCGC AACCGGTCAC TCANGTCAG ACGTTATAG AGACGGTCGT CGATGGCACT 60
 ACAAGGCGCG CAAATGCTTT GCTTATGAAT AGCACGGTTG AGGTGATAAC CGTTAAGGAA 120
 ATAGTGAAGG AGACAGTTTT CGTGACTGAG AAGGTGACTA ACTAACTCCA ATGCAAGCAG 180
 40 AACGCTTTCT GTCTTTTGT CCAAACCTAC CTGAACACCT AAACCTAGTT ATTACAACAT 240
 GAGTTTATT TACACAGTAG GGTGCCACAG CCACAGGAAA TATCCAAAGA AATTAGCTTT 300
 GCCTTGATAA AAGATATTCA TCCCTATTCA GCGACCCCTC TAATAAGCAT TCTCTAGAAA 360
 45 GTTCCTTGGC TTTCAITTTA AATCCTCGTG CACCTCGTCC GTAACAGTGT CTATAGTATC 420
 ATTCCGTATC ATTTCTGAAT GAAGTAGATT CCATATCAAC ACTTGCTTTG GTGGAAAGCT 480
 CATPATCTCG AGCAGTAATG GCTTCACCTC TATCCTGTTT CAACATACTT TTTTATAGCTG 540
 50 CCGGATTAA CCTCCCTGAA TTCCCTTAGG ATGCAGTGA GACCATGCC GATTATCAA 600
 ATTTATCTGT CCTTTAAANA ATTTTAAACC TTTGACNCCC CTATTATTAT TTTTATAGCT 660
 ATCGTAATGC TGCCNGANCC CCNVAANGAN ATGGGGTTTT CCNLTATTAN CTFTGGTTCC 720
 55 CCAANTTAAA ACCCNCCCCG GNCNCCCCC CCCCCACCN GGTGGGANAA T 771

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1338UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GATCAGGTTT TCOGGTACGT GAGAACGTAT CTAAGGCACA AAGGGCTTTG GGCGACTGTG 60
 CGGACGCTTG AGTTGCNAGA TACAGGACAA AGCTGTTACG GCGGCAACTG GTGCANCAOG 120
 AGCAGCCGAG GAGOGATTCT GCGCGAAGCG ACGGTGAATT CGAGCCAGCT GGTAGCAGGA 180
 GTGCCGGATC GTCTATTTAG TTGCGACGGG CGTCGGAACA GGATGCAOCT AAACGTTGCG 240
 GTAACACGGG ACGCTGAGCG GACGGCTGCT ACGCCGATAG CACGGGAGCG CAAACGACGG 300
 CAGCCGCTGT CGCCAGAGAT GTCTTCACCA CTGCGCGGTA GCAAGCTGCA GCGGCGGAAG 360
 CAGACACTTG AGGCCGGTCC GGGTCGGGCC AGTGGGACAC ACACGGTGGA CGAGCTGGCC 420
 GCGCAGCTGG AGCGCGGCTG CGAGCAGGGG TCGGAGGGGA AGCCGCGGTA CTGCTATGCG 480
 GTGCTGATCG GCGTTGCGAT CCTACAGTCG CAGGAGGGCA GCTGACGCTG TTGCNAAAA 540
 TACCGNTGNA TTTCNCNCNT CTCGCCCTAN TAACCGGTGT TTTTAACCCG GGGTTGGAAA 600
 ANANCTTCGG GACNACNINT TNCTTAAACA ANGGINTTGT TTTAAGGGGN GGNINCCCCC 660
 TCAAAGGANG GGCTTTTGG AAAATTAAGG GGGCCNITNA NGGGGGCTC NCTTNNOCAA 720
 AAAGGGGGAA TNATTTTNG GGGCCANATT TNNCAAAAT TVINCANTAG GGGGNTTNG 780
 NNAANTTINT TCNCTT 796

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1339RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

GATCATGGCC TTTAGGCCCA TGTCACCTT GCCCGCACCG ATCAACTCCG TCAGTGGGA 60

OGGGTGTGTG GGCTCGAGCA GCGCAATGTC CACACCCCTCC TGCTGAAAAGT AGCCCTTGGA 120
 CTGGGCTAGA AAAATCGCAA TGTGGTATGG CGCAGGCTGC CAATTCAATA GGAATGAAAC 180
 5 TTTGCTAGAC ATCTTGGTG CAGTCTCCGC AGCTACACC CATTCATOC AGGCTCATCA 240
 GCGGCTTTAT ATACCGCTGG GCCAAAGATG ATTGAATAAG GTTCGAGAC GGCTACTGGA 300
 ATACCCGTCG CGCCACAAGC CGGCCACTGG ATGCCATGGG CCAATGCGGA AGCCTCCTAT 360
 10 GTGACATGTA CTAACAGAGC AGCTTCTTTA TGCATTATC GAGCCAAAAC CAACATCTGC 420
 GGAATCACAC TTGACGGAAT CCGGCCCCAT GCGCAGCTGC TGGAAACACA AATCCAGCAA 480
 CTAATAGGOC TCAGTGGTAT AACGGCCCAT CGCTCTCTCA ACGCCAAGTC CCTCTCTGGG 540
 15 GAAAACATGT GATCAGCTGC TACATATTCA ACCCCGTCT TACCTCATAG CTGCGCATGT 600
 CCAGCCCTGA ACTGTTCGA CCTTCGTCT TCNGAAANC CTGATTGCTT TGCTTTAATT 660
 CCCCCCTCC NCCAACCATG TNCGCCCAT TTACTTCGGT TGCTTTTTTA TTTCGTGCAT 720
 20 TGTTTTTNTA AAAGNNCTG TTAANTAAAT NCCNTCATIN TGGA 764

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1339UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GATCAGGCA TTGTGATA GTGGCTTTGA TTGAAAAAT CCGATCATTA CCATGCTGAC 60
 TATACTCTA CTGACCAAG CCTTTGCAA CAAGACTGG GGCTTAAC TAATGTGTC 120
 40 TCGCCCAATG TATACTGA TATTTGGTT GATTGATGA GACCACCAA CTGTCTCTC 180
 TAAGCAACAG TCATCACTG CCGTAGCAAT AGCTACCTA ATATACAAC ACTCAGTGT 240
 GGTAGTAAA GAGAACAAC ATGACATCT AGCAATTGTT GCAGAGGTT TAAACAACA 300
 45 ATACGGCTCC TCTTCTTTA TCTGCGGA CGAGAGGCC GCATACAGAC TCTTGTTC 360
 TTACGGAAC TTAAGTACT TGAAGGCAC CTTCGCAG TTTGCTCTT CTATCTCAT 420
 GATAAGGAAG CTGAAGAGC AGTATGGCA CATATGAAA TTCCAGGATA TTTTAAATGA 480
 50 TATTTAAAGA AAGGTGTAC TATATATCT ATTCTTTGA TCGCTGTCC GAGGCTTCC 540
 CGGAAAAATG GTGAAACTT CGCTCTTTA CACACAGCT TTGCCCTTCA ACAGGATAGT 600
 TTGAAGGAC ATGTCTGTT GACAANNCT GAACCAGGT ACTGGTGNAA AATTINAANA 660
 55 TCTTTCTCC NCGAAANCN ANTTCTNCG AANTTAACG GAAAAAANC CCCCTCINN 720

CTTINTTTAN TAACCCCCC CAGGNTINTG ACCTTGATTT TTACAAAACC TTTTINTT

778

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1340RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GATGCGCTGA TATCGACAGG CACTTTTGTA TATTAGCAGT ATTCTTGACG AGATAATGCA	60
GTCAACTCCT ATATAGAAAC CGGATACAGT GGTA AAAACG CAAATGTAGG CAATTATATA	120
TTACTCTTCT CGACACCACT AACTTCTCGA TAGGGGCATA TCTTGTAAT TTGCATACAC	180
CTTTTCCCAA CTTTCAGTGG TCTGGTTGGC GTACTTTACA TGCATCTTGG CCCATTCTTG	240
GAAGACATGT GTGATACAAA ATTGAGTCTC CTGAAAATT ACAAATTCTT CTAAAATGCA	300
CTTTCTAATT AGCCAGGACC TGTTTAGTTG CTCAGCAATT GTCGGTTTGT CCGTTGAAT	360
TGCTGTCTGT AGTTTATCAT ATTCTGCACC TTAAAGTCC GGATTACTCT CCATAGATTG	420
AAGTTGTGCC ATATTATTTT CCACTCTCTT CTGCAAAATG GCTATGTTAT TCCCCGCCAT	480
AATTTTATAC CTATCAAAGA CCCCTTCAGT GCTATAATAA TATCTATGAA GGCTTTAAAC	540
TTACCGGATA GGTGTCTCTC CACTTCTGTA CGCTCCTTTC TTAGAGGTAT CGGCCACGCT	600
ATTGAGATGT TTTTGATATN NTGGAAATAT GANATTTAAA TATCTGTAAT AGTGCTCTTT	660
CCTATGGGT ANAANTGTTN CNGAATTATC AANCAATTCC TCCATCACNC NGCCAAGCAC	720
CCNCGTCTCT TCNAANACCT GCNCTNNGCC CCGTNCGGTT NNNNNA	766

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1340UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

GATCTGCTGT ACCTGAATGG ACTTTGTCTC CTGAAGTAGA AATGTAATGG CCCCTTCGGG	60
AATACATAAC AAACATAGCG GAGACAAAAA CAAAAGCGTT ATACAGGCAT CTGCGGTAC	120

ATCACCGTCA GCTCCTTGCA GACCAATAAG CCTTCAAGTT AAATATAGGC TAGCTATAAC 180
 ATATTATGTC GCTAAGAAGG GCCAAATCGT TGCCATCGCT TAAGAATATC GCTGAGGTGG 240
 5 CCAAGCCCAT CACCAAGGOC CCCCCGCTCC CCGTCTTTCG GTTTGAGGGC OCTGGGCTGT 300
 CCACATGTGG CTGGTATCCC ACCACCGTGC GCACAGTGCA CAATACCCCC AGTAAGGOGC 360
 AGACGACGCT GCTCTOGACA GCGAAGAAGG AGAGTGGGTT TTCCGCAATG AACCTGAAGG 420
 10 CCTTGGCGAA CGAGTGCOCG TCCCGAGGCT CAGGGTCTCC GGGCGGAAGT CGGATTTGAT 480
 CGAGCGCATTT GTGACTTTCG AGCTGAAGGG ACCGCTGGGC AGGCGGGGA CACGGCGGGC 540
 GTTCCACAGC CCGGGCACGA GCAGCGCCAG CGTATGOCGC CGTGGACAA GTTACCATG 600
 15 CCCGACATCG CGCTTGACAG AACGAACCCC GTGCCACACC CTGAGAAAA CTACATACTC 660
 CGGANICCNT CNTTGINOCN CCAAGGGGGT TTCCCTCCCC GTTACCNATT CCNAAAAGAT 720
 TTTTGCCNCG GAACCCANGA AGAAACCACC CGAACTCCCA GAAGGGGGNT TTNNNNANCG 780
 20 AACCGAANCT 790

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1341RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

GATCACATCC GATGCGAAAC TCGTATATTG TTTTCCACA ATGATGAAGG TGAGTGTGGG 60
 GCAGCAATTG TCOGGTTGAC GACTCCTATA GGCCCGGGCA TGCCCACTG ACCAGAAATT 120
 40 TGCAATGTGA TTCATGATGC AAATGGAAAC CCCATCCAAG TTTCACAGTC GCAAAAGAAC 180
 AGTTGGATCC TGACAAGGTT CTTCTGTTAG GCAGCTCTAT AGACACTCCG GTTGCTGTTC 240
 CTGCGGATGC AACGAAAGTG TCGGCCCATG CTTTACTCCA GGCCCTTTTT AACTCTAAGC 300
 45 AAAGTGAAGT AACTCCTGGA TGTATTACCT TTCAGCAAGT CAGAAACCTG ACCAGGTTCC 360
 ACTAGTTTTT TATTGAAGTC CGTGCTGTCT CAGTATTTGA AGCAGTTAGT CCCACGAATG 420
 AGAAACTTAA AGAATAATAG AATGGGGAAG ACTCAAAATT TACGGCTACC ATAAGACTCA 480
 50 CAGACTTACT CGACTCGAAC GTTTTGTGCC GCACTTTGTC CTGCGAGTCA TATACAGAGC 540
 CCTGTATGCG GTAAACACCC GGATGCGCTA CAGCAAGGTA CTGGCTACA AGACAACACC 600
 CTACGTACGC CGTTTCACAG TATGCAAATA ATNGAAGGCA TTCTCTCCNG ACTTTTTAGC 660
 55 NAAAGGNTTT ATNCGAAGTG ANCCCTGTCC ATACTTTATT CCCCNNANCC CNGTTTTTCA 720

AAAANCAGNG AACCATACNA TCGGTTTAAT AATGAACNTT CACNT

765

(2) INFORMATION FOR SEQ ID NO:481:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1341UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

GATCAGAGTA GATTTAGTAA AGAGGTAAOC ACCACTGTTC CAAGAAGTCC AGGGCCTTGG	60
CTTGACCAGC ATTGGTAAGT GCTGTGGCTG GAAATTTGCA CTAAACGGT CTGAGCTCAT	120
CTGGTTGGCC AAAGACCTAT GAAGTTTCAA AACACCAACT TTGCTGCCCA TTCTATATTG	180
AAATGTATGA CAGATGGCAG GTGCCTTACC GTACACTGTT TTATTGGTAA CTGGGTCTAC	240
ACCTTTCACG TTCACCTTTC CCACATGGAT CAACATAGAA ATTAAAAGAG AGCCAACCTT	300
AGCCTTGATA TTGTGGGGCC AAAGAACFTT AGACTCCTCA ATTGTGTAT TTCTAAACGT	360
GGTTTTTGCC CTTTGGACCA GCTTCTTGAA TTGGTTACTA TTGGCCCTAA CTTCCTTAAA	420
AATOGATTTT TCACTCTTCA ATAGTGCTTC CGATCTGTAT TCATCTCGA CAGCCTTACC	480
TATAGCCAGA ACGCTCCTG GTTGTCTTCA TACCTTCACT GACGCTCCA GTTAGAATTC	540
CAAGCCTTTA CCNATTOCCC AAATGTGTTA TGAANACACA TTTNCTING ANINACCCCA	600
AATTGAAATT ANGGGGNCTT TTCCANNCCN TGAAANAAAA TGINGAACGG NGTTTCAGTT	660
AAGCCCATNT ATCACTINGN ANCATTCNNN AAAAANGCTT CCCCCCTCCC TTTTAAAAAC	720
GGGATCTTNC CAAAAAACCN CCCCCTNAAT GAACCATTTT NCGAAANCCG GAAGCCCNNG	780
CCCTCNCCGN CTANATTCN GCAANNCAIN	810

(2) INFORMATION FOR SEQ ID NO:482:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 759 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1342RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

EP 0 866 129 A2

GATCCTGATT TTGATTTCGC CATGCTGAT GTTAATGCAC TCAGTGCTGA TGTCCTATAT 60
 ATCCAGCATG AATTATCCTG GTGGATATGC GCTATCTGCA TTCAACAAAT ATGTGCTGGA 120
 5 CAATAATATC TCGAATGCGA CCGTCCACCT AGATGTCCTC ACTTGTATGA CCGGTGCAAC 180
 GCTGTTTGGA CAGCTGCCGG ACTCCTACGG GATCATATAT GACAAGACTG AAGGTGATGA 240
 ATTATGAGAC GCATGGTCAT CGTTCGATTA TGTCAATTACA ACTGATCCCA ACAGCTCACT 300
 10 GCTCCTGTGT ACAGCTACA AATGGGAGCG CATCCAAACT ACTGAGGCTT TTGACCGCTT 360
 CGACCTTAAA ACTATACCGG AAATAATCAA CTCAGAAGTT GCTAAGGGAT TCCCTATCTT 420
 AAAAGATGCA ATACTCTCTG CAGACCTGCA ACCTGTGAAG GCTGCGTICA CAGATGTGAT 480
 15 CAGGTGCAGG GATTGAGTGT ATACATATAA AAGAGTTGAG AATTAAATAGA ACCAGCGCTC 540
 CGCTTACGGA CAGTTTCCAT ATAAATATTT ATTTATTAAA CTAAAAGTT CTGCGAGTTG 600
 AGGAGGAATT TGACTGCTGG AGATTCCGAC ATACTGAAAA CATAAAGTGC ACATTTACAG 660
 20 GATTGGCAG TTAATTGATT CCCCNTCCIN NNCTTAAAT GCTGATCNA ACTTNAACA 720
 TCCTATTGAA CCCCCTTTGG TGNITCAANC AANININIA 759

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 802 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1342UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

GATCGGGCAG GCGGGGAGC AGCAGTCGCG CGCTTCAAG GAGGCGCGAG ACTTGGGCGC 60
 40 CATCATCCTG ACCAAGATGG ACGGGCAGCG CAAGGGCGGC GGTGCCATCT CCGCGGTGGC 120
 CGCACGAAA ACACCGTGA TCTTCATCGG CACAGGCGAG CACGTACAG ACTTCGAGAA 180
 GTTCTCGCG AAGTCGTTG TGTGAAGCT GCTCGGCATC GCGACATCG AGTCGCTGCT 240
 45 GGAGCAGTTC CAGACCGTCT CCAACAAGGA GGACACCAAG GCCACCATGG AGAACATCCA 300
 GCAGGGCGCG TTCAAGCTGC TGGACTTTCA GAAGCAGATG CAGACCATCA TGAAGATGGG 360
 CCGCTGTCC AACCTCGCCA GCATGATCCC CGGCATGAGC GGCATGATGA GCGGCATCTC 420
 50 CGAGGACGAG ACCAGCCGCA AGATGAAGAA GATGGTCTAC GTGCTGACT CCATGTCCCG 480
 CGAGGAGCTC GAGTGGGACG GCGCTCTTCA TCGACGAGCC CGCCCGCATG CTGCGCGTGG 540
 CCCCAGGNC CCGGCACCTT CCGTCTTTCC GAAGTNTGAA AATATCCTCC NTTCCTCAG 600
 55 CCANATGATT GCCCCGNTT GCGCCANGGC GGCNANAACA TTGGCGGCTC CCGTGGCNTG 660

EP 0 866 129 A2

CCCGCCNGOC CCNGGNATGT CCCCCTCTCT CNCCTOCAA NGATNTNACC NGCCCNANCN 720
 TCNNTTINCT CAACCCNCCC NTGANNCCCN CATAATGGCT NNNCCGNGG GGNCCNGGGC 780
 5 CCCCATGCCC CCATTAGGCN AT 802

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1343RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GATCAACCAA TGTTTAAGG AAATTTTAA CGTTTTCGG GGATTGGGC ATCTTTCCT 60
 CTAATTGGTA GGAACATAG TCTGTAGCAC CCATGATATT AGCAAGTTTC CGCCGAGCT 120
 25 GAAGCAAACCT CTTAAGCCTC TTCACTTGTT TTTCGGAACA ACTAAACATT GCGTCCATA
 CCTGCTCCG AATAGCCTCT GAAGGACAAG CATTCAATAG TGTATACGGA GCATACCCAC 240
 TAGTTGGTAT CTTATAGTTA TTACCCATGG TGTCTTGGT GAGCTGACGA AGAACAAGAT 300
 30 GGCTAGTGCC ACTCGATTCC AAATCTTTGC ACGGAATCTT TATGTAGCTG GAAGATAATG
 ATTCTGTGTT GTTGATGAAG TCTTGGCCAA TAATGCTGAT GTTTTGGGAT AACTGTATAA 420
 ACTGCTTTCT GACTTCGGGC GACGCATATG CGCTGCTTT TTCAAATCC TCTAGCAATA 480
 35 TATGGCCTAC CGTATCTCC TGCTGCTCA GTTACTGCT TATATCTCG TCCGATAGCA 540
 CTGTTTTAA TCTTTTGCAA AGCACAACAT CTGTATTCAA GATATCATAA TCTCAAACAT 600
 CTGTTCATGA CATTCCCTGA GCTGCGGCAA CAAATGTTC ATCCGGATGT TGCAACCCGT 660
 40 TAAACTCCNC ACAATNCAAT CCCCCGGCAT AAAATCCTGA TTTGATCTAT CNAATGATNT 720
 NNNCCCAACC TCTTGTGACA ACCCTCNCAG TCCTTACAAC CCTACCCGTT ATGATTTTNG 780
 NAATTCCTAC CCTCNGCAT TTAGTGTTC NNNATACCTT TNGNCCCGG GNGGACTTA 840
 45 TCAN 844

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1343UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

5 GATCGATTAA AGGAAGCATC TGCTTCCCGT CATATCATAT AACATTGTAC CCGGGGCTGA 60
 GCGGGACCAG TAGCGAATTT GATAGCAGTG TTCTCCACGT CCCCCTCCA CTGTGAGCTC 120
 CTTAAAGTAT ACCGGCTTCA TACACCAGTG CCCACAATGA TGCGTACTTG ACTGTGAATC 180
 10 GAGAGCAITG GGCTTATACT GTGATTACGA TGAATGTAGC CAAGAGAGAA AAGGTTCAIT 240
 CACGATATAC AGTACTCACA TTCATGGCAT GCCATCCCCA AATTCCAATA CAGCCATTAG 300
 CACCAATGTA GCGCTACTAA TCCGGGAGC TTAATTGGCG TCAGTTCAGA GTGAATCTCG 360
 15 AGCTTAAAG TCAGATTGAT TAAGTAAGAA AATGACGATC AACAGGGTGC TCAAAATAGT 420
 TGATTACCAG ATTCGGGGGT GTGGTCTAGT GGTATGATTC TCGCTTTGGG TAAGCGAAGT 480
 TGCGGTTTAC TCGGGCTTAA CTACTAAACA TGTGAGAGGC CCTGGGTTCA ATTCCCAGCT 540
 20 CGCCCCAAT TTTTGTCTCT CGCTCCCGC GGGAAAGGTG AATATCAITT TACAAGTAGT 600
 TAACTCTCC CAGGTTACGT CCTTCTGCAG ACAAGTTGCA GCGGTTTACA ATGCTCAGGC 660
 TATTTTGGCG CTTCAA 676

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1344RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

40 GATCCTTGGG TACTAAGAGT TAGACTTTAA TTAATAATAT TATTTGTAGA AGATAGAAAC 60
 CATACTGACT CACGTCGTAT TTAACCCAAC TCACGTAACC TTTTAATTGA CGAACAGTCA 120
 AACCCACTT AGCTGTTACA ACCAAGAGGA TAGGTTGAGT CGACATCGAG GTGGCAAACA 180
 45 TAACITACAA TAGCTACTCT ATCGTTATAT TACCTGTTC AATTTTGTTA TCATAATAAC 240
 ATTTAATTAT TATTTCAATA ATTCTCAITA TTGTTGAGAC TATTTCAITA TGTATTATTT 300
 ATTAATTAAT ACATAATTGGG CTTTCGTGGA TATAATTATT GTTAATCCTA CTCATATATC 360
 50 TAGTCGTTGA ACGTTCTTAT AACTTTATAA AAAGGATTGT TATAAGCTTC GCTGCAGATT 420
 GTCCTTTATT ATTATAAAAT AATATTAGGA GTTCTTTGCA ATTAACCCAA TTTACTCAAT 480
 ATATTTAAAT ATTGATAATT AAATTCACA ATTTAATGGG ACTATTAAAT AATCCCTAGC 540
 55 GTAACITTTA TTCGTTTATC AAATACCATT ACAATATGTT ATATTTGTTC ATTATGCCAA 600

ACTTACGTGA TTGINCTACT TGTAGTATTA CNATTATAGC ACAGTTACCC CATCATATTT 660
 ATTTAATANA TACCCCAANT AGNTTTTTTT ANCATAAAAA GGANCTAATT TCCCTTTTTT 720
 5 CNOCAANTCC NNCTCTCTCA ATATTINTAA AAATTTTAAA CNNAANTAAG AAACCCCNAN 780
 TNAACCNCAN CTTTTTTCAN GGCTTTTCNAN CCTINTINAAT ANCCCN 827

(2) INFORMATION FOR SEQ ID NO:487:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 872 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1344UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GATCCTTATA AAATGGGCAA TAGACGTGTT ATAATATAAT ATACAAAATT ATAAATAAAT 60
 25 ATTTAATAAA ATATAAAATT AATAATTAAA GTATTATAAT AATTAAATAA ATTATTTATT 120
 AATAAGTATG GATTTTTTAAAC TGAAATTTGT TAAATGAAA TAAGAATTGC TAGTAATCTA 180
 TTAATAAGAA AGTAATGGTG AATACICTAA CTGTTTTCGCA CTAATCACTC ATCAGCGGTT 240
 30 GAAACATATA ATTAAATAAA GAATATTAAAT TAATTTATTA ATTATTAATT ATTATTAATA 300
 TTATTTAATA AATATAATAA ATATTTTAAT TTAAATTATG AATTAAATGG AAGTTGAAAT 360
 ACAGTTACTG TAGGGGAACC TGCAGTGGGC TTATAAATAT CTTTAAATAT CCATTTTTAT 420
 35 ACAAATAAAT ATATTTTTTA ATATATTTTA TAATACTAT AATTAAATAG TTAAATTTTA 480
 AATTATAATT TAATAATTTA ATAACCTATT AATTAGAGAG TTAGGGTACA TCCCCCTAA 540
 TGCTATGCAT TATGGTTGGT ACCACTCTAA TTAATAAACT ATAATAAATA AATACTAATA 600
 40 TTTTATATCA ATTAAATTAT AATTATTTTT TATTAATATT TTAATATTAT TTAATGAAAT 660
 ATATAAATAA AGTATTATAA TTTAATAATT AAATAAGAAA TGAAGANAAC GACTCTCANA 720
 ATTAAATTGC ATTATAGTT TACCATTAAA CAACATTCCC TTATTCATAT TATTINATCN 780
 45 ANTAATTAAT ATCTTATTAT TNATTAGAAG GANAGGNINC CNCCCTAAT GCTNNGCATC 840
 TTGTGGTACC NNNAATTAAA AAGTTTACAT NA 872

(2) INFORMATION FOR SEQ ID NO:488:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 835 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1345RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

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GATCCCAACG TCTGATTATG TGTGTGAATG CTGTTCTCCT GCTCCTCCTG AGTCTCCTTA      60
GCCTTGGCCT TGTACACTTT GCGTATGTT CTTGCTGCAA TATAGCCGAT GATTTCGTAC      120
TTCTCCAGCA CTGACACCTT ACGGGGTCTT TTCGCTGCC GATATGGCCC TATCGAGAAC      180
ACATTGTTAT TCGCCATTAG CATCGGCGAT TTGGACGTGC TGGCGCTGCC TTTGGTATCG      240
AGAAGCTGCT GTTGCTGTTG CTGGACCAC AGGCTCCGGG TGGATGCCTG GTTGGATACG      300
TTGAAATACT TATTCTGTTG TGTTTGATGC TGATTATTCA TACTATOGGA GGACTGTAAA      360
CGTATCCCCA TAAAATAGAG AGCTCGAGCT ACCACCTGAC GACTTGTGTT ATTTGTAGTG      420
TTAAATGGAT ATCGGCTATG TTCTAAGCTC GTTTTAAAGT GTAAAACATT GCAAATCCAT      480
ATGCACACAG CTCATCCGGT TCTACCGACA ACCCTCTTGC GACCGGAGCG GTGGAGCTGG      540
GGTGGATAGT TCCCGAGCCC CTATGTAGTA TATACAGCGT GCCACGGCTG CGCCTGGCGG      600
GCTGCAGGGC CTCAGCACGA NTGCCCTTC CNCCACTGCT TTATCCTCCT GAAAGCCGTA      660
CAACCNCCGG NNAAATACGG GGCACCCAAA GCNGCCCGAN GCGCCCGGAT AANAACNTGA      720
CCAGCCNTAG NGAGGCCCGG AAANAACANT GCGCTTTTTC AGCGGGCGGT CGCACAAACC      780
CCAAGGNGGN TCCCNNTTGG GNNTTTAAAT NGCCNNGGGG ANGCCCNNTT NCTCT      835

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(2) INFORMATION FOR SEQ ID NO:489:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 863 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1345UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

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GATCCGGCGT CAGCGCAAGC CAGTCTACTG GGGGACGGAG ACGCGCACAG CATTGGCGGA      60
GGGAGAGCTG GAATATCGCG ATGACCACAT TTGGAAGGCA GCTTACGTTT ACTTTCCGCT      120
AACGGAGGGC GCGAGCGCCA CGTACGCGA GCGCCTGGGC ACGTCCCTCC CAGAACAGCC      180
CATCGTGTGT CTCATCTGGA CGAGTACACC GTGGACTCTG CTGTCAAACA GAGCCATCTG      240
TTTCCACGAT GACCACGGT ACCTGCTTCT GCAATGGAAG GGTATGCTGG TGGTAGCCGA      300
GAGAACTGAA CTAGCTGACT TTAAATGGAG TGGTGACACG CCGGTGGTGG TCACCTCATT      360

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CCGCGGTTC T GACCTCCGG GGCCTCTATTA TACCAATCCA CTTCCTGGGG ACGCCGTTAG 420
 TAGGCGCTG CTGCATGGAG ACCATGTCAC GCGCGACACA GGTACTGGTC TGGTACATAC 480
 5 TCGCGCCAGG CACGGCCAGG AAGACTACCT AGTAGGTCAG GCGCAOGBCA TTGAAGTCTA 540
 CTCGCCAGTC GACCATGAGG GGAGGTATAT TCTGGATGAT ATTCTCCAC AACTCCGTGA 600
 TATGCTAAGA GAAGAGAGCG GTAAGCCGCT GAAGTTTACA GACCACAAAG ANTGCNGNT 660
 10 CTTTCATCAGT TTGCTANAAA AACCCAAGAT GCTCTGCAAT TCCCTGAATA CCACNCTONT 720
 NTCCCTNCAA TGGAGTCNAA NAACNTGTTT TCNAGANCTA CCCNCCGTIN GTTGCNAACT 780
 GATGGACTGA ACTTCCCCCN GGAAACCTGA AACTTTTATT TTTCCTCNCC AGGGGAAAAA 840
 15 NCGNTCAAGG TTCTCNAAAN CGA 863

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1347RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GATCATCATG CCAGCGCCCA TGCCGCGGC GGCACACCTT CACACCCACC CGTAACTGAC 60
 AATACTCGAG CACCTTCGTG CGCTGCGCCG CTGCGCGCTG CCTGGCCCAT TATGCAACCA 120
 35 CCCACAGTT TTAITCCACT TAAAAATTAC TTAAGCTGAC GTTACGCCCTG TTGAAAAATT 180
 TTGCCTTCAC GGAATTTTTT TGGGTGAGAT ATAAAAGGGG CTAAGTTGCA CAGTGAAGAAG 240
 GTGAAGTTTT TTGTGTTTAG ACTTCTTTTA TGACCTCATA GAAGGAATTT GGGAAATCTG 300
 40 ACTTTCAGC AGCCTCTCTC CAGTTGGAAG TGTTTACATA CTACTGCTAA ACGTCCGCTA 360
 AGTTAAGATT TTCTTTTCTT TAGTTTTAAA CTCAGTACCT TAITCCATAA AGCGACACTA 420
 CGATGCTTC TAGATTCCTC CTGCTCTCGA ACCTAACGAG ATCCTTGAGC TCTGTGGGGC 480
 45 GGATGCAACA GATGCGGTTT GCATCGTGA AGTCGATGAC TGTGCGGGAT GGGTTGAACA 540
 GTGCGATGGC CGAAGAGATG GACCGTGAT GAOGATGTGT TCATCATCGG AGAGAAGTTG 600
 GCGCCAGTAC AACGGTGCCG TTACAAGTCA CCAAGGCTT GTTTGACCGT TCCGGAACG 660
 50 CGGTINGING ANACCCATCA CCGAAANGTT TTTCGGCTCT TGCGTGGGTN CNCTGAAGG 720
 CNTGACCTA TGTCAATCAN TNGTTCACCT TCCAGCAGCA NGACANTTCT GAATCCGGC 780
 CAAATACANN TTCGTGTGTG CNACNVCAN TGTTCCAGC NAAGNGGNC NCGNNC 836

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1347UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

GATCCTACAG AACTCAACTC TTATATOCAG GACTCAGTCA CGGOGTCTGC AATCCGCAGC	60
AGCCACGGGT GCTCCAGGCT GGGTGGGCAT TGGATGGGIG GGCAOGAACC GAGTGGGCAT	120
GTATTCCTGA TAACTTAAT GTGTATGTTT ATGCTGGGCG AGCTGCAGGT ATTTGGCCGC	180
CCGCAATCG GGAAGCTTTC TGCTGATGT CAACAGCTGC AGGGGGCTCC TGGTAAATTT	240
GTGGCACGCA TTTTGCAAGC AAGTCCGATT AGAGAGCTAA TTAACCTCTGA AGCCCCCCTAA	300
CATATTTTAA GACGCCTTT CGTCAACTG CCACTAGAGA GTCTTGOGAT TCTGGTGAGC	360
GCGGTGTGTT TTGGCTTTTC GTTCATGTG CTGGAACACC CGATTCTATT GCTGTGCGT	420
CTTATCTTGA CATGGACCTG GTCACCTCTG GTAACCTATC TCTCTTTCCA TTGCTTTGCG	480
GAGCAATTGA CCGGTTTGCT CTTGCGATAC CTTCTAGTTT TGGGGTTATA CTGGTACATA	540
TATGATCTA AGTAAATCT GCAATATTAC ACAOGAACGT TAACTGGCC AGCTGGATAT	600
AGGCAAAGAT TGCAGATGCT GTGCTTTCCG CCTAATATGC GGAAAGATGA GCAGGCCCAA	660
CCCAATGCAG AGTAGGTTTC TCATATAGTA ACCATCGGCG AGAATGACAA CTTCCGCCCCG	720
CTTTGGAAGC ACTCCCCCTC GGAAGGAACA TCCNATGGGC GAATTTTGGC CACCTTANAA	780
TTNAANAAAC TATCATCGCC ATAATACATC CGANACAATT ACCCCCANAA TATCAAGTAT	840
CNGAAATTTT CNTANITTCN CCAATACGN	869

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1348RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

GATCCTTCGG CAGGTTACCC TACGGAAACC TTGTTACGAC TTTTAGTTCC TCTAAATGAC	60
CAAGTTTGAC CAGATTTTCC GCTCTGAGGT GGAGTTGGCC CCTCTCTTAA GCAGATCCTG	120

5 AGGCCTCACT AAGCCATTC ATOGGTACTA GCGACGGGCG GTGTGTACAA AGGGCAGGGA 180
 CGTAATCAAC GCAAGCTGAT GACTTGGGCT TACTAGGAAT TOCTCGTTGA AGAGCAATAA 240
 TTGCAATGCT CTATCCCCAG CACGACGGAG TTTCACAAGA TTACCCAGAC CTCTGGGCA 300
 AGGTTATACT CGCTGGCTCC GTCAGTGTAG CGCGGTGGG GCCCAGAACG TCTAAGGGCA 360
 10 TCACAGACCT GTTATTGGCT CAAACTTCCA TGGGCTTGAA ACOGATAGTC CCTCTAAGAA 420
 GTGCGCAACC AGCAAATGCT AGCAGCACTA TTTAGTAGGT TAAGGTCTCG TTGGTTATCG 480
 CAATTAAACA GACAAATCAC TCCACCAACT AAGAAOCCG ATGCAOCCAC ACCCACAATA 540
 TCAAGAAAGA GCTCTCAATC TGTCAATCCT TATTGTGTTC TGGACCTGTG AGTTTCCCCC 600
 15 GTGTTGAGTC CAATTAAACC GCAGCTCCAC TOCTGTGGTG CCTTCCGTC ATTCTTTTAT 660
 TTTACGCTT GCGAACATAC TCCCCCGAA CCCCAAAAT TGATTCTCCT AGGTGCCGAT 720
 20 TGTTCATAA AAACACACCC ATCCCTATTC GCATATTAT GTTAAATACA AG 772

(2) INFORMATION FOR SEQ ID NO:493:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 823 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1349RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

35 GATGGTTATA TATCAGTCTC TTGCTATAGA TTAATATAGA GCGACCACT AATGTACAAG 60
 TTATAACTAC TGGTAACACG TTATATAACA GGTAGGAAAC GGGGCGGCG GGGATTTTGT 120
 CCTATGGCTT GCGCAGGTAG CAACTGCTAT AAAGGGGAC GTTCTTCCG GAGCTTTTTC 180
 40 ATCTTGCGCA GTTCACTTG CTAGTTAGTT TAGGGCTAGG TCGACAAACA TATTCCACAT 240
 CGTTTTAATG GCTGGGTAC CTGATAACGT CAAGGGCGTG GTTGAGCTGG ACCCTGGTT 300
 AGCTCCTTAC GGGGACATCC TCTCTGGAG ACGGTTCCTT GCGACAAGT GGAGGCACGA 360
 45 TATCGAACAT GGGGTGCCC GCGGGGCGG CAGTCTAGTT GAGTTTGGC GCGACGATA 420
 CAAGAGCTAC GGGCTGACG CGGACGCGA GAGCAAAAGC ATAAGTACA GGGAGTGGC 480
 GCGCAATGCA ACCCGGGCT TTCTAGTCG CACTTCAAC GGGTGATGA GACCTGCAC 540
 50 GAGCTCCAGA ACAAGGACGA GTTCGGGTGT TCAOGGTGT TTCGGACCTG GCGGACGGC 600
 GAATTCATAA TCCGCTACT CACCTTTAA GTTGTGTTCN AACTTGCCAC CGGACCGA 660
 TACCGGTTG CCACNTGAT TCAAAGGAC CACCCACC AGAANCCAA GATTTGGGC 720
 55 NCCTTACAAG CGTCTGAC CCCCCCT ACATTCCACA CAAAGCCCC NGACCAACTG 780

ATNOCCTNAAA NNACAGNCNC TTGCTCTCAC CGACCCCGTT TGT

823

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1349UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GATCGCGAAA ACTAACGCAC CAAACCCGAC GGAAGCCAGA GCTCTCTTGT AAAGTGGCAA 60
 GATAGTGTAT GTCTGGCCGG ATGGCTCAGA GGATTTCCTG CGAGCATAGT GGCAGCGATT 120
 GACATATGGA GTTATCATTTG CAAAAGCAGT GGCAATAGCA AGACCGGTTT TGTTCGAACC 180
 GCGTTTCTCT TCTTTTCATTA TTGGCCACAA GGGATTGTTC GAGTAGAAGG CCATCTTCAA 240
 CACAACGCTC GCAACAAGGC CTAGAGACCA AGTAATGGCA AACTGCGCGA CACGCGCGTT 300
 GTCTTCACA ATGCTCTTCA AGGTCACCTG AAAGTTCATC GTCTGAGAC CCGTGGCAAC 360
 CGCAACGCTC ATCAACCTCC ACTCCGGTTT CTCAACTATG TAGCTCCGA TACCGATTAC 420
 ATTAGCAAGT AAAGGGCCGT ACTGTGTAAT CAACGTTGGG AAAAATGGAA CATAAAGCAG 480
 AACTGGGCTC AATACCGCCG CTATCACCCG CCTCATAGCC GGAGATACCC ATGTACCAGA 540
 GCGGGAAAAA CCATATCATA CACAATAGGG CAGTCAAGTT CGTCCAGAAC ATAAACGAGT 600
 CAAAGTACT GACAACAATG TAAAACAGAC TTGCTGTGAT GGTGATGGGC TGTCCGGCA 660
 GGTAAACGAG TTCTGTGCT CCTGGTGAT AATCACCTCC TCCAGCATT TCCTCCATTG 720
 CGCCGCGCC GAGTCCCTTG CCGGCTAGA NAGCNGGTG CTTGTCTTTG ANTGCACAAC 780
 CCCNCGAAG GCCTGTGCC TGGGTGCCN AACTTTNCCT NAGTCTCCC AGTTTGCNTT 840
 ACTTACCTC CNAAAAATTC CAAATATCCN GGACNCCN 879

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1350RP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

5	GATCTCTTGC AATTCCTGCT CGGTCTCTCT GTGATCTCTA TTGATCACTT TTTCGAGTTT	60
	GGTCGCTTGA GAAAGCGTCG CAAAGTTGTT CATAAGTTTC TTATAACGTC CCAGTTTTCG	120
	AGCCAGCACA TCGTCGCTGA TCGTGTGGAG CGCAATTGGA TCCCCATCGG CGGCCATGTT	180
	ATCCTTGACC GCGATATTGC GTGTGTATGA AGTCTGAACG GCTCTGTGGC CTGGAAGTAA	240
10	GGCGAAAAAG TAAAATTATA TAGAACAGGC ATGAGATTGG CTGGAAGTTC AGGGAGCCAG	300
	GCCTGTGTGG AAGCAGCTTA GAGAGCCATA GGAAGCCACA TCGCAGGAA CTAGAGATGA	360
	GACCCACCCA AGGTGAACTC GCCACGGCA CAGGGGCAGT CTTAGCAACG TGGTAAACAT	420
15	TAAAAATAAT ACATACGTTA CAAGCAGCGC GCATAGCAAC TGCTGGAGT CATGTTTTAG	480
	AGAAAAATAG AAAAATTATT ATAATATTCC TTGTGTATGA AATAAAGCTG CTTTGCAACA	540
	CGCGGCAGAG ATTCAGACCT GCTTGAAGCC GTAAAAGGAC GAAAAACCGA ACGAATAGAA	600
20	TTAAGATAGA AAAGCAGCAC TCGGCCAAGG CGAAGCGGGG CGGCAAGCC GCGCGGCTT	660
	TCCCTCNCNC TCAGCTGCAA ATGCTCTCA GTGGATCTG CTCCCCCTGT CCGCTCTCA	720
	CCTCTCCAC TCTCTGTCNT ATCCTTTTGA TGAAACNAGG CTGACGGGGG TGTTCACTCC	780
25	ATCTTCNCNC GCNCGCTCG ATAAATTGCT CAGNCCTACC TCTTGGNG	829

(2) INFORMATION FOR SEQ ID NO:496:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 875 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1350UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

40	GATCCGCATT AAGCGGACG ACGAAATCAA TACCAAGAAG CTCGACGAGG AGAAGGAGCG	60
	GCGCTCAAC GCCATCATCA ACGGGGAGC TAGTCATATA AGGTGCATA TAGCGCAATT	120
45	AAAGGTTTAG CGTCATCGAT AGTTACATAA AGTTAGAATG CATGCTCCGC CACGCGCGCG	180
	TTGACTCGG CGAGCCAGCG CGAAAGCGCG TCTGTGCGCG CGGGTAGGAA GAACCGCGCG	240
	AAGAAGTGA GTTCTCCGC CCACCGGTCG TAGAGGTCTT GGCTGAGTAC GTTGTACTTG	300
50	ATCGGGTCG CCTTGGAGAT GGCATTCATG AGCCACTGTG TCTGTGCAA CGAATGCGTC	360
	GCGCGCTGC TGTGCGACTT CATCATGAC AATTGCGGA ACGGCTGAA CCGCGTGATA	420
	AGCGCAAGCA AGCAGAGCCC CGCAGGTAC AGTCCGTGC TGTGCGTGG CTGGCGCGCG	480
55	CCGATCAAGC CCGCGCGCA GTACTCAAGC GTCTGCTGA GCGGCTCGG CGCGCGTGC	540

EP 0 866 129 A2

CACACTGCCG COGACGTGAA GTCCGCCAAG AATGCTCCTG CCCGCGCAG AGCACGTTG 600
 CGGTCTTGAT GTCCCGGTGC ACCACGCAGC TCTCGGAAG GAACTGGAGC GCCCCAACAA 660
 5 GGTCACGTGC GTACCGCCAC CACTGGCCCT TGTGCGGGC GCGCGCCGGT GGNCCGCTTC 720
 CANGTGGGGT TCAACCGCTC TACACAACGC CGGACCCNC TOGCCACCGC GAANCGGGGG 780
 GTATCCCNAC GTTTCGCGC GGNCCCCGN GGAANGGACC ACTTTCGGTC NOGANCNC 840
 10 CCGCCCGGT GCAAGNGGG AATTNTTAC CTTCT 875

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1351RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

GATCATAATG ATTGTCITA ATTCTTTTCT TAATTATTCA TTAAATAATT AATTAATATT 60
 TTATTAATAA AAAATATTTA GAGTTATGTT CGTTTATGAT AAATTCTAAA ACTTTGCAGC 120
 30 ACGAACTGAA GACAACATG TAACGCTGT AATTAATTAT AAATTATTAT AATTAAATAT 180
 TCAAAAAATG GTAAGATTTA TOGAGGATTA TOGAATTAAA TAACATGTTT CACTGCTTAA 240
 GTCTGTAACC GTCTATTGTT TTGATTTTAA TTATTGCTAA CGTAGTCATC AGGCGGAATA 300
 35 CTTTAATTTT CATTAAATTT ATTCTTTAAT TAATAAAAAA TAAATAGGTA TTCATTGTTT 360
 ACTGCTAAAA CTACTCGGGT ATCGAATCCG ATTGCTACT TTAGCCTTCG TTCTCAATG 420
 TCAATTAATA TATAATTTAA ATTTTCACTT TATAAGTCTT ATTCAATATA TTATTATTTC 480
 40 ATCTTTACTT GAATAATTCT TAAATTATTT TTATTAATTC TAATTATTAT TTTAAATAAT 540
 CATCTACGAA CCTTTAAGC CATTACGAAT AACGCTAACC CCTTTGCTTT ACGCGAGCTG 600
 CTGGCACAAT TTTGGTTGGA NGANTTAAT TATATATCTC TTTTAAAAAT ANAATCTCCC 660
 45 TCATATTAAT AATTTTATAT TGAANTAAAT TATCNTATT TAATAATTAT TGAATTTATT 720
 GTTACCCANA NTAANAANAN ATTATTATTT ACATCCCCNA GTACNGANCA CTTACATTG 780
 50 CCAAAATCCCN CGCGTTCCNA NAAATGATAT ATTCNANCAC GGATNTCTTC TT 832

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 863 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

EP 0 866 129 A2

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1351UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

10	GATCATTATA TTATAAAATA TAATAAGAA TATATTTAAA TAATAATAAT AATATGAAAT	60
	ATTATATTAA TTCTCCATTG GAGCAATTG AGATTAGAGA TTTATTAGGT TTAACATCAC	120
	CAATAATAGA TTTTAGTTTT ATTAATATTA CTAATTTTGG TTTATATCTT ATAATTCCTT	180
15	TATTAGTAAT TTTACTAATG AATTTAATAA CTAATAATTA TAATAAATTA GTAGGTTCTA	240
	ATTGATATTT AAGTCAAGAA ATAATTTATG ATACTATTAT AAATATAGTT AAGACACAGA	300
	TTGGTGGTAA AGTATGAGGT TATTATTTTC CATTAGTTTA TACATTTTTT ATTCTTATTT	360
20	TTACTATAAA TTTAATTAGT ATAATTCCTT ATTCAATTTGC TATAACTTCA CATGTAGTAT	420
	TTGTAGTATC AATAAGTATA ATTATTTGAT TAGGCTAAC TATTATTGGT TTTTATACTC	480
	ATGGTTTAAA ATTCTTTGGT TTATTTTAC CACTAGGTAC ACCATTAAIT TTAGTACCAT	540
25	TATTAGTATC AATTGAATTA TTATCATATT TTGCTAGACT TATTCATTA GGTTAAGAT	600
	TATCAGCTAA TATTATAGCT GGTCATTTAT TAACTTATT TAGGTTGTTT AATATTTAAT	660
	TTAATAGCTA TAAATATTTT AACATTTTAT TAGTTTCTTA CCCATGAATG CNAATTTAGT	720
30	ATGGTTGTTT ANAATTGGCC ACCCTANTAT CCACCTAANT TGAGGTTTTT TAAATCCNC	780
	ATTTTAAAAA TCCATTTATT TACATNNATT AANAATAANA TATTTAATAA TATCCANNAT	840
	TNAANATTTT ATAANITTTAA AAN	863

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1352RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

50	GATCCTGCAT CGTTTCGTG GCTGCAGGT TGATTTTGT GCTCTCAATT TTATCCTTTA	60
	TCAAATTCAC AACCTGGCAA TCCACCTCAT GCCTTATCTT CAACGAATGC CTCATCGTAT	120
	TGCTAACCT GAGGACCATC TCCACCTTCC GTTTAACAAG CTGACGGTA TCTGTGTCA	180
	ACAGGTTTAT GGCTGGGTG TOGACCCCA ATTGGGCATC CCAGGCAGTT ACGTATCTA	240
55	TGTGTCTCTT GGTGTTCGGA GAGAAGGAT ATGTAACTGA CTGCATGTTA AGAAGGCGGT	300

AGGGGAGATC CTGCTCCCGC AGGTCCCGGT CGAGCAACTC GCTGGTGTG ATGTTGATGG 360
 CGTCTCACA CAAATCGCTC AACAGCGAAA GCTGCTTGAA GGGGAAGCGC ACGTGGTGGA 420
 5 ACAGCGACCG TGCGTCTTG CCGAGCGGC TCGCGGGCG GAACGGGTG TGCTGTGTG 480
 CGGACAAGTT CGGGCAGCTC AGGGACGGAT GGAGCATCAC GGGCGCTGC TTOGCAGGGC 540
 CCAGGTGCT AGGGTCCGGC TCGGCAACG CGAGACCTTG TACTCCGCG CCGCGCCGG 600
 10 CTGGCGAGC GCGCCNGTCA GTCTTCTACA CCGCTTGA CTCCCGACTC CTCCGTNGAT 660
 GACTGCGGC GCTCTNCATC CGGTGCTGC ACACNCACAT CTCGGAATGN TTTCCACCAC 720
 CACCCNGNAC AACTTTCCAC ACCCGGAAAC TCNNVINGNNT TINGGACCT GTCTTTACNC 780
 15 TCCAATCCN TCTGCTGCAT TTTTGNAAAA CTCGCCCA CCACCCCTC N 831

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1353RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

GATCTAACTA TTAATGTGTT CCTTGAAATT GTGCTGAAAT ATAACGAGCT CTTAAATGAT 60
 GTCTATCTTG ATGACGATGT CGTCAAGTTG AGCCAATGGG TACTTCAAAC GTGTAATGAA 120
 35 TAAAAATATA CAAGCGCAA GOCCAATAAC CTTACCTA TATATCTTGT AATATATTA 180
 GTTAATTGAA CCATTACGT GGCATATTCT GCGCTGGCAT GGTATCCGTG ATTTTATAAT 240
 ATATATTTCT CGCAGGGGAA GCAGAAACAC TCAAGATCGG CGATTGCCGA TAAAAGAATT 300
 40 GCTCCCTGAT TGATTGTTGT TCGAAGGAGA TGCAGATGGA TTGTCCAGAA AAACCGGTTT 360
 TAAGACTCGT TCATCAAAC TGTAAACCA TTGCCATCG GCTTGAGTA TATTGCCAA 420
 GGTTCGCGG ATATTTCTTC TGTCTAATGA TAATGTCC ACAGGCTGGT CAGCGCTGA 480
 45 TGCAGAGCG GAAGAGGGT GGTCTATCAT AGGAGGAAAG CTTTCTTGAT CCGGGGAGC 540
 GGTCCGGCTG TCGCTAAAA ATGGAGGTGC GTCTAATGAA GACATTAGCT GCACAGGTCT 600
 AGGGGCTTCC ATATCAAATT CATCATCGT ATCTCTGT TCTTCTACG ACCCTGTCT 660
 50 TATGTTTGA TCTCCAGCAT ACCGCAGTAT ACCTCCAAT ATGATACGT GAGAACCCCA 720
 CTACCACCA GTGCCNAAA AGAAGTTGAC CCGCTGTAC CTTNATGCA TCCACNACC 780
 CACCCCCCA ATCNCCTGT ATGGTATGAC CCTCAGANAN CCGCTCNGA TC 832

(2) INFORMATION FOR SEQ ID NO:501:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 877 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1353UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

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15 GATCGGCGCA CTCTGTGGTT CATGTCTGTC ACAAGTTGAC CACTGTATAC CAGTTTGACA      60
   TCAGAGGGCG AAATCATCAG TGTGTGGCOG TACACAGAGC AAATAAACTC CTTTACTTCC      120
   TGCACGGTGG TGTGACTGT CACTTTCATA GTCTTCATCG CCAACACGGA GTCCGAAACG      180
20 AACTOGATAG TTACACCATC CCCGTCTGG COGTGGTTGG TACGGAACAT AATTAAAGCAA      240
   TCGAGAATG GGGTGGGCGC AAAGTCAAAG CCCAATACCT CCTGTAGGCT CAACCCGCG      300
   TGTTCGCGG CGTCTTCGGC GCCCAGGTAC ACAGGGGTAC GATCGCCCTG CAACTTGGA      360
25 TGCAAGCATG TCGTGGGCA CATGGTCTT GTTGAACAC AGGTCTTGC AGCTGCTGCG      420
   CTGTA CTG TTTACTATAT CACATGCCAT CGTCCGACG GCCAGCACAG ACGTCTTCAG      480
   AGGCACAAGT TGCTTATCA CGGCCACCAC TTTATCCATG GAAAGCGTGT TGACCTGGAA      540
30 CTTGAAGTTC ACATACGCAA ACTCACTGTC GGCATCGTAA GCCAGGTCTA CAGTGGCGCC      600
   TCGACCTGC TCGGCACATC CAGCTCCAGA TGGACCAACC CCGCGCGCA GCCTGCAATC      660
   TCCTCGCACA ACATGGTCAG ATTGAGCGG ACGCTGTTGG TATTGAGACA GTATTGCTCA      720
35 GCGGCGCAAG CGCATGTTT TCCCTGATG CATGATAAC AATGCCNTAC TGCNATACT      780
   NGCNACTGAT AANTTGGGGG ANGCCCCGCC NTTCACGAAG AAGATCCANG CTCCNTTCA      840
   AATAGNAANN CNGANTGAAC TGGCGNATNC CNAATCT      877

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(2) INFORMATION FOR SEQ ID NO:502:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 871 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1354UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

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55 GATCGAACAC GCCTGTGCCA GGGAGCTTAG GGTGTTGTGC ATCCAATTGA GATOGAAGCA      60

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AAAACCGACC ATGCTTGTG AACCGAAAGG CGGATGTAGC ATGGCCCTTT CCCAACGGTT 120
 GAGATCCTGG TTGCGCCCTC TTACCCCTGT GTAAATTTCT CGCAAAGTCA GCGTGGTCCG 180
 5 TCGTCAGCAG CGCCTCAAGG GCATGGCCCA GCTGGACAG AATGATCTCG CGGTCTGCAG 240
 AAGAGTCTGA GCTCAAGCTG AAAATTGGGG GGGCTTGGGA CCGGCGCTGC AGCAGCATTG 300
 ACGACGTCAT CTTGCAGCAC TTGCTCACTT GGGGTCTTTT CCGCAGCAGC GTCCGAGACA 360
 10 GGTGCCGACC ATTCAGAGGC CGGAAGTTGG ATAGCAGATA ATGCAGGTGC GACAGCACAC 420
 CAGACATGCG ACTGGTTGAC GATACATAAC GTGCTTGCC TTCTTTGGCG CGCTCCAGCA 480
 GTCCGAGGTC CCGCAGGGC GGCACGAAGT CTGGATGGC CTCAAATCGA AGTCTGCAC 540
 15 CTTGATCACC CGCTCGATGA AGGCTCGAA GTTGTACACC CCGACCGCC GGTCCCGGAG 600
 CGGCACCACC GACAGCGGGC TGGAACAGGC AGGTTCCAG CCGTGGGCC AGCGCGGGG 660
 GCAGCTCTGT TGCACTGCTC NINCCACCCC ATTGCTGAAC GCGCCNIGAT TACAAATTGT 720
 20 TGNCTCCCG GCGCGCTTG CCGCGTTGC CCTCCCGC CGGGCACCC CCGCNCNNNT 780
 GGATGANNGT TGNCTGATTN NCCAAACCG TTCANNITGT CCGTTTNT CANGNCANT 840
 25 NCCNNTCNT TGNCCNNT NAATGCCNC N 871

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1355RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

40 GATCATGGCC AAAAAATTGG GAATAGGAAA CTGTTCCAG TACTCATCAA GGTGAGTAAA 60
 AATGTTTGGC AGCAGTGAAG ATTGCATCCT TATCTTGCCA TTTCGGGATA GGACATTTGT 120
 TTCGATATAC CTGTGGTGAG AGGAAAAGAG TGTGCGAGT TGGTAAGTT CTCGTAAAAA 180
 45 CAAATAAACT TCTCTCTGG AAGTCTTACC GTAACGCAIT CTATTCAAAA TCCTCTCCAA 240
 GTCTGGCCA TCAACCAACA TATTATTTAA CGACTCAATG AAGATATTAC CAACTTCGGT 300
 TGAAATGCAC TGAATGGGT CCAATCTCTG TTGTATCTGA TCAATATTTA TTAAAGGCTT 360
 50 TGCAATCCAG TTCTTCAAGT TCCTTAACCC GTAGTTTGT CTAGTATGAT CTAATACCCA 420
 TAACAGGGAG CCTTACTGC TCCTATCTGT ACTGTCTCA AAAATATCTA AGCTTTCAAT 480
 AGGCTAAGA AGGAAGAATC ATGTGGTCT TCGAGCAGAA TGGTTTAAAG TTTTCCTTGA 540
 55 AGAAGAGTAA ACNNNCATTT TTGAAGTTTG TTAGGTAGCC ATGCACCAGC ATGAGCGCTG 600

TTTGCAAGAG AACGTTGCCC TTAAAGGCTG GGTGGGGCTC ACTGAAGATT TCTTCATACA 660
 ACCCGAGGAG CTCGATCTTA TTAGAGTGA TATCGGAATC TGAAGTATGA AACACCTTTT 720
 5 CGATTCTTGA GCCAAGGCCA TCTCCGACCA CAACTTCACT CGGGTTTGIG TATTTTATTC 780
 GGGTCTCCAA AGCCTCCGTC AGAAAACGCT CCTCTTTGAA GTCATCGAAG ATAACTTCAC 840
 CGCTGTGTAG ATTAACTA ACCAGGAAGT ATCGCGTGA TGAAGGTTGT CGCTTGACA 900
 10 CAAGACCCCA CACAGAAGCG CTATCACCCA GGACCCGAG ATCTTTGGTT CGAACGTCTC 960
 ATTGATGCCA TAGGTAGCCC TGTGAATAT ATTGGGTACT TCCCTCGAGA AACAGAGCT 1020
 TGAGGTCCCA CTGTTCTTTT TCACTGGGGA TGTCTCTGTC TGCTCCAGA CCCCCACTTT 1080
 15 CAGATTGTGG TGCATCAAGC GCTGCAAGTG GACTTCGAGA CGGGTGTCTG GGAATGGTGC 1140
 AGTAAGCAAA CTCTTTGTGC TTGTGA 1166

(2) INFORMATION FOR SEQ ID NO:504:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 887 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1355UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

GATCATGCTA TCAAGTGCG AGAACACGGA TAGAGCCTAC TCTGCAGGTT CGGCTCGCT 60
 GAGCGCGCG CAGAAGTGA AGAAGCCGCC AAATACCGCC TTCCGGCAGC AGAGGCTGAA 120
 35 GGCCTGGCAG CCCATCCTGT CGCGCAGAG CATCTCCCA CTGCTAATAT TGCTGAGCGG 180
 GGGTTTGGC CCAATCGGGA TTGGCTGAT CATCAGTGCA AACACGTGC AGAACCTGGT 240
 GATCGACTAC AGCCAGTGG GCAAGCACGC CACGTCCGAA TACAAGCCA TCCCCGAGAA 300
 40 CCTGGTGAGC TACCACTTCC GGACGTCCAT GTCCGAACAG CCTAAGTGGC GGCTGCATTC 360
 CAAGAATGAG TGCGAGCTAG AATTGAGAT CCCCACGAC ATATCGAGCT CGGTGTACAT 420
 45 ATACTACAAG CTGACGAAT TCTACCAGAA CCACCGCAAG TACGTGCAGT CCTTCGACCT 480
 CGACCGCTT AAGGGCAAG CTGTTGCACC AGACAAGCTG TCCGACAGT GCCACCGCT 540
 CTGACTAAG GACGGCAAG CTGTCTATCC CTGGGCGCTG ATCGCCAACT CAATGTTCAA 600
 CGACACCTTC ACGCCGTTC TCCGGGTGT CCAACGGGT CCCCCACTA CAACTCAGCC 660
 50 AACAAAGAAC ATCGCTTGC ACACGACCG CAACAGGTNN CAAGAAGAAC AAGCTACAAC 720
 CCGCAGANA TNGTGCCGCC CCGGCGCTTG GCACGAACGT TTCCCCNAA TGGTANNAC 780
 55 AANCCAACCT GCTGACTINN CTACTTGGGA GAATTTCGG TMTTGGANTG NNCCCTGCAG 840

NCTGCCNCCT NNTAAANCTN CNTNCAAAAA AAAAGCAACN CCCTCCC

887

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1356RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

GATCTACATA TGCATCAAAA CATGTGOCCTT CATGCGCATC AGTAGTTATG TTTGCGCTGA	60
GAGGCGAGCC ATTTCCAGCT TGTCTGCACA ACTCCATATC ATTTGCATCA TCAACCTCAT	120
TATCGCTATC ACCATCCTTA GTCGAGTATG GAAAGGAGGG TGACACAGCA AGGCCAGAGG	180
TATCAGTTGA AGACATATCT GTGCTCATGC GGTGGGCGCC ATCATAGTCC GATGACTTGG	240
TGGAGGATTT AAAGTCATTC TCGGAGGAT TCTGTGGCTC TACTGACCTT GCAGATTCTG	300
TTTCACTTTC GTACAGAATG GATCATCTTT CGAACTTGAG ATCTATCGGT TTGTGATCAT	360
ACGCGACTCT TTTTTCAAAC TTCTTTGTGG TCATTTGGCAC GGAGTTTATC AAGCTAGAGC	420
CCAAGGAATG CTGCTTATCA AAGTCTTCTT TAGCCATGGG CATTTTCGTAT CTATCATCTA	480
TCCCTTCGTT CGAACCATAC TTCACCTGGT AGCCATACCT TGTATTATAA TAAGAGTTGC	540
GATAATGCTT CGTACCAGAA CTACCGGCAC TGCTAGACTC CAATATGGCT TGGATGAGGA	600
CTGCGCAGCG GAAGTTTACT GGCATCCATA TCAATTTGGG CNTGGCTGCC ACATTGAGAA	660
ANANTAAGAA GAAGTACGAC TAATCCTCCA CTNGCTAGCC CGTCCNTAGC AGCGAACCGG	720
CTGCTGTCTN NNCATCCAC CCCCCTGCTT GCTTAGCTCC TACNCCCNIG TGGTTCCATA	780
ACCCACCCCG TGTACCCCA TCCCTGANC ATTNTGAGAG ANN	823

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 873 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1356UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

GATCTGAACC ATATTACCAA AACCAACAA AGAATTGGG CCCAAGCGAC CGTCCGCGC	60
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GTAAAGCOCT ATAACCAGCT TACGGCTCTG TGGGCGCCAT AGAAATTTGC ATTTTCAACG 120
 GAACCAACAC GTCAATCCCA AACTACACTT ATCATGCTT AAAAGGGATT ATCTTTTCTA 180
 5 ACGAGGAGGC CCGOCTGCG AGTAGGAAGC GGATCTTAGC GCGTCCGGC CGGCACATTC 240
 GGCGTTTGA CTGCAATATC CTACTTCTGC AGCGGAAGAT AGCGCAOGAA AATCTGCGGC 300
 GGAGCAAGCT CAGAATTATA TGTAGGACCA AACATTGTCA GCAACGCTG CGCCGAGTTC 360
 10 TGTATCGAG TAGGGGGATT TOCTGCGAAT GCGTTCTT TTTATCGTTT CTTTTTTGAG 420
 GGCATCTGC AGAAGCGATG AGSTCCAAAG CATCTTGTG CATCGATCAC CGAGCCACA 480
 GGCAGGTAG AGTAAAGCT AGTCACCATG GTGGTAGITG ATAATAGCG CGGAGGCGCA 540
 15 TTCGCATCT ACGCGGTAA GCTGCGAAAC AAGGTAGCGA CGCGGCGGG GCTTTTAGGC 600
 GACTACGACT ACAAGTACCT GTTCACGCG CAGATATTCA AGCGCCAGAG AAGCTTCAGC 660
 CATTTTCTCG ATCNATGCAA AATCCCCGT GTTGCTTGG TGGCNTTTGG GGVINCACNC 720
 20 CCGNNGCAAN NCTGGCGGT TNNTTNCNC NCCAATMNTG AATACCGNG GNGGGAANTT 780
 TGAAAGNNAA NCCNACATNC TTATTGGCT TNCNGNIGT NGAACGGGC TTNINNAAG 840
 GNGAATANN CCTTGNGAA TOCTTAANAA AAT 873
 25

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1357RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

40 GATCCAGCG AGGACATCGA AGAGGGACTA CTGTACGCA TGGACAAGCT TCGTGGCGA 60
 TTGATGAGCG AAGACCGAGA TGAAATGACA GATGGCGGA CCGTGGGAG CGTGATCTGG 120
 AAGGAAATGT TTCTGCGGT CCGTATGGTG TCCAGGCTCA TGGTAGTACC TGCAATGATC 180
 45 TGCTTTCCG TGATCGGCTT CATGGTGGG GTTAGCGACT TATAATAGTC GGTGCGGTT 240
 GCTGGCGCAA GCAGCTGGCA TGCAGTGTG TCCGACAAAT AGGAGTACCG GTTGGTGTTC 300
 TTATTCTGTG TGTTGTCAGA AATGTTTGCA AAGGAATAGA AACCATTTC CATGGTGTTC 360
 50 GAGGGACTT GCGAGTTCTG TGCGGGTGT TCGGCGACAT GACATTTCAT TTCTGTCTT 420
 GCGCCGCTT CCGCAGGAAA ATGCGGCGC TGTGCGGCA TGTCTCTTC CTGCTGTGT 480
 CCGTCTGTG CCATCTCCCC TAGGGGCTG CCTGAAGAG TTTCAAAGCT TTGAACTTC 540
 55 AAGGAGGGG ACGCCGGGC CAGGAAACGA TATCGCTTCA CTCCTCTCA GCTTCCGAT 600

AGGCATCTCN ATGCCATTTT ATTAATATAT TTCCCCCGTC CGAACCCCAA ATGTATGTCT 660
 CCGGGTTGGC AAGGGATTCC GACTTATATA TTATTTGATG TOCACCACAG GTTTCNNAAA 720
 TATTATACAT CNATTGCCNA ACCTCCCCNT TATNCATCAT CCGACCCNC NCATTTTGTA 780
 CNCACTAACN TGCACATNNC CCNATVINNT AACCCATCAA CNCACCTTNC CTGCCCATCT 840

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAGL357UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GATCCTCGCG TTCCCATGCA ATTGIGITGC TTGGGTGAC CCGATATGAC CTCAAAACCG 60
 GGTCOGAAGC CACCAGCAC TTGTGCTAT GTGACTTAGC CCGCTCAGAG AGAGCAGTGA 120
 CACAGATAGT ACGCCGAAG GAGGGTGGT TCATCAACAA GTCATTGCTA GCGCTTGAA 180
 CCGTCATAGC CAACTTAGC ATGTTGGGAA GCCAGGCCAA TGGCCTGCAG CCGTCTCCCG 240
 CAGCCGCCA CATACGTAC CGTGACTCAA AGTTGACCG CATCTTCAG CCAGCATTGA 300
 CAGGAGACAG TATCATTACG ACCATCTGCA CCATCGATTG GAAAGCCGAG TCCTCAACCG 360
 AAACGACCAA TACCGTCGCG TTGCGGTCTC GCGCCAAGAA TATCGCCCTC AACGTGGCA 420
 AGAATGAAAT GGACTGCGAC GCGAGAAAG ACAACATCAT CCAGAACTTG CGCAAGCAGC 480
 TTGACGAGCA GCAOGAGACC ATTGTGATGC TCGGCGCAG TGCTGCAGCG CCTAGCGGCA 540
 ACGGCTCGAC CAGCCCGCTG GACAGCCCTG GCGTCGGCG CAGCCAGCTT TGAGCGAGCG 600
 CAGCCACAA CATTTGAAAA AAGGNTGCT AAAGGTINGAA AACAGCATCC TCCAAGAAGA 660
 ANCTCCGAGC CATTTGCGAA AAGCNCTCG AANNAGGAAA TGATGTCTC CGAAGAACCG 720
 CANTTTNCA NATCTTINAA ATCTCCCCCT TGGAAATCC CCGTCCCCC CAAAACCAGG 780
 NINCAGGGT TGATTTCCNC NGCCCATTA CGGNTTACT TTCAAANTA AATNCACNCC 840
 CCCAGNCCN NGAAAATNCN TTCCCCCCN TMTGGNGTTC ACCGCCNA 888

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1359RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

10	GATCCATGTT TATTCACCCC GCTCACTCGC GTAAAGCATG CTTTACGTTG CTCACATCGC	60
	CGCCACCATT AACAGCGTAT CACATTTTAC GTTTCOGTGC AGCAAAAAGT CGGTCCGAAC	120
	ATAATGCTCC AATACCAAGA TAGGTCCGGG CAAGCGCCTA ACACGTGACA TCCTGCTCGC	180
15	CTCCCCACGG GCGGCTGGG CTGTGCTGGA TGAAACTCC CTCCAGCGTA TGAGCGGACG	240
	GGCATTGCGC CTGCCATTAC TGCAAGCCCC ACCGACAGGT TTCCCATGTC AGCATCGACG	300
	GCAAAACCGC AGAAATCGAT AAGTAGCAGG ACACGCGTCA GAAAGACCAG TGTGGTATCA	360
20	TGGCGCAGA GGAGCTAGGC AACCTGCTT TTCCGCAAC ATGCCCGGCC GCAGTTTGA	420
	ACGCGGGAGC GCTCACCAG GCGGGATTG CTAATGTCC TTCCGGCCAA AGGCGGTCAC	480
	AGCTAAAAGA GAGGCGCCA CGAAGGCATA TAGCTGGCAG GAAACGATAC GATTCAGCGC	540
25	ACTGCGAGCG TAAGGAACAG GAGCATCACA TCGAACAGTC GCTGTGGIN TCCATCCCTG	600
	AAGGTGACA CTAACCTGAA AAGCGGGGT TGGCACTAAN TACAAACNTT ACCACAGTAG	660
	ATGCCNAATA CTGCTGACAA ACGAAGTGG ATTNCTNACC GGTGCTGNG ANANAAATCT	720
30	NCCAAGAACN TTAACNCAA TTGGCCACTA CCCCTCTTGA TCCCTCTTNN ATCNCAAGGT	780
	TTGGGANCCG GNGNGCAAAG CCTGATGNN ATCCCTGACN AANITGGACT NNT	833

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 871 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1359UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

45	GATCGGTGTA GTACACGGTT TCCGGCGCG CTTCTGGCAG AGCAGCTCCG ATCACCGCGG	60
	TACCCAGAA CTGCCCGGGC GGTGCGAAC ACTAGTGCTT GCTGCTGATG CCGGCTTCT	120
	AGTCGTTGCC TATTTTATTC CTGCGCGCA TGTTCGGCT GTACGGGCT ATCTCGATGT	180
50	GCGCGAGCAG GAAGCTATC TTCCGAGAC CGTTCTGTG CATCTGGTGG CACCACGCA	240
	ACCGCCGAC GAGCTGGTG ATGCGCTGGA CGCCTGCC TGTGATTGG TTCTGGACT	300
55	ACCGTGTGTA CAATCCGTCA TATACATGG CATCCCGAT GCGCCACCT TTGTTGGTCC	360

EP 0 866 129 A2

AGAAGAACTG CAGCGCACTG CTGCGGTCAT CGCGCACAAAT CAAGGGGCOCA GTGGGCCCCAA 420
 CTACGAGTAT CTGAAGCTGC TCCACAGGCG GCTGCACTCA ATAGCCGAAA CGTTTGGGCG 480
 5 CCGCTTGTGC GAGCTGGAGG ACCATTATCT GGACGAGCTG CTGGAAGCGG TCGACCGTCT 540
 ACGGGGCCAG GCCTGTGCGG CGGTAGGTGC CTGATCTTCT GCTAAACCCA CGCCGAAACA 600
 AAGATAGCAC CCGCGGCTCC GGGTAGCGGC CGCGCGTGGT GACCACTTGC TAGCGTTTAC 660
 10 TTGCATACCC GTATCTGCTT TAAACGTTTG GAAGGTTTAN CATCAITAGT TNNITTTGTC 720
 GCTTTGCTGC CCTGCGNTTG GCAAGGGGCG CCTATTTTTAA NTTACCGCC GNTTAAACGNC 780
 NOCTGAACAA AAATGAATTC NITTINGANAN TCCCGNATTT TNAGGATATC CCNGTTTGA 840
 15 ATTGANAATA CTGATTTGCC NTTTTTNT A 871

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 850 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1360RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

GATCCTTCTC CTCGCAATC ACAGAATATA TCTCGCGGT CATATCCTTC GCGGTGAAA 60
 TAATGAACG TGAGTCCCGC GACCATGTGA GCGATGTGAT GTGGGCGAAA TGCCCCGCGT 120
 35 GGACCCGGTA GCGCACAAA GCGCAAACT GCGGCTCAGC ACTGACCCCT GGAGTCGCGC 180
 AAATCTGAAG AAACCTCCCA CATGCCAGAG CAAAGAGCTT ACGGTCTGTC GAAAACTTCA 240
 CGTGGTTTAC TTGTCTTTA AAGTTGAAAT GATGTATCAC ATTCTCTGTC TTTATATTCA 300
 40 CAAGGATTGC CCGACCGTCC ACGTCAACCG AAAGAAGCAG TGTACCTGG GCATTGACGT 360
 CGATCCTCG CTATATTCTT TCTATGCTCA TATTCAAAGG TAAACGACTT GTTACCAATC 420
 AGGTCAAACA CCGATACCTT GTTGCCAACG GCGGAGAATA GCAGCGTTC ATCTCTCGAA 480
 45 AACACCACAT TTCCCTGTCT GTATACAGTG CCTAGCAGAT TGGAAAACCT GAAATCAGAC 540
 TTTCATGTAG TCCAATGCGT TGCTTTGCTT GATCTTTTCA TGGTGTAGCT CATCTCATCT 600
 CGAATTAAAT TTTCGTACC ACCCAAAAA ACANATCTC CANCTGCATC TCAAGATTAT 660
 50 ATATATATGT TCGAAAATTG AANATOCAT CNTCTAAATG GTACACNGTC ATATGAATGT 720
 GTTNTTTTGC TCCANTATCC CNAACATTAC CCACTCCAGA ATGGGAATAT ATGCCAGGAT 780
 NTCCGCGACT TCACCTGTG TTGACANAAT TCTTGAGNTG CTGACAGCCG AGAAAAAGG 840
 55 TCAAGGTAT 850

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1360UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

GATCGATGCA AACCAGGACA ACTACTTAGA AGAGTCTTG AAAATTAAAA GGTATTGAG	60
TGAATTTGAA AATGACGTAC CGGATAAGAC AGATATCAGA GGAGTTCTCA ATCCGGTTGC	120
AATTGTTGGT TCCCGTGAAC ATGIGTTCTC TGAAAAAACC GGTGATTGG GAGATCTGC	180
GGCTGGAAG GAGCAAGTAT TCGAACATT CTTTGCACTG ACCCTTTGCT ATATTGGTGC	240
AAAGTTACAC TATGGCCATC CTGATTTTGT TAATGCTATA TTGTCTACTA CCAGAGGTGG	300
TGTATCGAAA GCTCAAAAGG GCTTACACTT AAGCGAAGAC CTTTTGTGTG GGATGAGTTC	360
CATATTACGT GGGGGTAGGA TTAAGCATTG CGAGTACACT CAATGCGGGA AAGGCCGTGA	420
TTTAGGATTT GGGTCCATTT TGAAGTTGCT TACTAAGATT AGTGCGGGTA TGGGGGAGCA	480
AATACTCTCA AGGGAATACT TTTACTTGTG TTCAAATCTC CCACTCGACC GTTCTAGTT	540
TCTACTATGC ACATCCGGGA TACTACTTGA ATATGTTTCC AATATCCCTT CTAACCCCTT	600
AATTANGNAA TTTANTCCCG NATTAATGGC GGTCTTGGTC AANCCNACCA AAAATNTNNA	660
NATTCNTITA ACCCCCCAAN CTGCAAAATT TATTGTTGCC ATTNAACCN TAACCAAGGT	720
NCCCCNTCNC GNTTNANCA TCCNNTCCC NCCGGINCCC TTCCAGTTT TGNAGAAAA	780
ATTTAAAAAC CNACNCCGGG TTNCCCCGAA AATGAAACTN NTANAAGNGC CCCCTTTCAA	840
ATTTTTTTTT C	851

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1362RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GATCATAAGC TATTGGGTAC CCGTTGTAGC CTAGCCTTAA AATAATCGAC ATTTTGGAAAT 60
 TTAGTTATTTG CGTGGAAATA AGGTATATAT ATTGCTTCCA AGTTTAATGT CGCTTTTAAC 120
 5 TCACTAAAAT ATGGATGTAA ATGTCTCTCA TTGGACTTTC ATGTTCTATC TATACACTAA 180
 CTGCGATGCG ACTCATTTGTG CTTCACTATT CAAAACATGT TTTATATATG TAATATGCGG 240
 ACGTAGAAGG CAACTAAATA TGAGAGGCAA CTTAGTCGCT GTCGCTGTG CTGTTTGAAT 300
 10 CGCTGGAATC TTTTTCATAC ATGATCTCGT CGCATTATC TTCTTTTAGA ACGCTAAGTT 360
 CCAAGTCCTT ATGAGATTCC TTGTTCTCTT GAGAGACCTC GTCATCAAAG ATGATCTTGG 420
 TGTTGGAAAC GACAGGCAGG TTTTCTGCTT GCGACCTGTG ATAGCCTTCA CTTAGCAGTG 480
 15 ACCCCTCGAG GGACACCATT CTGCCCGCAG TGTAGACATT TTTAACAGTA AATTTGAGTT 540
 TTCCGTCCAG CTGCTTACCG TTGCCGTGAC CCAGTGGCCT AGAGACCGGG CCTTGGCGAT 600
 CCTGTGGAG AATCGTTTCG CTGCTCCCGT TGGTACTCTC TTGTTATGA ATAAAGTCCA 660
 20 ACCATCGGA ATGTTATTTT CTAATGAAGC GTTGAACCTT CGTGATCCAN CAACCATNTT 720
 GTTGAGGTGA CNNTTGAAAT CCCCCNCA CNATCCNAT TTTNGGACA NCCNCAATTT 780
 CCGGCCCCN NTAANCCAG GNTATCTGNT CCANTGANTA CATCTCNCCT T 831
 25

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1362UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GATCATAGCT GCAGGCTGCC AAGCAGACAT GCTGACATCA TACAGCCAAG AGAGCAGCTA 60
 CGCTGTACCC GAGCTGGAAC AGAGGCTAAA CGAGTTTCGC ACTAAATGTA GAAAAAATGC 120
 AAGCCACTTT CAGGCACTAC TTTCACCTGGT AACTGAGATA GACCATCCCG ACAGCAGCCG 180
 45 GCTAAGTCAC CGTACAGTAG TCTTGACATA CATGGAATAT CGCTAAGGAA GGAGGTGTAA 240
 TAGGACACAA AATCATGAGA AGAGTATTGG CTTGTGCAAG ATGCGGTGGG CACAAGATCA 300
 AATGCGTGCA CAACAACGAG CCACCCCTGCT CTTACTGCCA GCACAAAGGC ATAGCGGAGA 360
 50 AATGCGTGTT ATCATTTCGG CCCAAGAAGA GGCGCAAGAA GCGGGAATA TACTTAGAAG 420
 GGGTTGCGAT GCGCTGGGC GGGTATCCGG TGCAGCAGTT GGAAACTGCA GATCTGCAAG 480
 AGCATAAAGC CAGAGCGGAC GGCCTGTATG AAAGCCAAGC TCCTGTGCAT GCGCAGGACT 540
 55 ATACGATCGG GAGCAAGCTG CGCAGATGTA CGAGCTGGCC AGCAGATGTA CTACGGCTGC 600

CCAGGGGTAC TCGACGGTTA TGTCGAGTAG TGCGAAGGTT CCCAGGCGGG TTGATTCTCC 660
 CGCCAATTGC CACCGGATT CTAAACCGAA ANAATGCAAC NCATGGAACC NGCCNACTT 720
 5 TMTGGACTG TCCCCAGTGC CCNATGCATN GTGCACTTGC AINGAGANNI TGTCATCCTT 780
 CCCCAGTGG NGTITANAT GANACCNCCC AAGAATAACC CCTGACCGTC TTTGGTCTT 840
 TTTGCCCCC NCCT 854

(2) INFORMATION FOR SEQ ID NO:515:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 853 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1363RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GATCATTATC AGCATTAAATC TTCAACTCG CATTGCTCT TAAACCAATA ACAAACCGG 60
 CAGATTGTC TCCAATTGCG TAAGGATCCT TTAACCCCTT GAGGGATACT TCAAAAAGGC 120
 CTTCACTAGG CCAGOGAATA TTAATCTTGG CATGGAACAT ATTCTAATT TTATCCAGA 180
 30 AGCCTATTTT CTGGATGGA TCAACTGGAG GTTTCGAAA ATTGTCTAAA CAATTCATGG 240
 CCTGTGTAT AGCAGCTTCA TAAGAGCCAC CCCATGTCAC CATGTGATG TCTTTGAGT 300
 GTATATCCAT TGTTACCTGA CTGTAAATTT TAATAGGCGT TAAAGACCGG CGGAAGCCCA 360
 35 ACGAATAATA TAGGTCTATC TCAGAAGAAG TAACGGAAGG AACAAGCGC ACAAATATCG 420
 TTAGTAGCTC CTGGTTGAT TGAATCATAT CCTCCAGTAA TAAAGAGGTC ACCATACAAA 480
 TGTATAGCGG GAAAGAACC TTGTTGGGAA GGCATAGCTT CGGCATATGG ACTAACGGTA 540
 40 GINGGGITAA CCTTNAANA GCCCCCTTAA TTCACCCANC TTGGCTTCCA ATNTAAAAGG 600
 GAAGCCNCCA NPTATTCTGG GTTANITTTG GAACCCCNIT TNCNCNCAAN TTTAATNAAT 660
 TNCNNITTT ACCCTTCCA CATNANGCT TAAANTNCA TGTTTACCC CCCNGCCAA 720
 45 GANNTCNCC ATTTTGGAAA TGTTANATC CANACCCCT TNCATNTIN NAGGANCTTC 780
 AACTGTCCNT TNCNCCAAA ANTTAATCC CCNAAAAAT TCTTCTCTCC TGGGNTTTT 840
 CCCCCCTTAC CNT 853

(2) INFORMATION FOR SEQ ID NO:516:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 858 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

EP 0 866 129 A2

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1363UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GATCGAGGAT	ATTTCCGTAC	GCTGGATGTC	GCTCGATGTC	AAGTACATGG	GTGATCGGTT	60
GGCCTTTTCA	GTGTGGCTTC	AAAATATCAA	GCACAATAAG	GTCTGTCTGC	TGAAGTCTGG	120
TGCGCTGAG	GTCTGGGCT	GTTCACAAA	AGACAGTCC	TTGGACTAA	CATGTGTGA	180
ACTGAGTGC	AAGTTTCTTC	AACTCACAGT	GCTGTGAGT	AACCTACTAG	CACTATTTAC	240
CTTGGGCAAA	GAAGAAGATG	AGGACGTGGA	AGGCTTTGCT	CGTAATATTT	TOGATGGCAT	300
GACCGAAGAT	CCACAACCTGA	ATGCACAGAA	TTGTGTGGAG	ATGATGAGAT	CAAGAGTTAC	360
CACGTTGCAT	AGCTACTTTT	CCCATCTAAC	TAAGGTTGAT	TTTTTTGTIG	ATAAGGTTAA	420
CCTGGCAGAT	ATACCACCCA	GCTTATTGCC	TGAGTTGTCA	TCTGCCGTIG	AGCCTTTGAA	480
ATACGAAGTT	GCGCTTTCTA	GTTTTACTTT	TCAAGTCACC	CGTTTTAGCA	CCCGAACAGC	540
CAGGTATAGT	ATCCTTTTCA	AAAGTCTGAT	AGACCGTAGG	GTCCGTATCA	CATTGTTCATC	600
GTTCGAGTGC	GCTCTCAGTT	AATGCCCTTA	AAATCCCTCT	GAAAAGGCTC	CTGAATACAT	660
CCGGTTTTTG	AAGTCCCAN	TTATATCCAT	ATGGTGANAC	TATACTTTTC	CTGAAAATTT	720
GACTGGTCCA	CGCTGTTTCT	GANACAAAGT	CAATGGTGGG	CAGTTTCTCC	CCTACCNIAA	780
NATTGAAATG	AAACCCCCAN	CTTGAACCCC	GTTCGCAATA	CTGTANGACT	ATTNTTCCN	840
CANAACCCCN	CCACGNAN					858

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 842 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1364RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GATCAGATCG	ACGTACAGTT	CCGTGCGCTG	GGCACACCTA	CGGACAAGGA	CTGGCCTGAG	60
GTCTCGTCTT	TCAGCGCGTA	CAACAAGATC	CAGGTATACC	CGCTCCGTC	GCGCAGCGAG	120
CTGGCAGCC	GCTTCATGTC	TGCAACTGAG	AATGCCCTCG	ACCTGATGTG	CGGTATGCTG	180
ACGATGGAAC	CGACAAACG	GTGGGACAG	ACTCGTTGCC	TGCTCAGTCA	GTATTTTGTA	240
GAGCTTCCGG	AGGGACACC	TCCTACGGAA	CTTCCAAAAC	TAAATAAGTA	ATGACTATGA	300

TAACCTAGAT GGTATACTCG GACGTTTTGT GTTTGTGCTT TGAGGOGATG ACATTGGCTT 360
 TTATGGTATC GCAGACGTTG CCTGAAAAAG ATTCAACGTC TCGGTAACAG ATTTGCGCAG 420
 5 ACTACTTGTT GAAAGAACAA AGACCAGAGC GCTGGGATGC TCACCCCAAT GACGAACCCA 480
 CTCGGCCTTA TTGGCGCTGG CTGCAGGTTT CTTAGCACCA ACAATAGGCC GCGACTGCAC 540
 AAGATCTTTC CCTCCAAGAA GCTGGTGAAC AGGATGCTGT TCCGACCTTG ATAGCGGACT 600
 10 GACCTTCCGG AAATTACTTG CCTTGTATAC GAGCAGTTGT ACACCCAATT AGACAGTTAT 660
 TACGGGCAAT TTGTATATACC CCNCGNCTTG ANGGCNCGA CMTTNTATCC TGAAAAGNTG 720
 CTNGAAAAAA TCCCCGCNAA NGAAAANNCC ATCGCCATCT ANTTGNCCTG AAACAACTGC 780
 15 TTTACTGCTG CCCAATNGAN ACCAAAATCN CGGCGGTACC TTGAOCTTNT CACCCGCTNC 840
 CT 842

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1364UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GATCTAGTGC TTCACAAGCT AGAAGCTCCA ACCATGAAAG AGCGATCGAT CCTGAGAACA 60
 35 CTTTTTCTGT GGAGGCTTAT CAATGCTCTT TCTATCCGCA GCTTCTTCCA GGCAGATGAA 120
 TACTGGCAGT CGCTGGAGCC TGCGCATGTT AAGGCGTTTG GATATGGTGG GCTGACTTGG 180
 GAGTGGCAGC ATGGGCTGGG CAGCTATGCA TTCCCGATGC TCTTTGAAAT GTCTACTAT 240
 40 GTGGCGTGA TACTGGGTGT GGCACCCGG ATGGCGCTGC AGGGGTGGC ACATGCGAGC 300
 GCGCTGTGTG GGGCGTGGT GCGAGCGGC GCGGCGGGCG TGCGCGGAT GAAGGCGTC 360
 TGGGAGCTGC CGGAGGCAGC GCAGGAAGTGT GTGGAGTACT ACGGGTATT GTACGGGCGG 420
 45 CGAGTGGTGA TGGCGCGGT AGCAGGTGTC GGGGAGTTCT ACAGCGTGCT GCTGGTGGC 480
 AAGCTGTATC TCGAGTGC GGATAAGGGG GAGGACCCAG AAGGGGAGC CGGCGCGGT 540
 CAGCGGTGT GCGCTGAATG CTGACCATGA CAACTTCTT CAACTGTTC TTGCGAAGC 600
 50 CAACGTTTAT CACTCCINCA AAATAACCCC CACNGCGNVC CCTCTAACC NATTTGGATT 660
 GGANCCGGG OCCANCTTGT GTTCTCTTGG GCTTCACCN CAACTTTNGC GSTGGCTGCN 720
 TTTGCCCTGC CTGCAAGGCC NATACTTTTT ATCTTGGCCT CCTGCGTGT TCTTGTGCCA 780
 55 AACTGTGCC CACCAAAGGT GCACTCNVIT ANCTGTCCC TAGGTTGCC CGNGCCCCGC 840

GGGTTTTTCN ATACCANTNA NACNCTCCT

869

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1365RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GATCTGCGGC CGCGGAAGA CGCAGAGGAA AGCGAATCGA GCGCGGGAGA GCGCTACTCG	60
ACGGACAAAA GCAGTTACGC GTCTTCGGTG CAGGCGGTGC TCAGAGCGAG GACAGCGTGC	120
GCAGCCAGCG CAGATACAGC AATGAGCAGT TCAAACGGCAG CCAGCGATAG CGCGGGCGGC	180
GCTAAGATGG ATGCAGCGCA CGCAGATGAC GCGACGGCA GCTTGGAGCT GCGGCTTGCA	240
GCCCTCGCCA CGCAGGACCC GGCTGTGGAC AGCGCAGACA CGCGAGCGG CGCGTCGCCG	300
GCGTCGCCCG CGCGCGGCC CAGCCCGCCG CCCANCGCG CGACGGAGGG GTCGGACGAG	360
GCGCGCGGC CGCTGGAGGT GCCAAGCAG CGGGCGGACG CGGCAACGGC GGCCGGCGGC	420
GAGCGGTGC GCGCGCGCC CACCAACCCC TTCGCGTGA TTTCGGTGG CGGCTCCAGC	480
ACGTTCAAGC GCGCGCGGG CGCGGACGG CAGGCGTGC GCACGTGTC CGCGGGCGAC	540
AAGGCGCAC CCGTGTCCG GAACGAGCAG AGCATGCTCA AGTTGCCCG CNAGCNCANC	600
TACCTGACC ATGAATTCNT CNACTGTTCA AAGANATTAA TTTCCTGANA ACNTGAANAA	660
ANCGTCCCT GTNCTTGAAG AANCCCCCN ANTAACNACC CCTNGACAG CTCNGATTTC	720
CTCNCCTTA TINTAAAAA TTTCAAATNC GGGTGGINCT TCCCCNCTN CCAACNTTT	780
TAAAANGTTC CCACGGCNIN NIGNCCCN NATTTGGCCC CCGTTCCNT TNCCNGGT	839

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1365UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

EP 0 866 129 A2

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GATCACTGA CGTTCATGGA GGTGCAGCA CTGCAAGACA GCGAAGCGT GGTGGGCGG 60
ACGGGGCGG CGGCGGTGCA GCTGTATGTG GGGCCCGGG GGGGCTGG GGGGGGCTG 120
GGGAGGGCG TGGACGAGTT GCTGGCGGA CCCTTAGCGG CGAGCCCACT GGGCCCGCG 180
TGGGATGTGT ACTTTATGCA GCTGGGCGG CTGGGGGCT CCGTTTCCA CTGCATGAAG 240
CGGCGTGTG GGTGGGTGAT TGTGGCGGCC TGCCCGGTCA TTGCCACCGG GTATAATGGG 300
ACGGCGCGC ACTTGCGCAA TTGCCACGAC GGGGGGTGG CGGCTGCAA CGGGGGGGC 360
AGTGGCTGC ACACCTGTCT CTGCTTACAC GGGAGGAGA ATGGTTACT GGAGGCGGG 420
CGGGAGCGG TGGGGAGGG CGGGGTGCTG TACTGGACA CCTGTCCGTG TTTGACATGT 480
TCGGTGAAGA TCGTTCAGAC GGGGATCAAG GAGGTGGTTT ACTGCGAGC CTACGGATG 540
GACAGCGACA GCTTCAAGGT ACTGGGGGG GGGGGGTCA GGTCCCGCA GCTACAGGAC 600
GGGTCCCCC GCACTTTTTA TTATATNNGC NGGCGCTTT CCNGCAACN GCTAAACTTG 660
CTGTTTTTNC ATATAAGGNC CCGCGGTNC CGACTNCAA GNAATNCCN AACCNITCTT 720
TNTTCCGAG GCGGGGAAT TTTCCCCGA TNNNGGCC CCCCCGTNN TGCCGTTACC 780
CANTCCCCCT GCCCAATCCT CCCCCGAAN CCNCCNCAA CGTCTCGNN TTNCTCCACC 840
CGNCTGNCC T 851

(2) INFORMATION FOR SEQ ID NO:521:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 823 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1366RP

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

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GATCCAACGG TCAACCAATG CCTCCGAGAT TGCCGGCATA GGGGATGAGA TTGCCAAAGC 60
GGAGAAGCAG GACAGCTCCG CGGCGGTGTC TGCCATGGGT GCGTCTAG GGCATGCAGC 120
GAGTCTTTC GGTGCTTTGA ACGTGCTTAA CAGTTCTGCC GAGCTCTTGA ACCAGCCGG 180
AGCAAAGCCT GCTGCGGTG CTCTCAAGGG CATGATGGAG GCTGGGTCTA ACACGACTAA 240
GGCAATTGAC TTCAATCATG AGCGTGCAAG TCATCCAAAG GCTGGCGGG CAGAGCAGGT 300
GATGGGTCTA GATATGGTAC TCCAGAATGC CGTGAAGTCA AGCGAAACCT TTGCAAATAT 360
CATAAAAATG CAGATGGCAT CGACCGAGGA GTCCGAGAAG GCGCTCCCA GTTTGTTGGG 420
CTTGTGTGCG TACTCGACTG ACAAGATCGA GAGCATGAAA TCCGTGATTA AGCTGATAGA 480
GTTGGTGAA AAGAGCCCTG ATGTATTGAA TCCTGTCTA GAAGTGCTGC AAGCTTCCGT 540

GAAGGTCAAC AGATTGATAC CCTCCGAAAG AATTTTNGAC TTACACCCAC ATCCTGGAAA 600
 CTTCATNTTT GCTGCGAGTT ACAAACCTGGC ATTTCCCAAT CTGCCATTIG TTCCCTTAAC 660
 GGNCCCCAAA GGTTTGACACA CCNCCNTCCT NCAGGNTTCA ATNCTACTC CTNNNCCNA 720
 CCNANGAATC CNNTTGGCCC TTNTTTAANN CAAATCNGNC CANATNTACC CCCAGGTTTT 780
 TTTTGGAAN CCTTTTANA CCTTCCCCC CCTCCTTIN NAT 823

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1366UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

GATCTTATCA GGATAAATGA TTTGCTCCCG GAAAGTCGAT AAATTGCTCA TATATGCOCT 60
 CTGGGGGAGA TAATATATCG GACTTTCCGC ATTTTCAGCA TTTCTACGGG GCATGATTAG 120
 CTTCGTAGGC TTCTTAGGT TAGTAAACGA TTGCAAAACA GGOCACAACC CCCAAGGAC 180
 CCTGAAAAGA GAAGACTTGC CGCAGCCATT AGGAOCTATA ATCAATAGAT GGTACCATG 240
 CTTCAACTCG AAGTTAAGTT CGGGGATAAG GACCTGATTA GCAGGTGTCA CTAGTGGAC 300
 ATGAACGAAT TGAATCTTAG AATCGTCGTA TTCTATAATG ACCTTTTTC CATCAGTCTT 360
 CGAACTACTT CCAGCGTCTA GCTGTGCTT GAAATTGTT AACCGTAGGG CCTCTCCCTT 420
 TAGCTGCTGG ATACTACGGC GCAGTTGAC ATAGCGGCCA ATAGATGGG ACCCAGTTAG 480
 CAGTAAACGT CTGTTGGTGA TAAATCAGC GGTGACATCC TCAGCCATAT TAGAACGAAA 540
 GAAGACGGGG ATAGAGCATA ATATCAAGC CAGCAGCGCC CCAGAGTAC TTCACCACAA 600
 AGCTAGTACA ATTCTGACAG TGCTCTTAAA TTTATCTCCC CCGGCTNAGA ATAAGTTACT 660
 GGTTANAAAN AAAAACCCAA TCCATATTC GGTNTTGTAC CNTGAATAAA CNNTNCCN 720
 TTGCTTGACC NCACTTGAAT TTATGACGA ATTACNCA TTTTCCCTG ACATACCGTT 780
 CAATTGNGG TTTGACCTCC CACTNATTAT GATTNAAATC AACCCATCCN GTCTTCNGC 840
 TTTCCCTGGN GATC 854

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1367RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

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GGATCGCCCC CGGTGCGCCC CGTGTGGCCC CGTGCCCCGC GCCAGGGCCT GCGCGCGCGC   60
CAGGCCACC GCGCTCCGC CGTGTGCCC TAGCGGATTG TTCATTCCCT GTGTGCGCTC   120
CTGACTGTCC ACTCGACTC TTGTATCCGC ACCTTCTGCG CAAGTGGCGC CCAAACCTCG   180
TTTTCTGTG TGTCCAGAGT TTCGCTCTCT GCGTGGCTA CTGCTACCT GCGTTTGGT   240
ATGGAGGAGA AGTGTGTGTG TATCTGATTT GTTATCTGCG TTCTCTCTC CTATAAGCTT   300
TTTGTAAATG AAAAAATTAT GAAAAAGGGA AATCTGTGGA ATTTGAAAT GCTGCTGGCG   360
CTGCGTGTGT CAACTTCAG GCGCGCGCTC TCGTCTACT GCTCTGTCT TGGCTAGCT   420
TTGGTATTT TTTCTGCTCG GTTTCGCTTC TTTTCTGCG AACGCAAGG GCGCTGGT   480
GCCTGAGGTG CCAGGTGGCT GCACAAGTGC GCGCGCGCGG GAACGAGCC GGTAGTTAC   540
CGGCAACTC TGCGCGCAT CCCCTGCGGA GCGTTAGGC AGGCTTATT TAATTGTTAC   600
GTAAGTCACG TGGAGCTAGC ACGTCTTGG CAGCTCAGC GCACTCAGC TAGGTGTGA   660
CTAATCGCG CGACTGGTG GGTAAANGA CCGGTACNC CGTTAAGTTG GAAAGCNC   720
AATAAATTAC NTACCNNTA AACACACGGG ANAAAAANAN NCCGGCNC NAAGNANTT   780
TTGCCCTTGA AGCGCGTGC CCAAGCGCG GNCNCCCCA GAAN   824

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(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1367UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

```

GATCTTATGG GTGTTCTCT AGGCTGAAA GCGGATATG GACAGTCGAA ATGGGCAGCA   60
GAATTTATTA TAAACGTGC AGGTAGCGT GGTACGCG GTGTATATT GAGGCCAGC   120
TATGTACTG GTTCCCTTC TACAGGAGT TCTAACGCG ATGACTTTCT GCTCCGTTTC   180
CTACGGGGAT GTGTCAGTT AGCAAAATT CCTGATATTG AAGGAAGTGT TAATATGTA   240
CCAGTTGATT ATGTGGCAG GTTAGCAACA GCGCTTCT TCTGTCATC AGGCAATACA   300
CATATGATGG TTGTAAATGT CAATGCGAAA CCAAGAATAT CATTCAGGA CTATCTACTA   360

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GCACTGAAGG AATACGGGTA CCAGGTAACA TCAGTTCTTT ATGACGAGTG GAGTAAGGCG 420
 CTTGAATCGT CGAGTGATGA AGAAAATCCT TTGTATCCGC TATTGTACCT TGTCCTAGAT 480
 5 GACTTGCTTA AAAACTGCGC AGTCCTGAAC TCGATACTAC TAATGCGAAA TTGTGTTTAG 540
 AAGAAGATTT TGGCGGGACG AATATTGAGC CAATTATCAT TACTTCGGTG TCATTAGAGT 600
 TGTTGGGTCC CATATCTCAT TTTTGCATAA TTTAGCTCCC NANAANAACC ACCTAAAGTT 660
 10 CCCAGCCCTT GGCNATATTC NCCTCTCCGA CGAACAAATT CCTTAATANC NCATACCNC 720
 GCNCCGAACA TACANCAACC CNTAAATACC NCAAAATGTN GACAACATGA NTGTTTATTT 780
 TTTTATATTT ACAACCTATT ATTAACCAAA TTINATCAC GATCCTCTNT GACGCCCTCT 840
 15 CTGACAAATT 850

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1368RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GATCATCTGA AGTAATATAG AATCTGCATG GCGGCAAAACC GTTGCGGTCC AATGTAGCGC 60
 CGGTGTAGCG GCCATCGGTA AAGGTGAGCA ACGCAGGGCC ATCCCATGGT TCCATCAAAC 120
 35 AGGGGGCCCA GTCAAACCAA GCCTTCAGGT TAGAATCCAT GTCTTGTGG TAGGCTTCTG 180
 GAACCATCAA GCACATCGCT TCGGGTAATG ACAGAACACC ATTTATCACT AGTAATTCTA 240
 GCACATTGTC CAGCGGGCA GAGTCGGATC CGCTTCTTC GATAATCGGA TAAAGCTTCT 300
 40 CCAGTTGGTC TTGGAAAACG GCGGATGCCA TGACACCTTC CTTGCGACGC ATCCAGTTTT 360
 TGTGCTCTT TAGGGTATTA ATTTCAOCTT TGTGTGCAAG CCAGCGCAGA GGCTGGGCAC 420
 GGTCCTAAGA TGGGAATGTA TTGGTTGGAG AAAAGAGAGT GTACCAGGC CAGGTGAGAC 480
 45 TTGAAATGAG CATTTGGTCAA GTCTGTGTAA TAATTATACA CCTGGCAGG TCAATTGACC 540
 TTTGTACACA ATTGTCCGT TATTTAGGAG CACACAGTA ACAGTTCTGA TACCGATGGC 600
 CGTTAAACCC NCTTTCTTT AAATNTAAA CTGGCATCCN GAAGTCTCTC GINATTANCC 660
 50 TGAATCTNCN CCCGATACTC CTGCCATAT TTCTTTNCN CAACAACGTT TTTGAAATGG 720
 TTTCCCAAAA CCAAGGAACC NAAAGAAATN CTNIGGACNC CTCCAACCN AACCCNNATT 780
 TAACAATCGG TACTNGCAA TTINTCAAG CNNAACCTGT NNNCT 825

(2) INFORMATION FOR SEQ ID NO:526:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 839 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1368UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

15	GATCGTGACG ACTTTGTGTT TTACTTCAAC CGTATTGCAA CGATCTTGGT TTGCGGGGCT	60
	TTGGATGACA TTGCTATCGT GGGGATGAA CTGCCATTGG TGA CTGCATC CGGATATCAA	120
	CTGGAGAAGC CTGTTTCATGT GAATTTTGAC AAGATTACGG CTGTGAATAT TGTGCGCTCT	180
20	GGCGACTGTT TCATGGCTTC CCTACGCCAA ACAGTGCCAA ATATATCCAT CGGTAAATTG	240
	CTCAITTCAGT CTGACTCTCA AACAGGTGAG CCGCAGTTAC ATTGCGAGTT CTTACCACTG	300
	AACATTGGCG GCTCTTTTGA CCAGGTCTTA TTGATGGATG CACAAATAAT CTCAGGGCCA	360
25	GCAATTATCA TGGCTATTCA AGTGCTAGTT GACCATGGTG TTGAACTATC AAAAATAAAG	420
	GTTATTGTCT ACTTAGCCAC TGAAATTGGA ATAAGAAGGA TAATAAATGC CTTTAACAAC	480
	AAAGTATCAT ATATGCGGGC GAAATTATAT CAGACGAAAG TATGACAGAT GGCCAATGTA	540
30	CTGGGCGAGG GTGAGATTCA TCGACTCAAG ATACTTTTGGC TGTGACTGAT TCAGAGCTTT	600
	TGCTGCCCAN GCAGGAATTA ANAACTTTTG GTGCTATTGC ATGTTACAAT ATTAGCATTT	660
	ATCATCCATA CCATAGCTGC TTTACNATAG CATNTAATTT TACTATCTTT NAACCCACCC	720
35	AGACTATTTT TCCCCCNCTA CTTTACNAA ANTTTAANCA ACTGACCCCC CGNTATAATT	780
	GCCATCCAA CACCCCCCNC CTCNTAANAA ANACCNACTT GGAACGAGTG GGAACCNCC	839

(2) INFORMATION FOR SEQ ID NO:527:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 851 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1369RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

55	GATCGCTAC TTGTCTCAGG AACTTGTAT CATGAGAGAT GATATGTGCA ACAGGTTTAA	60
	GCGCAATAGC ATTATTTTCC CAACAGTGA AGAGGAACAG AAACAGGAAT ACATGCTGTT	120

ACAGCAGGAG CTCAGGATG ATGAACGTAG TTGGATCTC TCATTAGTC AACTGATTAA 180
 GTCCAGGGAC CAATTGCTCG CCACTGTCCA GGAGTCCAGG AAGATAGTCA AAACCATCCT 240
 CGATCAGCAA CACCTTTCCG CCTTTACCTC GCAGGTGCGC CCTATAACGT GGGACTATGA 300
 CTACACGTTC CACCTGTCCG CAATACCCCT CACTATGATC ATTTGCGACC CAACTGCACC 360
 GAAATATGAT GTTACTTACA ACGGCTGCAA GAGTATCAAT CCAGGCTCAT TTCTOCACAA 420
 GCGGAGOGTC AACTATACTG AGTACACTCC TTGGTTACGG AAAGCAACAG AGGAAGAAAT 480
 TGTCGTGTAG GACTTTTAAAC TTACATATAA TGTCAAATAT AAAGGTTTCA GAOGTCGTCA 540
 TGTTCGTAT GGATATTTCT TGAAGTTTTC CCGTAATATC GTATGGCATA CAGTAGAGGG 600
 GGTCAATNGG AACCAACCCG CGTGCTTCTT CAACTGGNC CCCANCAAT CCCAAAAAT 660
 TGTGAAAAAC TTCCACCTAG ATTTTCTGGC CATGCGGAT GCGGCGGCT CTTTGATTCC 720
 TNCANCCCCA GANNAATCNC CCNCTTTCTT GTCATCCAT NOCNITNGC CCAATTCNA 780
 NGTTAAANG CCCCCCNC TTTCACCTT TNGGATTTIN NINGTTTCOG TCGGCGGCC 840
 CCGTNCAGAC C 851

(2) INFORMATION FOR SEQ ID NO:528:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 858 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1369UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GATCAAGACG AAGCAGAAGA AGACGGGTA CGCATGTACG TGCCACCTGG TGCGGTGGGA 60
 GCGGGCCAAG GCGATCGCTC TGGAGGGCGA CAGCGGCTG GGGCTGGTAA TATGGGTGGA 120
 CCGACGGTG GACACACGGG CGCGCACAT ACAGAGCATT CTGGGCGAGC AGCAGAGGAA 180
 GTACGGGGCG ACGGTGCCAA CCATCCGTGT GCGGTGATT AATTGGATCG AACATTGCGA 240
 GTTGTTTTTC GGCAAAACGC TCGACCGGAA CACACGGGAC TACCTGGTAA ACGTGAGCGC 300
 TGCAATGGTG GTGTGGGCG ATGTGGTGGG GACCTGCGC CCGACCTGA GGCAATATA 360
 TTGCAAAAC CTGAGGTACC TGATAGACTG GTTGGATACC CCTGAGAGGC CATGGCCGTT 420
 GCGGACTTTC TATCCGTGA AGGTATACAC TGCAATGGAC GTGGAGGCGT CGCTGCTGAC 480
 CGAGGTGAAA TACTCCCCAG AATAATGACT CCCTGGAGG ATGCGTTTTC CCAACGGCAA 540
 GAACTTACC ATAGTTCCNT GGACAAAGGA ACGGTGGAAA TGCGCGGATC TCCCTACTAC 600
 CCAATAAGC GTTTTGAAAA ATGACTACAT TNGAATCCN CCNACCAAAA TTGAACACTC 660

CCCGGAANNA NCATACNAAN CCAAAAGTTT GCTAAATATC TCTTTCQNVN GTACACTGAC 720
 CCNACTIVTT GCAGGGAAAG GNCITGTTTTT AAACCTCCAC TONGACTTNA TTTTACCCCT 780
 CCNGCATOC ACCNAANCAA CACCTINTON AACCATAGAA CNVITTTTCT TTTAAAACAC 840
 TNAGAAGCAT TTNAAAAT 858

(2) INFORMATION FOR SEQ ID NO:529:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1370RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GAICTTGTAC AACTGAGCCT AGGICTTGTT GTTGAACGGT AACCTCCACA TTCATTATTG 60
 GCTCCAATAT GGAGAACGCC GAAGTTGGTA AACTOGTCAG TGCTGATATG ATTAAAGGAC 120
 GCACAGTCAG CAGAATGGAT GCAGCTGCTG CGCAGTCTAG CGGTAGCGGC CAGCGTTTAA 180
 CATGAATCAC ACACGAGTGT AGAGGAAAGC CTGCGGTITT ACCACCTCTT TGCAAAGCCA 240
 CTATGCAACA CGAGATGATA GAGTTCAAGA ATGCTTCATA TTTCATGGA AATGGCCAAT 300
 TGICTTGGTT AAAGCGTGGG TTGGATCTA TGACAAGATA GTTATTATOG CTTCCTAAGG 360
 GGTACCATCC GTTACTGAAT AGTACTTTAT CTCTTCATT GTATTGCCGA ACTTCGAGTT 420
 CGAACGAATA TCATCATCT GTTTCAGAST GCTTCCTCTC TGTAGCAGTA TTAATGGITT 480
 CCTTGATGA AACTGCTACC TTGCTACTC TTACAGGCGC CTTAAATTCA TTGAGCAGCC 540
 GTCGCTGCT ATTTCCAGTG CATTCOOCC ATCCCATTC TCACTGTCTG ACCAGTCTCC 600
 TCATCCCTCA CNAATACCAC NAGGTTTCC CACTCGTTAG CTGCNNCANG ATCACCNNAT 660
 ANCTTTTNT TCCCAANIT CCGCGTCCN NCANCGNCT AAAANGGTGG NGGTANICAT 720
 GGGINTTCC CANITGNANT TNGCTTTTG AAAACAATC CCTTTTAAAGN TNNAGNCNA 780
 AANGGGTCC CTCTAANIG TGTCCTCTG GGCNCNNC CCAATNCCG AGAT 834

(2) INFORMATION FOR SEQ ID NO:530:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 840 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1370UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

5	GATCGCAGAG GAGGAGCCCA TTCGGACGCT TGCATGGAAG GAGGACACCT TTGAGAATTT	60
	TCTGGCGGAG GTGACATCCG ATGAGGCGCG CGAGACGCTG GTTTCGGAGG AGGATGCCGC	120
	CACCTACCTG GCCAAGCTTT TATGACGGCT GTCCGTGCTT TTAAATTGTT ACATACTGTA	180
10	CATAITGCTT TTAGTCGTAC CACATTTTGA TCAGCTCTTC GGAAACCGCG CTGGGGGTCA	240
	GCACGCCAG GTCTGTGATC AGCGCGTAA TGTGCTCGTG CGAGGTGTAG TCGATGGAAG	300
	GGCTTAGCAG CTGCTCTGAC TGTGCTGTC GCGAGAAGTC CAGCGGTCA CGCTCCATGG	360
15	GCAAGTGTG GGGGAAAGC GGAACATCC TTACAACTT GTGGGATTG CTTACCAGT	420
	AGAATGGCTT GGTGCGTTC TTGGGAGGA CCGCTACCGT GTACGTCCCC ACGAGATTTA	480
	TGATGCCGCC GGAATCGGCC ACGCCCTCCG CGCAACCG CACTGTGCGA TTTTGTGTAT	540
20	GATGGACCA CCGCGCTGTC CACGATCATC GTCACCGAT GCGCTTTGCT TGCAGCAGGT	600
	CATACAGCTG CTGCGCTGTC CCGAAGGCC CGTCTCCGT CACGANACAC CGGAAGCAAT	660
	CACTCTCAC TGTACTCAC ACGAAANCG CCGCAAACC AGTTCCAAA AAGTCTCTC	720
25	TGTTAGATCC NCCATCTTT GTNCITTTIN TNGACGCTG CCGAANCAA AAGTCCNIT	780
	CCNCGTTC TGTGNACCC CCGTCCANA TMTTTTTC CCCCCNCCC NATTTCTCT	840

(2) INFORMATION FOR SEQ ID NO:531:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 835 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
35	(ii) MOLECULE TYPE: DNA (genomic)
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1371RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

45	GATCGAGAAC AACTACGACA ACAGCCAGC AGACGGGCG GAAGCGCTCA AGCCGAGCTA	60
	TATTTTGTAG TACCTTGCTT CGCTCATGTA CCAGCGCGC TCAAAGCTGA ACCCGCTCTG	120
	GAAAGCCATC ATGCTGCGG GGTGCGAGGA CGGCGAGGC TTCTCTCGTT ATGTGGACCT	180
	CAAGGGGTC AAGTACTCG CCGAAGCTT GGCTACTGG TTTGGGCCC ATATGGCCAT	240
50	TTCTCTCATG CGTAAAGTC CAGATGCGA AAAAGAGTC GCGGCGTGC ACCTCTCAAT	300
	TGCGGAGCG ACTATCCTGG AGTCCATGAA GGTGTATTTC TACCGGATG CCGTAGTTC	360
	CCGTGCTTC TCGCTGCCA TCATCGACAA TGATGCCGT GTGAGCATGG AGCAACTGA	420

AGTGGAAAAC ATGACCTGGG GGTTCGCCAA GGATATTTCG GGCTATGGCA CCCAGAATGT 480
 CTGAGTACCG GCGGCAAGC GCGCACCTG TATACTATCT TGTCGGGGCT GCTCGCCAAC 540
 CGCTGGCTAC TCACATACAT ATCAAGATGC ATAATCAATC TGCTCATGAA CGCACTCTG 600
 TTTTGTGGAT ACTCTTCTCG CCGGTATCCT GAGTACGCTG GAGTGCAAAA AGAGCCACTT 660
 TGAAACAACA CGAGTCGCAG CTAAGNGAN ATCCGANTAA NCAACNCACA CTTCAATTGA 720
 CTTATGAAAT GCCCAAGGTT GATTGAACCTG ACGTCCTTGG AACNNIGGGN CGTGGAAACG 780
 CCTCTTCAN TTGAACCAAA GTCCACAANN AGGTATTTNT TTNAACCGTT CCGCC 835

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 850 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1371UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GATCCATGT GCGTTTGGAG GTCACGCCAC GGACGTGGAC ATGTAAGTGA TGAGCTTGA 60
 CCGGCAGCTC TTCATTCTGT CCGCACGCAA GAAGCTTGAG TTCCCGAAGT CTCGGGGGA 120
 GAGTTGGGGG TACCTTGGGT ATTACAGCGG ATACAAATTC GAGCGCATGG CGCTCTGGA 180
 CGTCCGGTG GCGGAACTC CCGCGAGGT TCTGGAGAGC CCGGCAAC AGGTCTCCG 240
 CAACGGTCG CAATACAGGA CTGTGATGAG AACCGCGTC GGGGAGCACA AGCTGGTGCT 300
 CGAGCTGAG ATCGACGCA TCATTGACTT CCGCGAGCT ACGGGGACA ACCTGAAGCA 360
 CTACGTGGAG CTGAAGGTGT GTCAGAAGAA CCGAACTTC TCAGAGAAAC TTTCTCTTC 420
 TTGGCTGCAA TGCTTCTTG TGGCATAAA CAGGGTTATT ATTGGATTCC GGGATGAGAA 480
 ATTCGTCTG AAGAGCGTG AGGAGTTGN TACGTACAG ATCCACACC TGTAAAGGG 540
 CACGGAATAT TCCAATGTAT GTGTGAGCC AATAGAGTG TATGGTGCTC TTACGAAGTG 600
 GCTATGTGAG CTCGGCGGG CCTGAANACA CTCAACTGT ACAGCTCTCC NGCTCCNIG 660
 GTGCTTACGT NTCNCCCT GGCNACAAT ACTCCCNAN NGGACNATT NTCCTGTTTG 720
 TTCCCAATT GCGCGGGCC CNATATAANN CANATTCCN CNTTNTTCC CTNTGNTTT 780
 TAAAAACCN TINTTCCAC CNATTNCCC AGANNACANA GGNNTCCC ACCANNCTN 840
 CCANCCNA 850

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 835 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1372RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

GATCTTAAAA TAAGATAGAA TGGTAATAAA TATCATTCAG GTACAATAGA TGCTGGTGTT	60
ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT	120
ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGTTA CTAAATCTTT AAAAATAAAA	180
TAACCATGCA TTGGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA	240
TGTACATGTA ATAGCATTAA ATGCATAATT ACTATTGCTG CAATAATAAA TGGTACTAAA	300
TAATGAAATA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TCCTCATAAT	360
CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA	420
GCACCTCAAT GTGACATTTG TCATATACT AAACAATAAC CTAAGAAAGC TGCTGCTATA	480
GTTAAAATAA AGATAATAAC ACCAACTGTT CATACAATAA CTCTAGGTGA TTTATAAGAA	540
CCATAATATA AACCTTTACC AATATGAATA TACATACAAA TAAAGAAGAA TGAAGCACCA	600
TTAAGATGCA TATATCTAAT TAATCAACCT AGTTGTACTC TCTCATAATA TGTTCTACTG	660
ATGANAAAGC TAATCCATAT TANATGAATA AGCAATNNCTA AAAAATACCN GTNAGAATTG	720
AATACTAACN TAACCTATAA AACCNAAATC NTCATATAA TGAGAAGGTG AGGGAATCAT	780
ACNACTATAA CNATTTAATA TATTGATTCT ATTNCCATTT TNNTNINAAT TTTTC	835

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 854 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1372UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

GATCTAGAAT TATTAAAGCA ACTATTAACT AATATCTATA ATAATAATGG TTTATCATT	60
AAATCATTA AGATAATTAT TAATAAATTA CCATTTAATA ATGATATATT ATTATCAAAA	120
AATTATGTTA ATAAAATAAA TAAATATAAT TTACTAATTA ATAATAATTT AAATAATAAT	180
AAAAAAGATT TAATTAATTT ATATACTTTA GATAATAAAT TATTAGATTT AAGTATCTTT	240

AATAATATAT TATTAGGTAA ATATTTAGTA GGTAGTAATA TCCAATTAAA GGTAGACTA 300
 TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAGGTAC ATTTAATAAT 360
 5 TATATATATC AATGAAGTAA ATTAAATAAT TTATATAAAT TAAATTATAT ATCACTTAAT 420
 ATTAATAAAC TTAATAATCT ATTTATTAAAT AAAAATGGTA TATTTAATAT TAAAATTAAA 480
 TTAAATACTA TTTAATAAAT ATTCTAAAGT AATTTCCTAT TTATTTTATA ACATTTTAAA 540
 10 ATGTTTTATG TTAAATAGAT AATAATCAAT TAAATAATAA AAATTAAGAT GCCACAAATA 600
 ATTCCATTTT CTTTATGAAT CAATTAACCT ATGGTTTCTA TTTATTTTAC NATTTATCNC 660
 ACTACTNATG TTTTTTTACC NNTGAATTIN ANAATATATA CTCNCNANTA NATATTNCA 720
 15 AATTATAATA TTAATTAAAT TTAATTAATC TATTATGATC CTNNNTNTAA ANATATCAGA 780
 ANAATTTAAT ATATATATNG AAATATNITT ATCCCCCGG NCACTTGAAN AAAANTATAG 840
 20 TTTCTTCCCC ACAT 854

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1373RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

35 GATCTTAATT TAAAATTTTA ATTAACATAT TATAATTTAG AAATATATAA TCTAGAGATA 60
 TATAATCTTA AAATCATAGG TAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120
 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA 180
 40 ATTTTATTTA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240
 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTTAATATT 300
 AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA 360
 45 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420
 TTTTATAATA TTTATTTTAA TTAGTCTAGT AATATCTAT TTAATAGTCT ACCCTTTAAT 480
 TGGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAT ACTTAAATCT 540
 50 AATAATTTAT TATCTAAAGT ATATAAATA ATTAATCTTT TTAATTATAA TTTAAATCAT 600
 TATAATAAGT AAATATATTA TTATTTTATT AACATAATTT TTGATAATAA TATACCATTA 660
 TTAATGNNN TTATAANAAT TATCTTNAAG GATTNNNTGG AAANCCTTNN TTTTAGAAAT 720
 55 TNGGTAAANG TGNNCTAAAN NCCAATCCCN AATTATTAAA TTAATTTAAN AANAANNANC 780

CTTTTNTTNA ATTAGTTTIN AATTTAACCC NCTCCCCINT TTAANAT

827

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1374RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

GATCAATGAT AAATCGAAAT AACTGATAC TATTGTAGCC ATTTTCTGA ATTAGCACT	60
GGAAACACTT TTAAACCTGT TCOGGAGTGG TCTCTGACTG ATTGGAGTTG AGCGTCTGC	120
CGCTAACTGC CTCTGCTGTC GTCTTAGCTC CGACGTTTTC CACTGCCCCG CGCTGGGTGC	180
CCACAGCGGT CTCTTCTGA ACTGCGAGTG GCCCCAACAT GTGGTCCACT AGCGTTGGTG	240
CGCCGCCAAG TTGCTGGAAT AACGCACCCA TCTTAAACCA GTTGAACGTG GCAAAATCTC	300
CATACGCTTC GAATTGCCTG AGATAGGAGT TCGCTGCAT GCTCTGGCGA AGAGCAGCAT	360
CCGCATGCTG ATTGGTGCTC TCATCTAGAG CGTCGCTGGT AGCATCTCCA TCATTTTGA	420
TGCTGTGCTT CTGGGTATTG CTAGCATCGT CTGTTTCGG ATACATAGAG CCAGGTACAC	480
TCACGTGATT CAACTCAAGG TAGTCTTCCA GCAGAAACCG CTTGGCCCCG TTGACAAACT	540
CCTCAGGGCT CAAAAGCTTC CCGCATTTG TCAGTTTTCG ATTGCGTATA CTCAAGCTTG	600
CAAGTCGCTG ACGCTCATCA CGGCATGOGA ATCTTGGGCA AAAGAGAATT GACCTCAGTT	660
CAATCGCCCC CCTTGCTTTA AAAACATATT AACTCTCCCN CGCNCNCAG GANAGAATNC	720
TCCCGTACTT CNANGNAGNC ANCTINIGCC NTCATCTCAA ATTGCGNACC TNGINANTTG	780
GANCCNITCC CGAGCCCCCTC TGCCCCCTTA TTGANGNCCG NCCCCGTTG A	831

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1374UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

GATCTTAAAG GGGATATAA AAGCTGTACA AAAGAAGATG AACAAAGCTTC CAACGCTTCT 60
 AAACCTTGAT ACTTCCGCCA TTGCCTTGGG AGATGAAGGC GAAACAAAAG AAAGTACCGA 120
 5 ATTTAGGGCT ATTATTAAAG AGTTTGAAC ACAAAATAGT TTCCAGAAGA TTTTATATGG 180
 GAATTAATAG ATAAGACTAG CATCTTTGGA AAACCTTTATA TAAACCAGGC AGATTAGCTA 240
 CCTCTACAAT GTCTTCAGA AGTCTCGTCG ACGCTAGGAG TCGCCTCTTT ATGTTTGGGA 300
 10 AAACCACTTG TTCCAGAACT GTCCCAATAT GCTCTGCCCT GGAAATATAA TAAGCGGAG 360
 CATCGCCATC GATTGTGTCG TCGTTTATAT CTACGTGCTC AATAATCTCA GGAATATAGA 420
 ACAAGGCAAG TTGTGGAAGG ATTCTTCTA GGCACCTCTT TTCCGACGAC CAATCTACCT 480
 15 TAGTTCCCAT TCTGTAGAGG AAAAATGGAA GTTTAGAAAG AGCGGGGACA TAATCCTTTA 540
 AAAGTAAGGG TACACTCTTA ATGCGAACGT TCGICAAATC GGTCTCGTCT CCACATATTT 600
 CAATCGAGTA ATAGTTCTCT AGCATTTCTCT CATGTCCACA CTGTTGAGTT ATTCCAAATA 660
 20 TCGAATGCGA CGCATTTATC ATCTTAGATA NGTTTGGTAT ATCGCTAACT TCGCAATCT 720
 CAACCNCAAC CTGATATNA TTTCCCGAAN TTTGNNAATN NNNATCCCAT TGANAAAATT 780
 CCTTCCTTAG GACCTATCAC CCAAATANIT AACCGCGNIT NANGATCCCT GNTTGGTCAC 840
 25 AACCNNGGT CTNNN 856

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1375RP

(x) SEQUENCE DESCRIPTION: SEQ ID NO:538:

GATCTTAATT TAAATTTTA ATTAACATT TATAATTAG AAATATATA TCTAGAGATA 60
 TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAATA 120
 45 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA 180
 ATTTTATTA TTTAATGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240
 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTIAA TTTTAATATT 300
 50 AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTTA TTAATATIAA GTGATATATA 360
 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420
 TTTCATAATA TTTATTTTAA TTAGTCTAGT AATATTTCTA TTTAATAGTC TACCCTTTAA 480
 55 TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC 540

TAATAATTTA TTATCTAAAG TATATAAATT AATTAAATCT TTTTATTAT TATTTAAATT 600
 ATTATTAAATT AGTAAATTAT ATTTATTTAT TTTATAACAT AATTTTTTGA TAATAATATA 660
 5 TCATTATTAA ATGGTAATTT ATTAATAAATT ATCTTTATGA TTTATGACAA CCATATATTA 720
 TAGANATTGT TAATAGTTGA CTAATATCCN ATCCAACCTN TATTNATTIA NAGATCATAN 780
 10 ACCTTTTATA CAATTATTTT NATATAACAT NTACCTNATT ANAATATN 828

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1376RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

GATCTATTTT GCCGACTTCC CTATCTACA TTATCTATC AACTAGAGGC TGTCACCTT 60
 GGAGACCTGC TGCGGTTATC AGTACGACCT GGCATGAAA CTATTCCTTC CTGTGGATT 120
 TCAAGGGCGC TGTAAGCGC ACCGGACCCA GCATAGATGC TGGGCTCTTC CAGCCATAAG 180
 30 ACCCATCTC CGGATAAACC AATTCGGGG TGATAAGCTG TTAAGAAGAA AAGATAACTC 240
 CTOCCAGGCG TCACGCGGAC GTCTCCACAC TCAGTTACGT TGCCGTGAAG AATCCATATC 300
 CAGGTTCCGG AATATTAAAC GGATTCCCTT TCGATGGTGG OCTGGAAAAT CAGGCCTTTG 360
 35 AAACGGAGCT TCCCATCTC TTAGGATCGA CTAACCCACG TCCAACGTCT GTTGACGTGG 420
 AACCTTTCC CACTTCAGTC TTCAAAGTTC TCATTTGAAT ATTTGCTACT ACCACCAAGA 480
 TCTGCACTAG AGGCGGTTGG ACCAGCTTT ACAGCCTAGG CTTGCTCACT GACTCCACGC 540
 40 CTGCCTACTC GTCAGGGCGT CATATTCTGC CCTGACGGTG GAGTATAGGT AACACGCTTG 600
 AGGCCATCC ATTTTCAGGG CTAGTTCAIT CGGCCGGTGA GTTGTACAC ACTCCTTAAC 660
 45 GGATTCCGAC TTCCATGGCA CGTCCCG 688

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1376UP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

5	GATCCAAGGA ACCTTTCCTT CTGGCTAACC TAGGGTACTT GTACTCTAGG CGAACCANGA	60
	CTTTTACTTT GAAAAAATTA GAGTGTCAA AGCAGGGCA AGCTCGAATA TATTAGCATG	120
	GAATAATGGA ATAGGACGTT TGGTTCCTATT TTGTTGGTTT CTAGGACCAT CGTAATGATT	180
	AATAGGGAAG GTGGGGGCA TCAGTATCA ATTGTCAGAG GTGAAATTCT TGGATTATT	240
10	GAAGACTAAC TACTGCGAAA GCATTGCGA AGGACGTTT CATTAAATCA GAACGAAAGT	300
	TAGGGGATCG AAGATGATCA GATACCGTC TAGTCTTAAC CATAAACTAT GCGACTAGG	360
	GATCGGGTGG TGTTTCTTCA TGACCCACTC GGCACCTTAC GAGAAATCAA AGTCTTTGGG	420
15	TTCTGGGGGG AGTATGGTCG CAAGGCTGAA ACTTAAAGGA ATTGACGGAA GGGCACCACC	480
	AGGAGTGGAG CCTGCGGCTT AATTGACTC AACACGGGA AACTCACCAG GTCCAGACAC	540
	AATAAGGATT GACAGATTGA GAGCTCTTTC TTGATTTTGT GGGTGGTGGT GCATGGCGGT	600
20	TCCTAGTTGG TGGAGTGATT GTCTGCTTAA TTGCGATTAAC GAACGAGACC TTAATACTA	660
	AATATGCTGC TGCATTTGCT GTTGCCTTC TTAAAGGACT ATCCGTTTCA ACCANTGAN	720
25	TTTGAGCATA CAGTCTGTGA TGCCCTAACT TCTGGCG	757

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 821 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1378RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

40	GATCCTTATA AAATGGGCAA TAGACGTGTT ATAAATATAAT ATACAAAATT ATAAATAAAT	60
	ATTTAATAAA ATATAAAATT AATAATTAAA GTATTATAAT AATTAAATAA ATTATTTATT	120
	AATAAGTATG GATTTTTAAC TGAAATTGT TAAATGAAA TAAGAATTGC TAGTAATCTA	180
45	TTAATAAGAA AGTAATGGTG AATACTCTAA CTGTTTGGCA CTAATCCTC ATCAGCGGTT	240
	GAAACATATA ATTAAATAAA GAATATTAAT TAATTTATTA ATTATTAATT ATTATTAATA	300
	TTATTTAATA AATATAATAA ATATTTTAAT TTAAATTATG AATTAAATGC AAGTTGAAAT	360
50	ACAGTTACTG TAGGGGAACC TGCAGTGGGC TTATAAATAT CTTTAATATT CCATTTTAT	420
	AAAATAAATA TATTTTTTAA TATATTTTAT AATAACTATA ATTAAATAGT TAAAATTTAA	480
	ATTATAATTT AATAATTTAA TAACTTATTA ATTAGAGAGT TAGGGTACAT OCCCCCTAAT	540
55	GCTATGCATT ATGGTTGGTA CACTCTAATT AATAACTAT AATAAATAAA TACTAATATT	600

TTATACCAIN AATTATAATT ATTTTAAANA NATTTAATAT TATTAATGAA ATATATAATA 660
 AGTATININA TTTNATAATA ATAAAAATGA NAAAAAGACC CCTAATAATA ATTTGCATTT 720
 5 ANANTTACCC TTACACCTCC CNITAAATTT TTACCCINAT ANCCNINITA ATTAAGGANG 780
 GNGNNOCCCN TGCTCCCCNN TGCCCCCCC ATTNANNTTT A 821

(2) INFORMATION FOR SEQ ID NO:542:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 852 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1378UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

GATCCTTGCG TACTAAGAGT TAGACTTTAA TTAATAATAT TATTTGTAGA AGATAGAAAC 60
 25 CATACTGACT CACGTCTGAT TTAACCCAAC TCACGTAACC TTTTAATTGA CGAACAGTCA 120
 AACCTACTT AGCTGTGACA ACCAAGAGGA TAGGTGAGT CGACATCGAG GTGGCAACA 180
 TAACTTACAA TAGCTACTCT ATCGTTATAT TACCTGTTC AATTTTGTTA TCATAATAAC 240
 30 ATTTAATTAT TATTTCAATA ATTCTCATTA TTGTTGAGC TATTTCATTA TGTATTATTT 300
 ATTAATTAAT ACATATTGGG CTTTCGTGGA TATAATTATT GTTAATCCTA CTCATATATC 360
 TAGTCTGTGA ACGTCTCTAT AACTTTATAA AAAGGATTGT TATAAGCTTC GCTGCAGATT 420
 35 GTCTTTTATT ATTATAAAAT AATATTAGGA GTTCTTTGCA ATTAACCCAA TTTACTCAAT 480
 ATATTTAAAT ATTGATAATT AAATTCACA ATTTAATGGG ACTATTAAAT AACCTAGCG 540
 TAACTTTTAT TCGTTATCAA ATACCAATTAC AATATGTATA TTTGTTCAT TATGCCAAC 600
 40 TTACGTTATT GTTCTACTTG TAGGTATTAC AATTATAGCA CAGTTATACC ATTATATTTA 660
 TTTATATATA TOCCATATAA GTTTTATTA ACATATAAAC TGTCATTAT TTATCTNTTT 720
 TATATAAAAT ATNATTATAT TAATNATTTA TTAANATTTA NACCNEATA TTAAATATAA 780
 45 TCNTTTTAA TAATAAATTA TTAAGGACTN TCCAACCTTT TTGAAAGACC CCCCCTNCC 840
 ATTAAATGTC NT 852

(2) INFORMATION FOR SEQ ID NO:543:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 845 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1379RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

GATCCAATTC TCTGGTAGT TTCCTTCCAT ATAGAGACTG ATCAACTAGC CACATTCCCA 60
 CAACAAAAGA GTTCTATCT AACGTGCCAT CGGTCCTTGT ATCTACCATG TCGTAGATTT 120
 GAGCCAAAGT ATCTTGAGGT AGATTGCTTC GAGACCAGAT ATCTGTAACA ACTAAGTICA 180
 ACATTAGACC ATCTCTGGC ACCTCTCTTG TCTCATCGTA GTTACCGTTA TTCCACCATG 240
 GGAGCAAGTC AAGATAAGTG TCTCTATTGC TGACCCACAT TCCCTGGTAA CGCTTTCCTT 300
 CCCTTTCAGT TACGTACCCA ACATCAAGGT GCGACTTCCA AGGTTTGCTCT TCGTTGAAGG 360
 AATTACGGTA TCGAAGATTT TGAAGTATCT TCTCGCGCTT TTTGCGGAT CTTCTTCCTG 420
 GACTTCGACT ACGGGAGTTG CGGTGCTTC CGTAATCTC TTCAGAGTCT TCGCTGTCAT 480
 CGCTTAGTTG ATGGGCTCT GAGCTGGAAC TGTCATTAG TATACCCCGC ATAGTGGTTT 540
 TTAGCCGCAC ATGCAATTTA CTCTGCACGA GAGCGTTATC GTTCTGGTAA TATATATGTG 600
 ACGTTGGGG GTGATTCCTG CTGGGGCCTA GCGCAGTTG CCGATGGGCG TTGAAAGCTT 660
 CATCCACTTG GANIGCTGCG TTGANANITT GGTATTAAATN CAGGAANATT CCTCCGTAGT 720
 CCAGTTCATA GGAATTTGTT CATGTCAATT ACAANCCTTC NACGGGAATC TTTTGGGACT 780
 CNIGTCAAGT CGANGNATNT GTCTCCGTA CANCTCCCGA TNCNCCAAAN TNNCCNCATT 840
 CNCNN 845

(2) INFORMATION FOR SEQ ID NO:544:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 855 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1379UP

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GATCCGGAAG TTAACACTGC CTGGGATTCA TAACTTGGCA ACAGCGTATG TCGGTGTGAA 60
 CATAGTCGAT GGAGCACATG AATTGGGGTA TCAATACTGA TTTTATAATG CTTTCTGGAG 120
 CCATTGACCT TCGTGACAA CCTCAAACAT ATTTGGAGCC AATGGTTGGA CTTTATGTGG 180
 GGAGATGCAG TATTGGATG TATGCACTGT TGGTAGTTCA ATCTTTGGG GACAAAAACC 240
 TGGTAAGTGA ATTGTCTCTT TGAAGCGCCA CCGCTCCAT CATCCAGCAG GTTTCCTAAG 300

TTTTTAGCAC GCGAAAGGCT CGCGCCTTCG TGTATACCCT TAAGTGGTGG TGCTTTGTGC 360
 TOGACCAGCA AGAAGTCTCTT TGTAGGCTCC ACTCGGTGTA CTTTCGGACC TTTACAATAA 420
 5 TACTCTAAAG TTTCGGTCAG GAATATTCTA ACCCTGTGGA GCACGAGATT AGCCCGTGGG 480
 TTTAGCGAGA GCGATATTGG TAGAAATGCG TCCAAAATA TATCTTTTGA TGCAATTACG 540
 ATTTTCATAAC TCAATTCTTT TTCCAGTCA CGTGATATGA CTATCGGTTC GGTATCTTCT 600
 10 ACAGAGTTTC GAGATAGTGT GCGGATAAGT TAATCGGAAC ACGACGTGGA CATTGGACTT 660
 AAGGTCCTAT GCGCTCAATG TCACTCAAGC AGGTATTTAC GTTCCCNATG TTAAGTAGAAT 720
 CTCTTGCTC GACNCCGGAN TNGANCCCCA AGAAAAATA TCCCCGCCNG AAAANAATTT 780
 15 CCTGGNGTG ACGTGTGNAT NACCCNACGA AAACNCTCTC CTTCGAANGT NOCTTATATT 840
 CNNTNAAANA ATANA 855

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1380RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GATCGCATCG ACCTGCCCAA AGTAAGGCAG GCTCTGAGC GAGATCCAGT CGACAAGGTG 60
 35 AGGAAGCGTG GTGTCTTAC CCTCGAACAC AATTGGCTCC TTCTGCCCCG GCAAGTGGAC 120
 CGCCAAGGTC GGCTCTTAG TTGGTACTG CACAAATACA AAGTCGTTC GGAGCAGGTT 180
 GGCCAGTTTC TAAAGGACT CGTTCAGGCC CTTCAGCCA CCGTCAACCA CCACTGGGGT 240
 40 CTTCGACTCC GCAAGCAGGT CCTCCAGGTC CTGGGGGCC TCCTTGCCCT CCAGCACCGT 300
 CACGGCCGCG TCGGCTGGC GCAGCATGTA CGCACAAATT TCCTGGGCT TGGTGGGCC 360
 CGTGTATGCG ATGCCCCCT CTGACGCCCC ACTGTGGAAC ACCTTCAGCG TGGGTACCC 420
 GCGCAGGTC TGGCCCGCG ATAGATOCAG CTCTGCTCG CAGTCCACT GCGCCAGCTT 480
 45 GATGCCCTTC TCGGCCAGCT CCCCAGCCG CTTCAGTAC TCCGTGCCA GGTGCTTACA 540
 GTGGCCACAC CATGGCGCAT AAAACTCCG CATCACAAGC GGGTCTCTCT CTAAGAACTT 600
 50 CCGAACGTC TTCCGGTCA ACTTGACACT GCAGAGTCT CTGGTGCACT GGCATCTTGG 660
 GCTGTGCAA CTGTGCCAGC AACCGCGAT GGACAACACA AACCGCTTGT CCAAAACNT 720
 TCTGCTGGG TCTATCTTAC CCGTGGTTTN GTGNACTCTG TGGGATCAA ANCCGNTN 780
 55 CNATTTTTGT TTTACTGA TCCAGAATTC ACCCTTCTC AAAACNNTTN CCGAAAAGA 840

NCGNGTN

847

(2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 860 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1380UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

GATCTOGCCT	GTGTGAGTG	ACGCCGAGTT	GCGCGAATTG	TAGCAGTGCG	AGAGGAAOCT	60
GCCGACGGTA	TGTTTGCCA	GCGGACAAC	GCGCAGCTG	CCCAACCGA	CCGCGTCCAA	120
CTGCTCCTGG	TACATCTTGA	CCACGTCTT	GCCGATGCA	TCCTTGATGT	TGAAGCCCTT	180
CGTCAGGGG	ATCAAAGTGC	CGCTCGATAG	CGATGTCTGC	GCCACGGGAT	ACGAGAAOCT	240
AAACCCGAGC	TTCAGTTGGC	CGCCCTCGCT	CTGGAGCACT	TCAGAGTGGT	AGCGCTTGAC	300
AAACGCCATT	GTGGCCTTGG	CGATGAAGCC	GAACAACCTG	TCGTATGTTA	CGTCGTCTGC	360
AAGGAGCTCC	TGGGGATCT	TGACTTTCAA	CTGCTCCAGC	TTGAACGTGT	GATCACCGTT	420
GAGACGCACC	GAGCACACC	GGAATTTCT	GCGGCAAGG	TGGCGCGCA	AGAAGCTGCC	480
CTCCTCAGTG	CCATTTGGGC	TGCCATCAC	GTACGAGGG	ATCATGGAA	GCCACGGTA	540
CTCCCGTCCG	TCTCTCGTT	CTTGAGACCT	GTTCATACA	TTGATGAAG	TACGGGTCA	600
ACTCGCGGAG	TTTGTCCTCC	GTCACTCGA	AATCCTTACA	TATTTGTGCC	ACTGCTCTC	660
GACTTTCCCG	CGTTGGCTT	GTGCAATCT	TCNAAAANAT	CCTGGTACTG	TAAANATTAG	720
ACTTCGANAC	GTGGTGGAG	TCTTTCNNGC	TTCCTACTC	NCCNGCCNTG	TCNTANTATT	780
TTGANGGCGN	TCCAATAAAA	AACCTTTTNG	GGGTCNCAA	GNGAOCCTCC	ACCCTCTTTT	840
GTTCCCCTNT	CCCNNAATGA					860

(2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 835 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1381RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

5 GATCATTATA TTATAAAATA TAATAAAGAA TATATTTAAA TAATAATAAT AATATGAAAT 60
 ATTATATTAA TTCGCCATTG GAGCAATTTC AGATTAGAGA TTTATTAGGT TTAACATCAC 120
 CAATAATAGA TTTTAGTTTT ATTAATATTA CTAATTTTGG TTTATATCTT ATAATTCTTT 180
 TATTAGTAAT TTTACTAATG AATTAAATAA CTAATAATTA TAATAAATTA GTAGGTCTA 240
 ATTGATATTT AAGTCAAGAA ATAATTTATG ATACTATTAT AAATATAGTT AAGACACAGA 300
 10 TTGGTGGTAA AGTATGAGGT TATTATTTTC CATTAGTTTA TACATTTTTT ATTCTTATTT 360
 TTACTATAAA TTTAATTAGT ATAATTCCTT ATTCATTTCG TATAACTTCA CATGTAGTAT 420
 TTGTAGTATC AATAAGTATA ATTATTTGAT TAGGCTAAC TATTATTGGT TTTTATACTC 480
 15 ATGGTTTAAA ATTCTTTGGT TTATTTTAC CACTAGGTAC ACCATTAAAT TTAGTCACCA 540
 TTATTAGTAT CAATTGAAT ATTATCATAT TTTGCTAGAC TTATTCATT AGGTTTAAAG 600
 TTATCAGCTA ATATTATAGC TGGTCATTTA TTAATTGITA TTTTAGGTGG TTTATTACTT 660
 20 AATCTAAANC CACAAATATT TAACNITTTN TTAAGTTCNN CCNATGAATG CTATTINAGT 720
 ATGINTGTTA GAATTINAT CTTATACCNG CTTANINIGA AGININAATA CNOCNTATNA 780
 AACTATTTAT TCTTATTAA ATTAACANTT NAACNCCNA TTANTTINTA TNCTT 835
 25

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 863 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1381UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

40 GATCATTTGIC CAATATTCOC CACTGCTGTA TCATATAGAT ATTGATTATA ATTTCTAAAT 60
 CAACGTGATT GTTCTAACIT TAATTAACAA TTATGAATTT TTGGCTAGTT ATTATTTTTT 120
 AATTAACTAA TACCTAAATC ATTATAAGCT TGACTTAAAA CAAATAATTA TTACATTATT 180
 45 CTTTATTTAT TATTTAATAT TTAGTTAAAT TTTAAGTTCA TTATTCITTA TTTTACTCA 240
 CGAGTACACC ACTTATTAAT ACTATTAAT AATAATATTA ACGTTTGATT CGCATGTGTA 300
 ATGTCCTTAG TTAGCGCTTA ATCTGAACCA ACATCATGTT CTCATTATTA TTAATATTT 360
 50 TTAATTATTT TAAATAATTA TTTAATACGA AAGTTATAGG ATTGGAACCT ATGAAATCAT 420
 AAAGATTTAT AATAGCTCAA ATATTACACT TTAAACCACT CAGTCAAACCT TTCTTAATAT 480
 ATATACTTA TATATGGTTT GATAATTTAC TTATAATATA TAGTATATAA TTTAATGATA 540
 55 AACTCTTATC ATTTAGGTGC GTAGGGTTCA CCCCCCTATT GCTAGTCAGC AATATGATGT 600

ACCTCCTAAA TGATAAAGAA GTATAATATA TAAATATTAA TATTAAAGTA TTTAATGAAT 660
ATTATATTAA TTTATTTAAT TATTATTTTT ATTTAGTAAA TAAATAAATA TTTCCACTTA 720
5 TTGAAATATA GGTTCCTINGA TTAGAAATAA GCNATNATAA TGINCCATTG ACTATTAAAT 780
ANTGIGCTCN CNNGACTTCC CTATTTCNCCN NNGANAANTC NGAANATCAG AANANAGATT 840
10 CCNANATNTT TAATNNNNCCC CCA 863

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1382RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

25 GATCTCACAC GTGACTAAAA TCACTAACAC CACGTGACTT CGTGACCGTG GCATOGTCCC 60
ATTCTGTGCG TOGCTAGCAT TCTGCCCGCG CATCTGTGTC AGGCCACTGC GCAGCTGACC 120
ACGCCGTACC ACGGCAGGCT TCACGACAGA CGGCAAGCTC AATOGCTATC TACGGTTTCA 180
30 GGTGGAATTT CTACCGGCA TCCGATTAAT TGCTTTTTTG GCTTCCTTTT GCCCCCTTTT 240
TTCCAGIGGG TTGCTTCCTG AAAACAGGGA GCTAGCTTCC CGTAGTACGT AACAGTCGTA 300
GAGGGTATAG CATCGCTGAG CTCGAGACCC GGTGATGCAA TGTGCACAAC CCTCGTCTGC 360
35 GCAAAACGGG CACGAAGATT GAAAGTATCC AGGAGTGCAG CCCAGGGTCA TCGAGACAG 420
AATGGGOCAG AAAAAGCGAA AAAATGGACG ACGCTTTTAT ATATATATGT AGCGAGGCG 480
GGCGTTCCCA GAACGGGACC CGACACAAC TGTGTAGAA TTTCTATCTG CAAGGAATCA 540
40 AATACAAAAT GGAATCTAGA TTGGGATGGC TAACTOGTTT GAACTACGAC ACTGGTCTCTG 600
CATTGAGAAG AACTCCATCA TCCGACAAT GGTCTAAGA CCAACCAACC AGANACTTNG 660
TGGANCTTAA AAAGGNGGGT TGAACATCCT GAGAATGAAC TTCTOGCNOG GTCTTACAAT 720
45 TNCACCATC GGTGNTCNAA NACCCNNAAT TCGAGATTNT NCCNGTTAAC NITGGCCTTG 780
CTTTGAANCC AAGTNCCTGA ATNAAATGIN CCTNTCGAAA NITANTACCN TCCCCTACCC 840
50 AAANC 845

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1382UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

25	GATCTATAAC AGGTGCCAAG TTGGCAGATT TGTTTCAGGG GCTCGACGAT GTAGAGTCCA	60
	GTAGAATGCT CTGTAAACCC AGAGCATACT TTGCGGAA GTCTTTATCT GTTGAAATCA	120
30	ACTGGGGTAT CCGCTTTGAT GCTGTCCCGG AGGTTCATGC CTTTCTTGAT CGCCTTGTC	180
	AGTATCTGGT TGGTAAGCTC AATGAGCTCC GCATGACCAC GTCCCATATT GTTTTGAAAA	240
35	TAGCAGCCAG AAGCAGGGAT GCGCCCATCG AACCCCCCAA ATACTTGGGC ATGGGTGACT	300
	GTGACAGTTA TAGTAAATCG TGCAGATTAG GTCTTGCTAC CAATATTCCT GGGTTTATAT	360
40	CTGCAGAGAT AAAGGCAGCT TTTCGCATGC TATGCTGCCC CGCAAAGGAA CTGGGTGGTA	420
	TAGCCGTTCA GTTTCTTAAA CTGAAGGAGG CATCCATTTT TCAAATGCCC CGTCAGCTCA	480
45	GGTTTCATT TGGTACAATC AGACCTTTAA CAACTCCAAA GAATCGTATC ACAGCGTCGG	540
	TTACAGAATT GCCAAGTGTG GTTTATAAAA GGGCCACTCC TATTAAGGAT TTTTTTGACC	600
50	GGCACAAGAG GACTCAGATT CACCATCACC TGATTCACCT ACATGATGTC TCGTTCAGCC	660
	TTGTGCGAGT CATTCCTGGT GGATTACCTA CGATCTTGCG GAAAAATCCN AAAAAACATT	720
55	GACNATCINA AACCAGACTT CTTTNTGTCN ATTCCCAAAA AAATTGGGNN GNGCCGNGGT	780

TNNATCCCAN CATGCCCTTA AAATTTAGAT CCTTGACCTT ACTCCNANTT GNTNCCCNAA 840

5 AAAAAAACTA TCAATGTNTN CT 862

(2) INFORMATION FOR SEQ ID NO:551:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1384RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

30 GATCTGCATC GCGTCCACCG TGGACTGGGC GGTGGTGGGC GGTACCGAA AACTGGGGG 60

ACTCGGTGAT GGTGCCGGCA AGCGTCTCGT AGCGGATGGG CACGACCTTC GCAAAGTAGG 120

35 AAAAGAAGTG GCTATGGCCG TTCGGAACCT CCATGGGCGG GCCATTGAGC GGCCCGGGGT 180

TGCCGGCAAT TTGGGGCCCA AAGGAGAGAC TATGGATCAC GTGGTTGAAG GAGAGATGGG 240

40 GGTGTTCTTT GTAGAAGGAA TCGTCGTGGG CGTGGCCCTT GCCAACGTGC GCAGAGCCCG 300

GGCGAAGTG AATGTTCCCG TGAACGCGGT TGAGCTGCCG GGTGCCAGCG ACGCGGCATC 360

45 CCTCGTTGAT CTGCTCTGCG AGGCGCTCCG TGTAGCCCTC GCGCTTGAC TGCTCAAAGC 420

CTTTGCCATC GAAAGTGGCC CAGTTCATCT CTGGGTACGC CGCGCGCAC TCCCGGCACG 480

50 TCTGACAGCA CACGCGCTCG CTGCGCGGCA GGTTCCTGTT CTGGTCTGG TCGGTGCGC 540

CATACACGGC CACAGTAGTC TTGGTGTCT GTAGACGGCA ACGTCTCGCC ACTCGGAATT 600

55 CCTCCTTCCC CACGTCCGTC CNIGTTTGTC CACCNTTTTT CCTTGATCCT CCTCCACNA 660

ATTCACTGTG CTCCTGTTC TCINTANNIC CATTTCAATC TCCCCCGGAT CTTGCAAACT 720
 5 TATATCNAAC CCCACTCCNC TCTGCTGCCG TCCTTCAANC ACTGNGCGTC TCCCTCCCCA 780
 NTCCCTCCT ANCAAANACN CGTTCACAAC ACCNCTATN CCT 823

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1384UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

GATCACTTIG TTGTGTCTG CACGATAAAT GGCTCGGTA CAGAGTTTGA CGAGTGTTC 60
 TTGGCTGAGA CCGACAGGT CAATCTCAGA GTTTTACTA TTCATTAGTG AGTAGATTGA 120
 35 CCGGTAGTTA TTATCAAAGG CCACCGGGGA ATTGTTAAAG AAGTTGGAAA CAGATGATTT
 CGACATGGTA TAGTTCGTGA GCTTAATTAG AACGGGCAGG TCTGAGCTCT CCGCGACGGG 240
 40 AGTACTGTTT TGAATGGGTG GCACAGCCAG TGGCGGTGG GCGTGACCA TGCCAAGCTG
 TGGCCCCCT GTGAGGCCG CTGGTACTGG AGCGGCACG CTTATCGGCG GGTCTGCTGG 360
 45 TGTOGGCGAT TTGGAATAC GGTGTGTGCA CGCTGCTAGG TATTTTTCG GCTCCGCTGG
 GCTCATCTTC TTCTCGGTCA AAGCAGGGTC GAAGTTCAGA ATACCCCTAC TCTTGTCTC 480
 CTCTGCAATC ATGTGCAACG TTTGCGCGAT CTTCCCCAGC TTGTGGTGAT AGGGCGCCAG 540
 55 GTGCCCCGAG TTCCGGATCA GCTGCGCTTT CATGCCAAAG TTAACGAAAT TCTTGTAACA 600

GGGTTCGACG CAGCGCTTCC CAAGCGGTAC CGCAGCGCAA ATCGTTTTCC TGCTGGTACT 660
 5 TGTGTGTCNAT ATTGAATCNA ACAGGCCCCC CAATAANCCCT GTCCACGGG CCCCCTTCCCT 720
 GANNAAACCA GCATCACACC GCNAAAAAAC GGGCCCCACN CGTCGTATC NAACTTACCC 780
 10 CTCAGACTG NNATATCCANN GCATNCNCCCT TTTTNTTCCC GTGTNCTGA AANTNCNAAG 840
 CCCCCACCT 849

15 (2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 862 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1385RP
 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

35 GATGACCTC GTTCATCATGG GCAAGCAGGC CACCGACAGC GACAACAACA ACACCGGGCA 60
 GATGCTGGCG GGCTTTCTCA ACTGGCCGCA GGCCACCAAC GCGCGCGGTG TTGAGCTGGA 120
 40 CGGACTGGC ACGCGTGGCA CGTCAACCG CGAGGTGAG GCGGGGAGG AGGTGTCAG 180
 TGGCGGCTG CCACTCGTGG TCACCACGGA CCTGGCGCTC AACACGCGC GCTACGTCAC 240
 45 GCTGCCCAAC AAGATGAAG CGAAGAAGAA GCGATGGCG AAGCTCAACC TCGCGCGTT 300
 CCGCGCGTC GACTCCGCG CCGCGCTCAA TCTGCTGCG TTGAGGAGC CCGCGCGCG 360
 50 CGCGCGGCG ACGTCTGCG CGTCCGTGGA CGAGCTGCTC GCCAACTCA GGGAGGCCAA 420
 GGCGTTTAA CACCTATATA AACTAACAGC CCTATTTCC TCGCGGAGC CAGGTCCCG 480
 55

CTCTCCAGCA GCCCCGGGG CTGCTTGCGC AGGTACGTCT GCTCGTACCA CGCCTCCAC 540
 5 TCCCCGCGCT GCGCCCGGC CTGCTGTACG CTCTTCAGC ACGCGCGGC ACTCCTGTC 600
 CCACGCGCG AGGTGTCTC CCGGTGCTG GCGCCCGCG CTATCTTGCA ACNCGCCAG 660
 10 CTGCGAGTTT CGCCCGCCCC CCGCGCATGT NNCCNCCAA CKNITTTTA CACNGGATNT 720
 TNCCNITTG TTNTCCNINN NTTCNCCC GTGGAANTGN TTTGCCNTTG CTGANAATG 780
 15 CTANCCAACC CCCCAATTG ATNGNGCCCC CCAAAATNA ACTTCCACT TTGCGAGAC 840
 CCGCGCTGT NCCCTTNTT AA 862

20 (2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 851 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: PAG1385UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

40 GATCCTTGAG GGCTGGTTC TGGGCTTGA GCGCGGGCC GAGGCGAGC TCGCGCGCC 60
 GCGCGGACC TACGCGCGG CCGCGCTCG CGAGGTCAAC GCGCGCTCG AGGACTACTC 120
 45 TGGGTGTCTG TGGCGCGCG CTGGCGTCC CTGGTGGC ATGTTGTTCG ACGGCGAGT 180
 TGGGAGTGC GTGGCCCGCT GCGCATCCA GCAGGACAC GAGCTGCGG AGCGCTGCGG 240
 50 GCGCGCATG ACCGACGCG AGGTGCAGC ATTTCTGGAG CGCTACCTGG TGTGCTACGA 300
 CGTCTACTAT GCGGTCTGG TCGCGAGGG GCTCGGGAAC CTGCACGCG TGA CTGTGGG 360

GCTGGAAGGA GACCGAAAAG TTACGTATGT TAGCCAGAAG AATATGTAAT GCGAGTCTA 420
 5 TAGTTCTCTGG TCCGAGATGT CCTCCACGGG GATGAGATAG CCGCTCTGGT GCGCCTTGTC 480
 GCGCGTGCGC GCGCGGGGGC CCGCGGGCGA CGCGGGCTGG CGCGGGCCA TGCTGGGGGG 540
 10 CCGCGTGGAC GGCAGCACGC TGCCGCGAG CTGCTCACTG GCGCGGCCAG GAAGGCTTCC 600
 GTCTGGGCTT GCGCGGGCTT CAACGCTGTC AGTGGGGGA ACGCTGCCA NCAAGTTCTG 660
 15 CCGCGTGTCC ACTGCGGGG ACTTNTTAAA CACTCTGCT TTCTTGAAT CCTTGAACNA 720
 NCGCGTTGC GCTTTCNAC TTTATGANC CCCCCAAC CCTTTCGNG GCGTGGGGC 780
 20 NCCCCGCCC NNNCTCTCG CCGGTTCG TGCTCTTAC CCTTCCCTT TNCNTTAAAC 840
 GTTANNTIN N 851

25 (2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 857 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: PAG1386RP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

GATCGCACT CATTTTACCT ACAGGCTGGG CTTTGAAGA AGACGCTGC ATGGTACAAT 60
 50 GTCTAGCCA GGATCCACC TGTACCAAG TTGGCAGAG AACCGAAGCT GCATGACCA 120
 GTTAGCGCA AGTACAAGG CGAGCTGGAT ATAATGACG ATAGATTAAA CAGAAACACA 180
 55 GAGACGTACA AGACAGGCG TGGGAGTTC GACCGGCAGA CGCGCGCGGT GCACAAGCCT 240

TCTAAGCTGC GGTITATCGA GGACAAGCTG CGGTGCTGT TTTTCAGCA GCATCCCTGG 300
 5 GAGCTGTGCG GGCCGAAGGT GCTGGTGGAG AACATGGGAA ATGAGCAGTA CGACTGGTCG 360
 CGGATGTTGC AGCTAGGCAA GCGCTTGAC GGTGAGTCTG TGGTGACGG GACCTGTAT 420
 10 CTGCTGAAGT CCGGCGCGCA CCGGAGATG CTGGCGGCAT ACGACCAGG CCGGTTTGAG 480
 TTCTATCGTC TGAGGATGCA GCAGGAGCTG GAGGAGCAAA TAGCGTACGA GGAGGCCACG 540
 15 ATGGTTGGCG CTGTGTTCAA GACAACCGCT GTGGAGCAG GTCTGCAGCA AGAGCAGAAG 600
 GTCTCGACA GTGGAAAGAA GACTTTGTG CCGGTTTGC CCGATTITT GCNAAAAAA 660
 20 ACTCTACAAA GCAGTCCNTG GGCNACCC ACCGAGAAA AAGAAGAAC AGGACNNTGC 720
 CGAACCCNAA GACNCCACT GTGNACTCN TTGCCAACTT TGTATAAAT TCTTACNNT 780
 25 TTATTCCTT NGTACAATNC NANNTACTGT TGTGTGCCAT CATGTGCCCC AACAGGTTCC 840
 CCCCNTTGA NAAANGC 857

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1386UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

GATCCATGCC TCGTTATAAC TGAGCAGAAG TGTGCATCG AACAGAGGCG TTTCCTTGTT 60
 55 CCTTGCCAGT TCCCCCATC CCGAAGTTGC ACTGCAAAAT GTGAATCATT GATGCTTGT 120

CGTCGCCATC GGTGCGCTGA AAGATGCTGT TCCGGTAGAC CGCATTCTGT CAAGCGGAAC 180
5 TCTAGGCGGC GCGGTGAGAG TCCAGATGAT GAATCTGAAG TTGAGGCOCA GCACGTGTGC 240
TTAAAAGATT GTAATCGGGT GCTGCTTTGT GGTATOCACA TGTGCAATTA CAAATGCCAT 300
10 GCAGGCAAAT GTCTCCCTG CTTAGAATCA GATTOCAATG ACCTTATCTG TCCCTGTGGT 360
AAGACAATCG TACCAGCCCC TGTCGGTTGT GGAACAAAGC TCCCTGCGTG CACTCATOCA 420
15 TGTGAAACT CGCTGCTGGA TACTTGGCCC TGCGGACACA GTCCACCTTC GCATAATTGT 480
CATCCCTTAG ATGAACCTTG CCCCATGTA CCATCACAGT CAAGAAAAC TGTGCTGCG 540
20 GTAAAAAGA GATCAGGACA TTCTGCTACA ATGATGATTG TGTGTGTGA GACCGTGTA 600
GAAGCCATGT CCTATTGCAA TCACTTCTGC CAATTNCTG TCATTCCGAT GCAATGCCA 660
25 GCAAACTTGT TAGCAAGCCT GTGGTCNACC ACCGAAAGCC GCACNTGTTT GTTAGGGAAA 720
TGCNTGGCNT NCGNATGCTT GAATCCCTGT NNNAAAAAA AANNCCGTC CGTTGTCCAT 780
30 CNCCACCAAT NTCNTGATT TGCTGGAAGA GAANGTTCG ACACCNCCCC GTCTGNAAG 840
AATGTCAAT CNNGN 856

35 (2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: PAG1387RP

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

EP 0 866 129 A2

	GATCAACCAC TCGTGTGCCT ATACATAGGA ACCAAAAAGC CTTCTGGCCT GGTCTCAAG	60
5	TAGTATGTGA TAAGTTTGA ATCCTTGTA GCGGTGCCT TCCGCGACC TTTCATATTT	120
	TCGGTAAAAG CCTCCACAAG GTTCCTATCT TTATCCTTGA AGTTGTCTCC ACAGGACTCC	180
10	CACAAGAAG CCCCAGCAAG CTTCTTATCT TTCACGTATT CCTTCTTTAT TTTCATTGAA	240
	TCCACATTGT CGTAGACGAC AAGAGTTTTA GTATTAGGAT CGTAGCTATA TGCAGAGACC	300
15	CAAACATTGT CAACTTCTC TGGGCGTGA GCTAGCGCA ATTGGTTGTA TAGCCACATA	360
	CCCGGTTCC CTTCTGATCC TCCGCTACA CCAGAATATT TCTGGCCAAT TAGTTGTTC	420
20	CCATCGCCCC GAACGTTGGT GAAGCCACGG CCATACGCTG CCATGCGAG TCAATTTTT	480
	CTGGGCTGA CCTTAAATTG TTCGGTCATC ATGAGTATCG CATCATGTGC ATTCAACTCA	540
25	TCAAAGTTGT CAATACCCAT ATCTTCATAC CGACGCTTAT CTAGGTGGA TTGTACGGCG	600
	AATTGTTAGC ATTGTACAAG TTGCTATGGT AGCCTGTTGG CTCTGACCAT GCACCGTGGT	660
30	ATCGTATGTC ATCATATCCN CATGCTGAAA ACTGTTCACT CNCAACCGGA AATGCAATNT	720
	CTGAAGAAGC NGGCTGCCAG CTINATTGAA CCGTCTGTIN TCCCCGGGCC CNANATNTTT	780
35	CCATCTCINT GTTNGCAGCG GINCTTTTNA AACTGGNTC GNNCNCACCA	830

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 857 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1387UP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

5	GATCACCACA ACACAGAAGC ACGCAACGCT ACAGGACTTC CCTGTTCTTT TGCTTGACACA	60
	CGTCCAGCCC AGAGGACGAT TACACCGCCG TCAGGGTTGG CTAGTCTCCG GCAGCACAGG	120
10	CTCCTTATCA CATTTTGCAT TTTCACGCTC GCACATGTCA CAAATAACCA AATACATCCC	180
	CAAAGCAGC CTTTCTCTCT GCGCGTCTT TCTCATCGG TCAGACTTGG TACTCGCTAT	240
15	GAGCGGCAAG GGCACGCGCG CAGGGAGCTC ATCTACAGGC ATCGGGTGGC GCGCCAGCG	300
	TCTGCAGCGG CTGCGGCAGC TCGTAGCGCA TCGAGATCCG GCAAGAGGCG CGTCAGGTGC	360
20	ACTTACGAGC ATCGAAGAGT TTACTAGGAG ATGACAGCGC CTGCACGTCC CTGAGGCTAG	420
	CCTCCCGAGG CCGCGGGGCC GCTTGGTATA GGGTTTACAT AGCAGAATGG CACGAATATT	480
25	TGCTCTAGGC AACTGCAGG ACGGAAGGGG CTTCATGCGA AATCCTTGCA CCGCCGGGTG	540
	CCGTATATAA GGTGACGCAG CTGCGCAGCT GCGCGGGCA TGCTAACCAC GACAGGATGT	600
30	GGAGTGGTGC GCGATTATAT ACGACAAGCC GCGTGGAGG GTCGGTGCAC AGGCAGGACA	660
	CCTGGGGGAA ATCCCAANTC GTTGAACAAG GGAAGTGGTG CAGCGGGCGC AATCTACAAG	720
35	AGTTGTIGAN GCGGGCCGTC ACATTGCGG TTNCACTGAC CCTGTGCGA TCCANGAAGA	780
	GGNCTGGCAT NTCACANAAC CTCGCCACAG CTGTGACTT GAACTCCNGC CTACCTTGAT	840
40	TTGCANNCCA GAAAAAN	857

(2) INFORMATION FOR SEQ ID NO:559:

45	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 821 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1388RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

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GATCCACCCA AATTCGTCTG TGCTGGACCA GCTTTCCTCA CAGTCTCCGA GGTAAATCAGG 60
 CTA CTGCGTT CCTATTTTAT GGCTTCAAT AACTCTTTAT ACTTAATTTA GACGTTAACT 120
 TCCACATCCG GTATTTTTC AATCTGAGAT ACTGGCAAGC ACGGCTAGCT TTAGGAGAAC 180
 TGTATCCCAT GACTTGTGGA CAGGGGCTTT ATGAAAAAAC GCGTGTCCGT GTAAGGATAT 240
 AGAAAACATA CTGAGATGGC TTTTGTGCT GAATCAGACA TTCTTAGGTT ACATTTTGGG 300
 CCTGGCTGTA CAAGGCACTA ATATGAAGAT AGAGTTATAG CGCGTGAGAA GGAAAGGCTC 360
 CACTGGGTGT TGCAATGGGAT TTCAGGGTCT TGATAATAAT GCCAGGCAAT CATATAGATT 420
 ACCACGAGGG AAACATCAAC GCTATTTAAG GTCATCCTTT TTGACATCTG TOGAGGAAGT 480
 GCGAATAGCT GTAAGGCGAA CTCTACAAGA TCGCGCCGTC TCCAAGACCA ATGCTAAGCA 540
 CCACAACCTC AATGAOCTGA TTA CTGCGGA GCAATTCCTT CCTCGAAAGT TGGCAGCTCG 600
 ACTGACTGGT TTTCTGCCCA GAGATCAATC NATTGATCCN TNATCCCTTA CATCNCCGGA 660
 CTITNGAAAA CCCAAATTAA AATTCGGNAN NCCAAAATCC NCGGATTCNC CACCCCTTGAA 720
 CTACCCACNC GGCCCTATTA TTTTATAATT GCNNACAANN CCGATCCCC CGNNAACCGN 780
 GTAAANCGAA AACCCCCCGG NNITCGGACC NNCNTTTTNC T 821

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- 50
 55
- (A) LENGTH: 838 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1388UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

GATCCAGCGG CTGGGTAGCA TGCTGGCCGA GGAGTTCGGC TGTCTGGTT TTGCGGCTG	60
AGGCTCACTT ATAGGTGCGG ACTTCGATTG CCACTTGTGG CCAAGACTTG CTTCTTTACA	120
TAGCTAAATG CCACTGATCA TATAGACTGC TTATTCCTGC TTAAGTGCT CAAAGTTCCA	180
TACCATCTCC GCGTACTCCT CTATGCAGCG GTCAGTCTG AAGAAGCCAA CGTGGCGAC	240
GGACAGGATC GACTTCTGGA GCCAGGCCCG GCGGTGCGG TGGTAGACG GGTCAACGAG	300
AGCGTGGCAG GCTATGTAGG AGTCGAAATC GTGCTCACC AGGTAGTAGT CCGCGTCTG	360
GGCGAGGGAG TCCACCAGAG GTTGAATTC ACGCAGGTCC TGAGGGGAAA ATGCGCCCGA	420
GGAGAGCGTC TCCAGTACGC GAGCAATGGG GGCTGGCAAC TCTTGGCGGT GATACCGGTG	480
CCGCTAGCGG AGGTCTTGA CATCTTCTGC GAGATTACCA AAGAGGAAGA TGTGTCTTC	540
GCGATCTCG CGTGTGATCT CGACGTGGC GGCATGACG GTGCGATAA TGAGACACCA	600
TTTATAACGA ACTTCATGTT NGAATTCCN GAACCTCATT ACCCGCTGTC AAANGTGCTC	660
ACTAATCGGA ACNCGGANAA TATTCGCCCC GAANATGTAT CCGAATGAA ACCCTCAGA	720
AATACNATCC CTCTCTTANA CACNGCCNC TTATTACCTA TATNGCTGCC NTTTTACCG	780
GGCTTINCCC CNAANACC TTGAGAAGNC CCGCTNININ GGNCCCGIN CCGTTTTA	838

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1389RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

5	GATCTTCTTT TTGAAGCCCA CAGACACAAA CTGTGATGGA GTGCTGGAGA CGCCAGCTTT	60
10	GGACGACTTC CTTTCTTAG ACCGGGAGT CTTTTCCTA GGIGTATGTC TTTCCTTGGT	120
15	GGCGTGTTG CTCACAATTG CCTTTAGCTC TTGACGACA ATCTTTGTGG ATAACCTTTG	180
20	GCCATCTAAT GAGCCCTTTT CAATGACACC TTTGATCCAA CATCTTCCAT TCCAAAGAT	240
25	ATTGGTCACC ACCAACATAT TAGTGGAGTT ATCTTTCCCC CATGATAAGT AGAATCTGGT	300
30	ATGTATTTC AAGCACCTC CCGAGGGTAC ATCTGGCGTC TTGTTATCT GCTCCACTAC	360
35	TATGTGAGAG TTCACATCGC AATGTAGGAT TTTTCTCTGG ATCAAGCATC GGTCTGCTT	420
40	AGGACCAACA GGATTGTTTA ATGGCTTGAT ATATTCATAT TCCCTCACAT TATCTGAGAA	480
45	TTCAGACGGT ATAGCTGAAA TATTATGATT AGCTGTMTT TCTAATATCT TTTGCAAGTA	540
50	GGACGTGTCC TCACCAATA ACAGCTTGTA CAAGACACC AATGGTGCTG CGATGGAATC	600
55	GAATCATCAA CAATAACATC TCCTGGTTGC TCGTATAGGT GTTCTTGTG GGAGGANGCT	660
60	ACTAGGGCGA TATNGTAAA TATTAAGANA CANTTGTTGA CTGTTNGAAC TGCCNCGTAC	720
65	TTGATTNTAT AAAACCTCIN AATGTTACCG TTCNACNCT TNGAGANTIN ANCCCTCNAA	780
70	TCCNTCCNC GTGANITTC ATCTCCCCC NICTATACTG ATACNT	826

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 839 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1389UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

GATCGTGGC ACTTTCAACA TTGTGAAOGA CTTACACCG GAAGAAGAGG CTGOCATCCG	60
COGTGAGAAC GAGTGGGCOG AGGACOGCTA GOCACGGCCC GOCCTATATGT ACCATAAGTA	120
GCCGATATCT ACCGCTGCOG GCGCGGGCCC CGCCCGCGCC ACCGTTGCGT GCCAGGAGCT	180
GGTCTGCCGA CTATCCGTGC CAAOGTAOGA AAOGATGCTG GTTTATGTGG TCOCOCOGCC	240
GCTGGTTACA ATTAACCGCC CCAGGTCATC GGTAGACCGA GCTAGCTACT CGTTGTCTCTG	300
TAAGTGAGTT AACGCACAAG GGGAACTATT CGTGTGGTCA GGCAGCAGAG ACGCTGCAGG	360
ACATACTACG AGTTATTTCT CATAACTAAA CATTTTIGAA ACCTTTGTG CCGGGGCCAG	420
GTCGTTTTCG AAAAGGCGGC GGAATAAACA GCGAGGAGAG GTAGATGCTC TTCTCAGGCA	480
GAGGCTAGCA AGGATGGCAG AACAGCGGAA GCGGTGCGG TCGCTCAGAG AGAGCGCGCG	540
GGCACTTTTC AAGAAGCATA CCGGGGAAGG GCGCGGGAA GCGCGCGCG ACAGTGCCAA	600
AGACGGTTAC GACCCGAATG GCGAACCGCG GANCGGGCCC GAGCGGTNAT TTCAAGTTGG	660
CGCNGGGAAG GCGCGANTTT NAAACCGGTG TNTAGACAAA AACTTGTCCA GTTCNCACCC	720
GTNGTTTACC AANNNNNNAA TCTCCNCCC NCGGTNGGTG GCNGAACCC CCNCTGGCTT	780
ACGGGGNCCA CATCTCTOCC CCCCCTOCCA TTAAANACCC CGNCNCTTT TNTCTGNCC	839

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 740 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1390RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GATCAAGTAA TCAATCAGTT AATAATATTA AGAATATAAT ATGTAGACAT TTAGTCTAGT 60
 CTATTAATTA TTAATTATTT TGTAATTTGT TGTTAATTGG TTGATATTTT ATTGATTTTG 120
 TTGACATTTT GTTGACATGT TGATATGTTA TAAATATATA TTTAATATTA TTTTATATAA 180
 TTATTATTAT TATCTAGTCA TAGACTCATA TAAATATGAA TATATTCCAT TATTAATTGT 240
 TTAGGATAAA CATAAATTAA TATAATAACT TATTTTAAAG TTCAATAAAT ATGTTCATAT 300
 TTATATGATT AATTCATAAC GTATTGATA TAAATATCTC ATACCCTTTT ATGAATTAAT 360
 TAAGCGGTAT TAAATTATTC TGATTGGATT AAGTTATTAT TTAATTTATG TTCCTAACAA 420
 TTAATTGATT CCATAAATAT CGATATTTAT TATTATTTAT TAAATATTA ATGATAATAT 480
 TGTAATACTT CAATTATTTT ATCAAATGGC AAGTAATCTA TTAATCTTTT AATACGATTG 540
 ATAAGAAAGA AAAGAATATC ATCTATCGTA TAATATATTT CAAGTATGAC CTCTTCAATA 600
 TAATTAGAAG TTAAACTTGG TAGAGAATTA AGAATTTAAT ATGAGTCTTA CATTAACCT 660
 GATATGAACC TTTAATCTAC TTATTGTTTT AACCGTTGAA GAGAGAATAG TTAATCTNAG 720
 TATNACTTAT ATATTGATAC 740

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 773 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1390UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

GATCAACTA AGAAACCTAA TAACTAATA GAACCTATTA GATAAATTAT AGAAATTTC	60
CCAAATACAG GTTTTTTAGA ATAAGTTGAT ACAATATGTG ATATTATACC AAATAGTGGT	120
ACAATTATAA TATATACTTC AGGATGACCA AGAATCAAA ATAAATGTTG ATATAAATA	180
GGATCACCAC CACCTTGTC TTTCAAGAAT GATGTATTAA AATTCTATC TATTAATAAT	240
ATAGTAACAC CAGCTGATAA TACTGGTAAT GATATTAATA ATATAACAGC AGTAATTAAA	300
ATTGATCATA GAAATAAAGG TATTTTATGT AAGTTTATC CATTAGTTCT TATATTTAAA	360
GCTGTAACAA TAAATTAAT AAGTCCTAAT AATGAAGAAA TAGTAGTTAA ATGTAAAGAG	420
AAAATAGCTA AATCAACAGA AGCACCAGAA TGTGATTGAA TAGAAGATAA AGGAGGATAA	480
ACAGTTCAAC CAGTACCTAG ACCAGATTCA ACTATAGTAG ATGTTAATAA ACAAATTAAT	540
AGTGGTGGTA ATAGTCAAAA TGAATATTA TTTAATCTAG CAAATGATAT ATCAGAAGCA	600
OCAATTATTA ATGGTAAATA ATAATTACCA AAACCACCA TTAATATAGG TATTACTAAA	660
AAGAATACTA TTAAATAAG ATGTCAGTA ACTAATACAT TAAATAATTG ATTTTGACCT	720
TGTAAATATT GTTGACAGGT GCTGATAATT CTATTCTAAT AATAAATGAT ATA	773

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1391RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

GATCTTTTTC	CTCCAGGTTA	TTCCCTTCCT	GGACACATTT	ACGAAGTGTA	TTTTCAGAC	60
CTGACTCGCG	CATTTAGGTG	TTACGTTAAA	GCCTTTGAGC	TAGATGCOGG	CGACCTGCTC	120
GCTGCTAAAT	ACATGGTGG	ATACTATAGT	GACCTGTGCA	ATTGGCAGGC	GGGGCCAAC	180
ATCTGTGACC	GTGTAATCAA	GAATGATATG	CATCTCAATT	CCGTCAACTG	GGGTACAGA	240
GTTCGGGTG	TTTATTATTT	GGAGCTTCAA	CAGGAGGCTG	AATGATCGA	ATGGTTCCAA	300
TCTGCTTTAC	GGATTGATTC	GTCTGATGTT	GAGGCATGGA	TAGGCGTGGG	ACAGGGTAC	360
GGCGCATGTG	GCAGAATCGA	AGCCTGATC	AAGGTTTTTG	AAAGGGCATT	AGAGCTGTCT	420
CCAGAACATA	AGTATGCAGG	GTTATTCTCT	GCTATATCAT	TATGCCAGCT	TTCAGAATTC	480
GAAAAAAGTC	TCGAGGCCCT	GAGAAAACCT	GTGAATAAGT	ATCCACAAGA	AGCTATCTTC	540
AAAGAAAGAC	TAAGTGCAAC	GTGGTGGAG	CATGCTTTGC	AGTTCCTCGA	CCAAGGTAC	600
CTGATAAAAG	CGGCAACTTG	CGCTGCTGAG	GTCATATCGA	TCATAGAAGG	CATTGTATCT	660
GAACAGGTAG	AATATACAAC	CAATATGTGG	ATTACTTTAT	CAAAGGCTTT	GAATATTTTT	720
ATTTCCACGC	GTTCCTCAGTT	CGACAACTT				749

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1391UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GATCGCCGCG CAGATTGTGC AGAAGTGCT TGCCTAGGG TCTCTTACGA CAAAGGACTA 60
 CATGCAGTCG TTGGCTTCCG ATGTTTCTGT GAATGATGTG GCGTCCATGT TTGTGAAGCT 120
 GGTGAACTA GGCTTTCTGG TCCCGCTTTC CAACGTGCAC TACATGCCAC TGGCCGATCT 180
 ATGGGATGTG CTCTACAAGA AGGAATACAA TGCTATTCCA AAGAATTCCA CGTTGTGAGA 240
 TGCCAAGAAA CGTGCAGAAA CAAAGGCGAA GACGAAGGTT CAGTTCAATA CGTTGCTGAA 300
 GAATGTGCGA ATGAGCAACG TACTAATGAC TGATATGCAG ACTTCAATGA GACGTGTCCA 360
 AGACAATCTT CCTCTAACAT TTAACCTCGG CCGGTACATG AAGCACCGGC GTTCTCGGCA 420
 GCTTGTACAG TTTGCACGTT CCGGTGTGGG GAGCGTACCA GCCATGATCT ATAAGGTGGC 480
 ACTGAAGATA ACCGAACAAT GTGCCCGTGC GCTTTCAGAT CCGCTATGTG AGACAGGCTT 540
 AATGCAGGAA CTTGAGGAGC AACTGGCTAT TCAGGAAGAT ATGGCGCTAG ACGATGAGAA 600
 GCTACCGGGC GTTACATTCA ATGGGGTGGG CATATCCAGA AACTTACCAA ATAACATGGA 660
 CCTACGTGGC AACTGACTTT CTATGCCAAG AAGATCACCA GAACGTTGCA CGCACCAAGG 720
 TCAATCCCAT AAGCGGNTGA AGGCTGAAGA TGGGATGGCT GTAGCAG 767

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1392RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GATCCCCACC ACCGTCAACC GGGTGCCCGG CACCACCCGG TTGTGAGGT ACCGGTCGCA 60
 CGTCAGCAGC AGGTTGCGCG GCATCTCGCC GATCGGTACG GACTCCGGCA CCTCTCGGAG 120
 CTTCAGGAAC TGCTGGTCTA CGAAGCGCGA GCTCTCGTGA ACGATCATGT ACGGGTCTTG 180
 GCGCAAGGG TTCCCCCGCG CGCTGCCATC GTCATTGAG TGGTCTGCA GGCACGCGCG 240
 CGGTAGCGCC ACGTTGCTCC CGCAAGCGA CTGGAAGTTG TTGAGGTCCA GCGCGGTGCT 300
 GTGCCGCGAG TTGCGGCACA TCAGCGCAAC GTGAGTCCA CGTGACGTCA GCACCGACGT 360
 TGACACCAG ATCCCCCTCA GCGCAACCAG CCGCGAAACG CTCTGTGAGT CCAGCTGCGG 420
 CAGCGCGGTC TCAGCGCGCG CGCTCTGCAG CTCCACCTGC ACCGCGCGCA GCGCGCGCGC 480
 GTCTTCGGCC CGGAGCGCGG CCATCGCGCG CGCTAATTCC GTCACCGCCT GCTCAAAGAG 540
 GGGCACGTC TCACAGGCT CGTCGCGCAC AGTTTGTTACA GCGCCTGTT GTACCAATCA 600
 GATGCTCGGT GTTGACGCGC AGCGGTACG CCGCACCAGC AGGTTGTTGC GCAACTGCTC 660
 GCGATATAAN NAACCGCGCG TCNAACGAAA CTCGCGACA AANCGCGA AGAGCGCACC 720
 NCCTCGANC GGTGTTGCG CGCCGCGCTC CTC 753

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1393RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

GATCACGGAT TGCCCCAAGT ANTGGGCAAC AGTCGTCAAN TCTGACATAT CTCTTGCAAA	60
TGCTAGCCTC TGGGGGCTTG AACTAACCAT TACTTCTAAT ACCTGGCTAG CTGCCTCCAA	120
ATCCGGATCC AAAAAAGCAA TATTTATACA TAACTATACA CGAAATCTCA GTTCATCGCT	180
AGCTAGCTCA TCGTATCCGG GACTGGGAGA GGAAGTCAAT GCTGTGGAAC CCTTCGAATA	240
TGGCAGCGTC GGCGATGTTG ACCAAGGACT CGCCTGGGOC AAACATGCGG ATGCCACNTA	300
GGTGGGTGTC TTTCGCGTTC TCGTGGTTAG TCAAGACCTC GATGGGCAAA AACTGGCACT	360
TGAGCAGGCC GTCGGAGGGT CGGTTGTCTT CGAAGGTGAA CTTGACCCAC CCATTGACTT	420
GCGGACTTCT AGGGTCTTGT AGTAGGTGTC GTCGGAAGGG CTGTGGCCAG CGTATATGCG	480
GAGCGTCTCC NANGTGTAGG ACTCATCGAC GAAGAGCGAG AAGTACATGG CAAGCTGGAT	540
GATGTCAACG CGCTTGCTGA AGAAGACGTC TATGGTGTGT GGCTGGGAGC CGTCGCTTTG	600
CCANAANGTG GCGGGGTTAT CATCCNAAGG CGTTTTCAT GGGGTANCCG GCCTTGAANG	660
AAGAAGGCTT CCANTAGGCC AACNAAGTGA TATCNACTTA CCTGGTTTCT CCAATGTTTG	720
CAAGCCCNCC TGTTATTTTG NCCAGAAAAG AC	752

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 773 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1393UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

GATCCAGGAT ATCATGCCCC AAATCCTTGA AGCCGCTGCA AAGCGCCTCG TGCAAATCAA	60
GAATCTGCAC ACGGCAGAGA ACTTACTCTT CGTATTTTGC TACCTGACTT CTATTGATGC	120
GCGGCAGACA GTGGACTTTC TTTCATCAAC GATCATCGAT GAAGGCGGCC GTACCGCCCT	180
CCAGGCTATC GTTCCCGGTT GGCTAGAAGC ATTGCGAGTT CTCGCGGAG AACATAAAAT	240
CAAAGAGAAC ATTTTATCCC TTTCGAAGCT TTTCTTCTT GAGGATCCCC GTATAGCGGG	300
CATCACGGTC AATGGGGATC TGATTCCCCA CGATGGCGAC ATCATAATCA CCGCTCCAT	360
GGCCAAGAAA ATGCCTGATA AGTACACGCA GATCTCCGCG GCGAGAAGA TAGTCAAGCT	420
CTTTGTTGCA GAACTAGCCT TCAGCAAAA CCAGCTGAC CCTGGCCGTT ACCCTAAAGA	480
CGGTCCTGGC CCTGCTGACC CACATGACTC CGAGGAGAC TCAGCTGATG AAGACTGGGA	540
GGATGTGAT GACATCCTTG ACTACGAAAA ATTGCGGAG TACGCGGATG ATAGTGACAT	600
TGACGACACG GTGACAGCCT TTTATTACACA AGTAACATCG AAGAGGATGT AACCACTCTG	660
CTTACTCAAT TCTTCAAGGA AGCGTTTGCC AGAAATGCCT CTGGCTTCCA GGAGATCTAT	720
AGCAGGCTCA CTGAACAAGA GAAGAAGAGC TATCTGCATG CATGGTATAG GAT	773

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 755 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1394RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

GATCTGACG ATTACCGGT ATGATTATAT CCCAGCAACA TGGGCACAG CGCACACAC 60
 AGACATGATA CTGGTCGGTG ATTGCTGGC AATGTCCAG CTGGGTCATG TGTCACGGT 120
 GGACCTGGAT CTGCAGGAGT TCCAATACCA CGTCGGGTG GTGTGTACAG CACCAGGCTC 180
 GTCTTTTATA ATTGCAGATA TGCCATATGG TAGCTTTGAG CGAANCATTG AGCAGGGAGT 240
 AGAGACGGCG ATCTGCTTA TGAAGACATC CAGCAGGGTG GGTGCTGTTA AGCTGAGGT 300
 TGGCGGGGAA GAAAACGACT ACTGTCTTGA GCTTGCCGA GAGCTCTCA GCGCGGGAT 360
 CCCAGTAATG GGCCATGTCT GGCTGACCCC GCAGGCGATG CATGCATTGG GCGGGTACAA 420
 GGTTCACGGC GCAAAGGACT TGGGCCAGGC GCTGGCGGG TACCACCGGG CTAAAGATCT 480
 GCAGGCTGCA GGCTGTTTTT CCATGTCAT CGAATGCATT CCAACTAAAC TAGCCGGTAT 540
 CATAACCGAG AAATCAGTA TACCTACTAT TGGCATTGGC GCGGGCCCC AGACAAGGG 600
 GCAGGTGCTC GTACAGTGG ATCTGCTGG CATGTTGCCA NGGAAGGCC CAAAATTTTG 660
 TCGNGAATTC CCGGACTTC CNCGGGACG CCATANGTTC CTTGTGCCCC CTATGTTGAA 720
 AANGTGCCA NGGCTCTTC CCNAAAGTNG GGCCA 755

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1394UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

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GATCGAACTC CATGAAGGAG CGTAATGGCC TGTGGAGCT GCACCGCACT GGGTGGGTAC      60
ATAGCGGGAT GTAGGAATGC GGGGATAACG ATTTCGAAAA GCTGACTGGG CTGCGCCTCT      120
AGCTTCAGCT CAAGCTGGCG CAGCAGCGTT GCTATAGGCT GTTGTGGCGA CAAGGTGAC      180
ACTTCAGTTG CAGTAGGAGC AGGTAGCATA CGACTAGTTA TATCGAACTG GTGCCGTAA      240
TGAGGATGAG GGTCAATTTC TGGCTCCGAG CGCTGGCTAG CACCACAATT ATCAACCAAGT      300
CCATACCTCC ATGCAATTCT GAGATCTTGG CTACGTGCGA CCGGTTTTGC ACCCCCTCCG      360
GCTAAGTTTT GCACCGTGAC CTTGATTCC TCTTGGGAAA TGGAGATTT CTTTACCTCT      420
TTACGTGTGC CCTGGAATAT CCCCAGCAGC TCTTCGCAT ACTGAGTGT GAGCGTGATG      480
ACCACCACAT GGTATTCCC TCCCAGCTGT GCGCCGCGAC TTCCGCGCG GTTATGTGCT      540
GCTCCCTGGC CTGCAAAGAG CTTTCCAAGT ACCGATGCAA AGTCTGTACC CCTTGTCTCT      600
TCCACCAGAA GCATCTGGCC CATTTGCAAG CCCATATGCC CTAGGAGCCG ATCCATATCT      660
GCACAACCCG TGGATGTTGT GGGATGCGAA GTAACCGCG ACGGACGCAA GCCCAGATGC      720
GACTGCCTGC CNOCTCACTG TTGGATGCCA ACCTCTCCAC GCTCTINGAA ANC      773

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(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 746 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1396RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

GATCAATCAT TCTAGAGCTG GAGCAAAGGA TACCTATAGG CTTGCOCTCGT CATTGGCCCC 60
 TTTCAATTATT ACATACCCAT CGTTCCACAG CGTGTCACAT TCTGCCATTG GAGAGCAGGA 120
 CACCCAAGTT TTCAAACAGA ACAGCOCTGT TCTCTTGGTA AAAGTTGGAC CTTCTAACGG 180
 TGTCCTCATC GAAGCOGTG TCGCCACTGA GGACCTTGAG GCGGTGGAG GTGGCTTTGA 240
 TGTAGTCGTT GAGCATAGGA ACCGGGTGCT CGCAAGCTT ATTGAAAAT TGGTACTTGT 300
 TGGCTGTGGA GCTGANCTGC AGGGGAGAGC AGTTGGGTCT TCTTTTGGAG GGTGGCCAGC 360
 TCGGGCTCGA GCTGGCTGGT GACTGTGTGT AATTCTGTGA GCAGCAGCAT CCOCTGTTGG 420
 GCAAGGGAGT TTTGGGCGGA CGCOGTTG GGATCCTTAA CCGGACACG TGGCACGGG 480
 ATGTCGAAGA CCAGTTGGCC GTAGGTGGAG GTCTTGTCGA CCTGGATGGT GTAGTTGATG 540
 CGCACGGGGG GGATGGGCTT GATGTGGGCG TTGACACCTG GGCAGCTCG GTGAGCTTGA 600
 GGTACTTGGG AGGCTCTGCG GCGGGCCGCA GGAACCTAAC GATCATGGCG TCACCTTGA 660
 TGACAACTTG TCGTCGTTCT GCGTGCTCTT GCGGTGGCCG CTNGGTCTG CGACNAAGAA 720
 CTCTTGAACA GGATTCTTGT TNAACC 746

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 772 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1396UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

GATCGGTTAC TTAGAGGGAG TGCAAGACCT GGCTGACTT ATCTTAGGGT TATTAGCTAT 60
 GACGGGTGTG TTCGGATTTC TGTCCAAGGG TTTAGATGCC ATCAACTCCC TGAATTCCGA 120
 CTACTTTGCG TTGTGGGTGG ATGAACAGAA GGCCATGACT TTCGTTGAGC GTATTAGATA 180
 CTACAATTGG ACGTTTGAGG GGATCTGTGT GGTCTGCTC GGGCTGATGT ATGCCGTGTA 240
 CGTGGGGGGG ACCAAACTAA ACGAGCGGG CTCGGACCGT CTGTTGGAAC AGCTGAACAA 300
 GTTCTTCTGG GAGGAGCTGC AGTTTGGGG CGTGGGTTT TGTCCCGGG ACAAGGGAGC 360
 GCTGCCATAC ATCAGCGATC GGAATGGCAC ATGGTGCAAC GCATTGCTA CCGGGCGCAC 420
 GTGTGTGGAC CATATTGTGG TGAAGGCTCA CTACCCGGG CGCTTCAACC CTGTGGGGCT 480
 GCTGGTGGAG AAGCTGCTGG GGATGTCTT CCGGCAGGTG GTGGACCGCA CGCGATGAG 540
 TTTGTGCAGG TGACGGTGAC CCCCAACGGG AAGTGGACGA AGGACGAGAA CAGCGGGGTT 600
 CAGCGACCG AGGACGGGCT GAACGGTTC CGGTTTCATG CGTCGATGT CCACAAGAAC 660
 GGGATGAACG ACTCGCGGG CAAGAACTAC TTCTCTCTCT TGACTCACNC GTCCGANGGC 720
 GAAACTCTCC CATGGAANTA CTCTTCATGT CCGANAACAA CCACTGAACA AC 772

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1397RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

GATCCCATTA TTCTACAGCA AATATTACAC GCGCGGGGA CCCTGACAA TGCAGAATTC	60
GATGCATACA CAAACATAT TACTACAAAG CTTCAAAAG GTGTCTCTCC CACAGACGCA	120
TTTCTAGGCG CACTCAAGGT TTACATCTCT AATTGCAGTT TGAAACGTTT ACGCTTGCG	180
AAAGCACAG TTATACTTCT TGATAAAATT GCGATATTCA TCAATACAAA TGTGGTCCAT	240
GTGTCTGTGG AATCGATACA TACGATACTG AAAAGTTTAG CTGAATATTT TATTGATGCC	300
AAGGAATATA AGCGACTCAA CAACGTGTC AATATTTTCAT TCAACGCATA TGTGATGTAT	360
AAGCATGAAA GCCTTATACG ACTTGCGCA GATCTCGAAT TATTTCTCTT TATGTCGGTC	420
AAACAGGACT GGTCATGTT TACCAAGTTC GAGAAGTTA TTTCTGTGCG TTCAGGAGAC	480
ATCTCAGTAT CGCTCTTTGA ACAGTGTTC AATGTTTATG TTATGTTGCG GGATCCCTCA	540
TTGGCCGGCC TATGGGATGT CTGCTTGAAC AAGTCGTTGA AGTGTTCAC GAAATTGGGA	600
CTAACTAGTT ACACAGACTT TAAGGCATCG TCCGAGCCAA TGCTAGTGTT GGTATACAGT	660
GGATTTGTTT CTGATATTTT TACAATACCT TATAATGGCT GGGCTCGCT ATCGAAAATG	720
TTATTCATGG CATTAAATGG GGTCTATAAA TTG	753

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 767 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1397UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

GATCTGAAAT ATTGCTCACC CCCACCGTGA CCTATGTAGA TGAACGTGCT GGAGTTCTGT 60
 ATCATTTCTGA CGAATTCATC CTCTTCTGGC TTTGAGCCAG TTAATATCCG TGTGAACCC 120
 AAGTCGCAAC AAAGTCTGGT AAAATGTTCT TTAAGGCGA GTTCAGTCTT GGTCAGTCC 180
 CCATGCGGGT TTAACAACAT GGAAAGTCTG CTGTCTAGGT TAATCTTTGG AGAGATCTCT 240
 CCTCTGAATT TAGTTAGTAG CTCGTGAAGG AAATTTATGG ATGGTAACGG GCTCAGAGAA 300
 GCATCGGAAA ATATACTGAG AGATTCCCAT GGAACCAAC TGCAATCGGA GCTTATTACC 360
 AGAAACGTGT GTCTAACCT TGGGCGCTCT GGTGCGTTGG CATGATAGTC GTGAATTAGT 420
 TCCTCAAGTT GAATATGTAT GAGATGAACG TCAATCTCAT CATAGGCATT TTCTTCGCCA 480
 TGGAAAAGCA ATATGTCAAA GATGAAGTAT ATCAAGTCTT CCATGAATTC CACCTTCTTT 540
 TCGTGAGGAA GGGCATCCCA ATCCACCTTT AAAAATAACT CTAATATGAA ATCGTCCACC 600
 TGTTAGAACA TAGACGGGTT TCCTACTGT CTCTTGTGTT GAAGATTTGT TGTAAACCT 660
 TTGAAATCCT AATTTGAATA NTGCAAAATG GTTTTATCCA ACTGTTTTTG GNTGAAGAAA 720
 CCGGGAATC CCATATCCAG ATCTCATGGG GGGGTCNAT CTACATC 767

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1398UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

GATCGCTCTT CTTTGAAAGA ATATGTAGGC ACCCTCTCCT ATCTTGCGCC GGAATTGGTT	60
CGCTGCAAAG ATATGAAGAC GATGACACCT GCAGAAGCAG AAAGAATCCC AGAGTACGGT	120
GCAGCAGTCG ACATATGGGC TCTTGGTGTC CTCTGCTACT TCATGATGAG TGGCTATATG	180
CGTTTCGATT GCGAAGACGA TGGCGAACT AGTGACTCCA TCTTGAAGGG TGACTATTAC	240
GTTGACGAGG AAGCTGTGTC CAAAGCCAAT GAGAGCTATA ACAGCTGCTG GAACTTCATG	300
CAGCGCTGCT TTACGATGGA TGATAATATC CGGCGGCGCG CACAAGAACT CATGGGCCAC	360
GCATTCATGC GGAATACITT CCAATGGCT GGGGCAATG ACTTCGCATC TATCCCGCTA	420
CTCGAGAGAT CAAGATCCTC GAACTCCCTG CACCCTTAG CGCGGCATC ACGGCAACG	480
TTTATCTCGT CTGGGCTGCC GGTATTAAAC GAGCGCCCTG TGCCACGTGT TGGCTCGCGT	540
GAGCGCAATT TGGATAAGTT GCGGGATACT TTGGGAAGA CCTTTCCTTC ACTTCGCTTG	600
AACCTATGCG CTTTGTGCT CAAGCGAATA CTCTAATCC TAATAAGAAG AACTCTACTT	660
TTGTTCTTGA GCCAGCTCCT CCCACGGGGA GTCTAATGAA TGGGTGTTTC ACGTCACACC	720
GGAAAGTAAT CCAACCTCAA TACGCCAGTC CTTTGGCGCA GAAGCTCCGG CCAA	774

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1399RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

GATCATTACT CGCAGAACT GAGATGTTAG GGGACCAAA CTCITTTTCTT TGATGAGATA 60
 CGGGAGGATG CCTCGGAGA ACCAGAACAA TGCAGCAAAA GGCAAGAAGA ATGCCAACGA 120
 GAAAAGCAGC CATCGCTGCA TATGCAGTCC CACCCCATAG TAGTTCCTTG CGCCATATGC 180
 CTGGGGGCAG AGTGTATCTA AGCTTGTTGA AATACCCCTCN AATATTGCGA AAGTGATATT 240
 GGTGTCATG GAAGCCAGGG AAACCGCTGC CAACTCATTC TTCCAGGT GACCCACAAC 300
 TAATGCACAT ACAACCGGAA ACATCTGCTC AAGCAGAAAT GTAAATATGA GCGCACGGA 360
 GTAACACAGA AGCACCAGAC TCTCGGACTT CACGGTGGCT GGTTCGTCTG CGAGATCTCT 420
 GGACCTCGG AACGGCTGG AGGGGCCCC CTTCGTGCCA ATGGAGTAGT AAGACAGCTT 480
 TCGGGGCGGT AGAACACGCA CTCTGCTT GTCCGACGGC AGTTGCTGCT TAACCCGATG 540
 CATGAAGTGA GTGTAGTGCA CCATGTCCTG GCGGGGCCCC TCACATCGA CGGCACGAT 600
 GTCTCGGG CTGCGGTAA CAGTCGAGTA CCGCGTTG TGCTCTCCA ATATCCAGTC 660
 TACATTCACT GCAGAGGACG GCGCGCTCA CTGCAAGCG TCGACGGCAG CGAGACTGTC 720
 CGGACAGCT CTCCTCGTC AAGCAGCCC TCCTCC 756

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1399UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

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GATCTTGTAC GAAGGCCGCG GAAGAATCGG TGCCATCGTT TCCAACAGAC AGTTCCAGTT      60
TGAAGGCCCA CCACCACAGG CTGGCTCCAT CTACGCCAAG GGTGGGCCCC TAACCGAGGA      120
GGGCAACTTG GGCCTAGGTG ACAGCGACGT CTTCTACCAN TGTCTGTCCG GCAACTTCTA      180
CAACCTATAT GACCAGAACA TCGCAACACA ATGCTCTCCA ATTAAGCTCC AGGCAATCAA      240
ATTGGTGCAC AACTGCTGAA CAGCCACAAA GGTATATAGT GCATATATTG TATTAGTTAA      300
ACTAGGAATT TTGTGTGGCA GCTAGACTGC CCTACGTGGA TTCTCGTTG CGGATCCTGG      360
GCTGCCGCTG GCGCTGACGC ACAAGAGCAA CTGCACAAC ACTGGCGTAC CGCATGCTTC      420
CTTGTGCATT TTGCGCGGG TGGACGTGCG TGACGTCAGC GTGGCAOGTG ATCATAATAT      480
GTCCCGGGCC AGGCCCCCTAT TGTGGCGGAC AGGAATGCAT GCGGAGGTGC AAAATGGTGC      540
AAAATGGTGC CGATGCAAC TCTAGGCCCG AGCTGAAACA AGATTACCTG GGCAGCCTAA      600
ATTTGCAGCG GCTGCTGGC AGCCACATG TGTATTGTGC TTTTACAGTT CTGCTGCGG      660
CTGTCCAATA CAGCCGATCG CGACTTTGCT GCGCACGGCC CACTAGGCCT GCGGACAAA      720
AACTGCAGGC GCGCGGGCGT GAATGGCGCC GGACGATGTG CTGCGGCGGA ATTCC      775

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(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1400RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GATCCTGTCA AATATGGCCA ATACCAAGCA GCGCGTGTT GTAGAGCATG TGGTTGAACT	60
CAAACCCCTCA AGCAGCCGGG TTTTGGACTG TGCACAGGAG ATATTGTCTC CATTTCACA	120
GTCCAAGAAC AAGCCCAGGC CGGGGGACTG GAATTGTCCC TCTTGTGGTT TTTCTAACTT	180
CCAACGGCGC ATTGCATGCT TCGGTGCTC CTTCOCAGCC ACTAGTGCAG TGACGGTCAG	240
CAAGCTGTAC AAGCCACAGC AGCAACGCGA TTATCAGAAC CCACACCACG TOCCATCGAA	300
ACAACAGGTG CAGCACCCGC AGATTCACGA CCAAGACACA CAGCAGCAIT CTCAACATTT	360
CAACATCCAG CAGATGCCGC AGCAACTCCA AATGCAACAG CAAGCGCACG GTACCGTTCA	420
AGGGGGCAGT AGCATGCAGC AGTACAAGCA CAGGCTCAG CACGGCTTAC AGGCGTATCT	480
TGGCTGCTAC CAACAGCAGC AGGCGAAGTC ACAGCAGCAG TACCAGATGA ATCAGCAACA	540
GGTGCAGATG ATCGCTGGCG ACGCCAGAGA CGGTATAACC GGTACAACAA AATGGTGCAG	600
GGCAACGGGC AGAACGGTAA TTCTTGTAAG GAAATGGCTC CCTGGGCAGT AGCAACGTGC	660
CCTTCAGAGC TGGCGACTGG AAGTGCTTGA ACTGTCTTTA CCATAATTTT GCCAAGAATA	720
TTGTTTGTCT GGGTTGTGGT AATCCAAAGA CGGCCAT	757

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 775 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1400UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GATCGGCGGG TACTTCAGGT CATCTCTCTC CACCACCACC ACCAGCTGCC CGGGCCCCGG 60
 CTCATACAGC TGGTACGCCA CGCGAACATG TCGCTCCGCC TGCGGCACAT CCGCCTCGTA 120
 GAACTGATCC GCAGCCACCA GCGCGTCCG CCACTCCCCG CCGCGGCTT GCGTCAGGT 180
 CCCCCTAGC TGCGCGACCG GTGTGAGCTG CACCATCTCA GGGGGCATCA GCCAGCTCAG 240
 CGTCGATGGC ACCACCAGTG CCGCCGAGTA CCGCTCCCGG AGCTTCCCCG TGAACTCGAC 300
 CTGCGGCTCG GCCCCCGGA GAAGCGAATG CCGGTCCATA GGGCCGAGGC AGTCAGTTG 360
 GTGTCTGGGA AGACGCTCAG ATTGCCATTG TTTGAACTGT CCACAGTTAG AACTTGCACT 420
 ATGCTACCTC CGGGGCGCT GCGCGACCC ATAGTCACAT ACTATCATCC TCACACAAC 480
 CAGTACTTGC TCGAGTCCC AACTCAAGCT AACGAGTACC AGACTTGGTT TTGGCTGTTG 540
 CTGTATGCAT TCCAATGGTT TGTATAATCG AAAAATTGTT CAGTTGCTCA GCACATCTCA 600
 TACAAGCAGG AACAAGACG AGTCGCGAGC CAAAGACCTC TTAGGCATTA GTATCGGTAG 660
 CTAGGATGTC GCCAGAACAG TTGCGACAAG TACACGCACT TGCAGGGCGA ATTGGAGGAG 720
 CTGGTGGTGA CAGACAGAAG CTGGAGACG AGCTGCAGGA GAACAAGATC GTGAA 775

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1401RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GATCTGTGTG TTGGCAATAC CCTGTCTTAC GTTGAAAAGA AGTGTCTCTG AGGTGTCCAT	60
CAACAAAAAT ATTACCAGTT ACAACACCCA CCCGAAGTCT ATTGGCCAAA ACATCCAACA	120
ATGTGTGCTT ACCTGCACCT GAATAACCCA TCAGAGCAGT CAAAGTOCCA GCCTTTACCC	180
AACCATCCAC GTTGGTTAGG ATCTCTCTGG TTTCATTCTT AATCTGTATA TCATAGCAGA	240
CATCTGCCA GTGGAAAATG CTATCAGAAC CAATCTCTG AATAAGTTG CCGGATTGGT	300
CACTTCCTAT AGTACTAGAT TCCTTTCTG GTGCATTACC AAATCTATG TCGCAGTTGA	360
TGGCCTTTT ATTTTGCTTT TTTATTTTCT TCAAAGTTGA CCTTAGGAAT ACAGCCATTT	420
CACCTTTTGT CATCCACTT TTATTATACT CAATTAAGAT CAGATAAACA CCTAAGAAGA	480
AAAATGCATA AGCAAGAACG ATCCCCCAAT TCATCCACTT GTTTTGGTG TTGTAACCAT	540
AAGCAAATC TATGTAACGG GTCCCATTTA CAAAGCTCTG ACCAGGAAT GCTCCCAACG	600
ACAAGCAGAC TTTATTGAA ATAGGGAATC CTCATAGAA ACTACCATG GGTACCATTC	660
GAGAACATTC GAATATGGT CGTCAAATT CATTCGCAAC CATGGCTTCC ATGATGGGTG	720
CGA	723

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1401UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GATCTGCTGA GATTAAAGCCT TCGTGTCTG ATTTGTTTTT TATTTGGAAG TCTGCAGGAG	60
CAGGCTTTGA AATAGAGTTC TTATGTTATT TAACGTCCGG GTAAAGAGTA TACAAGCATA	120
TGTTTATGCG TATGCTAGTT ATATGCTTTG AAGAGGTGGT CTGCAGCTGG CGGTCTATTT	180
TATTTTATTT TTTCATTTC CTAAGACTTT ACATTTTTTT TTTAAATTAT TTTTTTTGCG	240
CTAAGACTGT GAACAGCGAT TTTAGAAAA AGCGAAAAG TTCAGGAGGC CTCAGCTACA	300
TGATATCCCA GGCTTTGTAT TTGTGAGACT GCACTCCCGG GCTAGGTTGT GACCAAGAGT	360
TGACGTGCGG CGCGGTGCGG ATTGCAGGCG TTCACAGTGT GGTAAATTTA ACAATTTATA	420
GAGAATAGAG ATGCCCCGAGC TTAATCAACT GTGCGGCGCG CCAAATTGGA TTTTTTGGAG	480
TTTGTGATTT TTCACAGCAG ACGAGAAAGC AGGACAGGCG GCGCGGCGCA GGCAGTCCCC	540
CCTGCAGGCG TGAGCGGACA CAGAGAGAAA ATACAGGAAG ATGAATACTG ATAATCTACA	600
GATTTCAATG ATATCTCATT GATCCGCTGA TTATCAATGA AAGTACCCAA TGATCCATGA	660
AGCCAGTAGA TGTTAGTATA TTTTATTAAA TATATGCACC TTGTTATCC AATCTCTGTT	720

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

EP 0 866 129 A2

- (A) LENGTH: 719 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1402RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GATCAGGAGC CCATCAAGGC GCCTAAAAAT CGCATCCCCG CTGTGGTTT TCCCGACTAC 60
GCGCTGTTG CTTGAAATAC AATTACTGCT GTAGTTCCTC CTGTGATGCT GGTTCGAAATG 120
TTGGGGGCGG AAAGGGTCTG CCTGCTGAAA GGAGCTGAAA GGTGGTGACG TGGTTCGGG 180
ACTACTAGCG TCTGCAACCG TCTTTGAGCC CAAAACACGG AGGCGGATTA CATTCGCGTC 240
AGCGGGCGCG AGGGTAGAAG ACCTCCCTG ATGGGAGTTC ATGCTCTTAC TCGGGTGTG 300
GTAATAGTAC TCACCACCAC TGCTCGACGA AAGCGGAGCA GGGGTTAGCG CTGCCATCTG 360
TTGTTCCTC CTGCGACGTG CTTCTAATG TGCCAAACGC AGCTGTGCT GTTGCTCTG 420
GTGCGGTCC ACCTTGGCCA AGAGTCCGG ATCATCATGC AACATCTCCA GCACCTCCAA 480
TTTCGCCCCCT AAGCCAGTG ACTCGCTTC CAGGTGCTCC ATTCTCGAT GCTTGATCAT 540
GACCTGCAGA TGGAGCTGCT CCAGAATCTC GCGCTTCGCT ATCTGTATT TTATCGCTC 600
CGTCTCTCG CTCTCAGCC CCAGCGGCC CTCTCCGCA CGCAGCCGC TGTATTGTC 660
GTGCCCCAGG GAAAGCTGT GCGGCGACTT CGGTGTCGC ACCTGGTAAT ATGCGGCG 719

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PAG1402UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

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GATCAAGTTA TGGTTGATCA AAGOGTCAAT ACCCTTTTCT CTAAGCATGT GCCAGGTTTC 60

CTTCGCGGGG CGTAGGTATG GTTTCGCGTA CAACGCAATG AAGCAGTAGG CATAGTGGTT 120

GAAGTACTCT GCCATOCATT CAAAGACACC AACAAACGGCA TOCAAGATTA ACCACAAGCA 180

25

CTGCATCCAC CCACTGTGGG ATATCCCGGA AATAATCCCA TTGOGAAGCA GCTGAATAAT 240

CTGCCGCACT AGTTGAATCA GAGACACAAT CAGCGAGCCA AAGCAAATGG ACCCAAAGGA 300

30

AGTGGTCAAC GCTCTCTTTA ATGAGCCAAA AGCTGCCAA CGTGGCATGC CTGCGTCCGA 360

CTTCGAAAAA TAGTACCAGC AGCCGTAGAT GCCCGCGATG GTGCAATGAA TCACATTCTT 420

35

GATGACCTCA GAAATGTAGA ATCCACAGAA GAAAACGAGT ACCAAAATAC CAATTAACTT 480

TCACGTGAG CAAGAGCCAC CAGATACATC GCAGCCACCA TTCTOGCTCT TCGGGTCATA 540

40

CTTTATGTAG GTGCAACCA AACTACAGA GAATATGACA GAGAAOCAG CCGACACAAT 600

GGTACCTAAT AATGACACAA GCCACGTCTG TGGATGTTTC TTCATACTG ACATGACCGT 660

45

ACGCAAGACA GCGACACTAA ATGGAATCCT TGAGGCATT AACCAGTAGC ACACCGCCGT 720

CAGAAT 726

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(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 731 base pairs

(B) TYPE: nucleic acid

EP 0 866 129 A2

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1403RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GATCCGTTCC TTGAGAAGCA CCTAAGCCT GAACTCCTGG CAGAAGCGAT CAAGGGAACC	60
TCTTGGGAGG GTAAAGTTAG TATTAACITG GTAGACGGAT TCGAOCCTC GTATTACTTC	120
GTCAGCACGT TCGTGCCGGA ACACGCAAAG TACCATGCAG AAAAGTTGGG TCTAGTTTGA	180
GATTTGACGT TCGGCTGTT AATTGGTATA TACTTACATA TTTAGTCATA TGACGGCTTC	240
AAGTACTCTG ATTCTGCATT ATAAGTGCAG CCGAATGCCA GCTCCGGCA GTAATGCCAA	300
CGCAAACCTGA ATTTGCCGGT AGTTCAACCT TGGCCGGTTG CAGCACCGGT ATGCTCCGAG	360
CAGACTCAAA CGTCGCTATT TGGCGGSTAT CTACAGCCTC GTGGGGATCT CCTTGCCCAA	420
GACAGCCACA GATATCACTC TCCAGCCCCC AGGAGTAGAG TTCACCTTTG TGGTTTAGAG	480
CTAGGTTGTG GTAGTCTCCC GCAGATACAG CAATAAACTT CTGGCCTTGT TCCAAATTCA	540
TCTTCATGAA TGAGTCCTCG ACGATATCAC CATTATTCAC CTTCAGGGTG TATGTGCTAT	600
TCTCGGTACA TAAACCACT GTCATGCAAG ATGCTCAAT CTTGTTTTAA CCGTCCATCA	660
AATGGCAAAT CAACGGTTTT TGAAACGCCA TGAGTGTATA TCCACAGTTT GCGCCCATTG	720
TTAGTAATGT A	731

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1403UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

GATCTCAATA TCAACCAACT TGTGACGTGG CTTAAACAC CATATGCGGA GGACATTATG	60
TCCATCACCG TGTACAAGGA CAATGTTTTT GCCACGCACA AGCAGGGCAT TACGGGGTTC	120
CACCAAGGGA ACGTGAACIT CTGGAATGCT CACCAGGGAC TGTCTTTGAG TAGCGAAATA	180
TTGGCGAAGA GCTGTACCAG TAATCGTATA GATCGGATGG TTAATGGGGG AAATGATGGG	240
TCATTAGGTT TGTGGAATAT TAACGAATGG CTGAACGGTA CAGCGTCCC GGGTGGATCA	300
GCCCCGACCG AAGAACAATC GCTTCCCTCT GCGAGCGGC GAAATCTTG GACCGAGTAT	360
CAACAAATCC AGTTAGATAA CGATCACATG ATTGCAACAC TCGGGGAATT CATTAGTTAC	420
CAGACTGTTT CCAACTCC AGAGCCCCAA AATATCATCG ATTGCGGTAG GTGTGGAAC	480
TTCTTGCAA ATCTCTTAC TAAGCTGGT GCTAACCATT GTGGGCTTAT ACGTGTAGT	540
ACAGGCAGCA ACCCGGTGGT TCTCGGCAG TTCAAGGCA ATGCAGCGC GCGCAACGC	600
ATACTATGGT ATGGCCACTA CGATGTGATA TCGCGGACC ACGTGCAG TGGGACAACG	660
ACCTTTCAG CTCACTTGG AAAATGGTA TCTTAAGGA AGAGCGTGT TGATAAC	717

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 710 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1404RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

GATCTGCAAC GTTACTGATT ATCCTGTAAAG CCTCTTTTG GGTAAAACA TCCTGTGAGT	60
TAACAGTCGT GTTGAAGATA GAAATAAAG CAGTGTATGA TGATGCTGGA ACAACCTGG	120
ACATAACCAC CACAAGATCT AGAAGTGTGG CACTCATTTT TGGCTGGCC TTCACAGTT	180
GGCTAGAGCG CTCCTTATCC ATGGCATCTT TTAGTAATGC GCATACGTTA TCAAACGTGT	240
TAGACAGGTT TTCCGCAGAA GTAATTTTCA AGTATGCCTC GATGGTTTC AAAATATAGC	300
TCCGAGCGTT GGGTGCAGTC TGGTGTAGA CATTGAAAAG AACGGCCAAC ATATTGGGCG	360
ATTCTGCGGA GAGGTATCT ATGTTTTTCT CCGCTCTGT CGCGGGAAT TGCTGTCCA	420
TAATAATGTC GTCTTATAC GCACCATCTC TGTATAGAAG ATTACTTGTG ACCAAGACCT	480
TCAATCCATT GCATATGACA GTACGCAGTT CAATCTGGA ATAAAGTAGG GACGCTAACT	540
CTGCAGCAA CTCATCCGTG AATACATCGT TTAGATCTTT TGAAGAAG CAGAACTGAG	600
GGAAGGTAGA CCACAATTGG TCAACAACAG TCTGAAGTAA TGTCACCTGG ATAGACTCCT	660
TATCCAGTTT CTCAATGGTG GACTCGAAAT GACGAATGGT AGGAATAAAT	710

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 715 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1404UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

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GATCTTCAGC AAGATCAGCA CCACTTGACG CACTACAAGA AGTACCGGCA CTGGCGGTGG	60
CAGGCCAAGC GCAGGCTGGC CGGCTGGGAG TCAGGAAAAG TGGAGCAGG TCGTACAGGA	120
G00CGAAAAC G00GAG00GC TGG0GAAGCT GGG0GACGGG CTGA0GGTGA C0G0GCTGAC	180
GGCAAGATG AGCTACTACC GGCAGCTCCA GGAAGCGTG AGCTCGTTC TCAGTTCTGT	240
GTCGCAACTA ACGACGTCCA CCGGGGCGCC AGAATGCGAC TTCACTGAGC AGTTCATCAC	300
CTTACTCGTG AACACCTACC ACGAGATGTG TCTGGATGCA ACCGTCACAC CGTTCGACAA	360
GACTAAC00G CCATCTGCTT TTCTCAACAA GGTAG0G0GT GCTG0GGTGG AG0GTTCTGA	420
GCAGCAGAGC ATCGCCATCG GACGTCCGGG CGATAAATGG TTGTTGACCT GCACGGGGAA	480
GCGGCTTCTA CAGGAAATAA AGCGGGAGAC CGAGGACGTT CCACAGGGGT CCGTGGGCTC	540
GGTGG0CTGT TCATGAACC ACGGCAC0CT ACAG0G0GAT CTAAGCT0CG CTTTTGCAGA	600
GGAGGG0GAT TTCTTCTACT GGGAT0CGGA CTTC0CACTG TT0CAAGGCA TCACGGCAAA	660
ACTTCTAACC GACACTGGAG ACATCTCGGG CAAAATACC CCATGTCTTT GGATC	715

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(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PAG1405RP

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(x.) SEQUENCE DESCRIPTION: SEQ ID NO:589:

10 GATCTTTCAT ACTTTCGGGT TCGTGTATA TAACTAAGAT TGGACAGAAC TGCAAGGGCC 60
 ACAGAGGAAG AGCTGCTGCA TTGCACATTA GGCAGGAACA GCGAATGTCT ACAAATGCAC 120
 15 ACTACACACT ACCGCTCTCA GCGATCCCA ATCTCAGATG CGCACAGCAA GGGACCCAGT 180
 TCTTTGCCCA TGCCGCTGTA CTGCGAGGG GCGCAGATG GCTGCTAAC CATTAATGCG 240
 20 AGCGCTGTGG GCTCGCTGT GGGCCCCCAG CCGGTGATAC CTCACTCAT GCACCAGGTG 300
 GCGGTGACA AGCACGCTCA TATCATGCCA GCTCGTACG CGCTGCGACA GAGCTCGCCC 360
 25 CAGGTACCGG CGATTATGGG CGAGTTAGCG ATGCTGAAGA AGTCGATATT CCAGTCGCTG 420
 AACGCGAGT TGACGACGGA GGAATACAAC AGCATCTACC AACATTGAG TCAACTGCTG 480
 30 GCGTCCCTCC CACGCGCGGT CGAGCATCT GCAGGCGAGC CCCAGCTGG ACTGCGGTG 540
 ATATCTCAA TTATGCGGG AACAGAGCCC CAGGAAGTCC AAGTACCTT CATCATAGCA 600
 35 TCCTCGAGT CACAGCAGG CCAGCGTAC ATCTGCGGC CGTTAGCTC GACAATGTCT 660
 ACCCACCGC TTTCACCGG CATGTGGTA GCCAAACCGA ACTACTCGT GAGCACAAG 720
 40 AAGAATGTT 729

(2) INFORMATION FOR SEQ ID NO:590:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 715 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1405UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

5		
10	GATCCAAATA ACACCAAGGT TTTCATCGGC GGGTTGTCTT CGCTCGTGAC TGAGGATGAG	60
	CTACGGGCTT ACTTCCAGCC ATTCCGACAG ATAGTCTACG TGAAATGCC GGTGGGCAAA	120
15	GGATGCGGCT TTGTCCAGTA CGTGATCGC AGTTCCGAG AGAAGCGAT CGCCAAGATG	180
	CAAGGATTTC CAATTGGTAA TTCGAGGGTG CGGCTCTCAT GGGGCAGGAG CGCAAAGCAA	240
20	ACAGCCGCTA TGCAGCAGGC GTTTGCCATA GCACTACAGC AGCAGCAGCA GCAGCAGCAG	300
	CAGCAGCAGC AAGCCCGGCC GCAGCATTCC CAGCAACATC AGTATCAGCA TCAACAGCAT	360
25	CAACAGCAGC CTCAACATGT CATTTCTGCA CAGCGTTGC TGCAGCAGCA ATTGCAACTA	420
	CAATTTCCCT ATCAGCATCA ACCTGCCATG CCGCAGGCT ACGGTTACAC ATTGGACTCG	480
30	TTGAGGGCA CCGGTTGAA ACATGTTCCA ATGCAGGGTT TTCTTTCCGG TAATATCGGC	540
	TTCCAACCTT CTACGGCAAT TGATAGCTCT CCAGCAACGA CCTTGCTTCC CAACCTTTCT	600
35	TGTTGGACT ACTCTGGGT TCCACCTTCC ACGTCAGGT TCACTTTTCA CCCAGAACT	660
	CTTTAGGCAC AGCTTTCACA ACATGCCCTA GATTCTCAAC AATGGCAGCG TGTC	715

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1406RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

5
 GATCTCCTTC CAGTGACGCT GATGCACAAC TGCGGACCTC AGCCCGCGTG CCTCACGTGA 60
 10
 CCACAGTGGG CATTTTCTCA GTTAGCGCTC GTTTAGCTTA GCTATACGAG GGATGGCACC 120
 ACTTAGGGCC TGCTGCGGAA CCAGATACGA TGAAGCCGCC CAAATTGGAT AGAATGCTGC 180
 15
 CTGCTGAGC CGCCGTCATA GGGAAACGAC CAAAGGTTCC GTCTGCCGCA TCGTATGTAT 240
 GIGTCTGTGT ACGAGGACCG AAAAGTTGAC TTTTAACGAA GTAGATTTTT TTATTAGATA 300
 20
 TTTAAGCAGG TATGCGTTAA CGAGCAGCTT GCAAGGCGTA TACCAAGGCT CTGTGCGCTT 360
 ATCATTAGCA GGGCGACATG TCAGAATCCT TGCTACAGAC AGTGGTGGCG TACGTGGAGT 420
 25
 TGGTGCTGCA CCACTTCATG GGGTTGCTGT GGACGCAGCA GCTGTCCATA GTAATAGTGG 480
 CACCATTCAT ATACTCGCTG GTGTGGCAGA CGTTATATTC ATTCAGGAAG GATAGAGTAC 540
 30
 CGCTAGTGCC GTTCATGGTA CCCTGGGTGG GTTCGCGGCT CCGGTATGGG AGGGCTCCGT 600
 ACGAGTTTTT TGGCAAGTGC AGCAGAAGTA TGGGATGTG TTTGCGTTCA TGCTGCTGGG 660
 35
 CCGTGTGATG ACGGTGTATC TGGGGAACGAA GGGCCACGA 699

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 709 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1406UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

5	GATCTTCAIT AGAAGCGG GATTAGTCAA AAAGTGCCGG AATGTTCCAT CCACTAGGCC	60
	ATCTGCCTTC ACCCAAGGAT TGCAAATGCA GACAAGGTTT ATTAGAATTA TACCGATTGC	120
10	CCTGCGAGC TAGGAGCTCG GAGCTCAOGA COGAGCGATC CCGCTCGGG	180
	TGCCATGTAG TAAGACGAGC CTACGCAGAC ATTGGGGGCG AGCTCCGGCA CCGGTGTGGC	240
15	CAGCCCGAAA TCGCATACAT GTACGTGTGA CCATTGTGCC AGAAGAATGT TCTCGGCTT	300
	TAGGTGCAA TGATAGAGC CGAGTCGGTG GCAGTAGAAA ATAACCTGC ACAGCTGCAG	360
20	GAAGACCTTC TTAATCAGTA GGCCATCCTT AGCAAAGACT TGCTCGTTGA CAATGGCTGA	420
	GAAAAGGTG CACGTGATGT AATCCATAAC AATAAATGTT GOCAGGCTTG ACTCCATCAC	480
25	CTGATGTATG GTAACCACAT GTTCGTGGGT GTGCACAGTC AGGTGCATCA GCAGCTCCTT	540
	ATAATGTGGC GCGTGGGCA GCTGCTCTTG GGATAATGTC CGGATCGATT CCAGGTCCAC	600
30	AGATGGTAGA TACAGCCGGT TCTGGAAAGA TTGAAGAAGT GGTACAGCTG CGTGGCGAAA	660
	ATTGTGACG GCGCTGAGC CTGCTCTGCG CTGCCGCTGT GCTGCTTCA	709

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 707 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1407RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

EP 0 866 129 A2

5 GATCAACCAG ATAACTATCT TAAAGAACAA CCGAAAATG CGCAAAGCAC ACCACGGGTC 60
 10 CTTGGGTGAT AGACTGATAG AGATACAGAA AGTAACTTCT GTGTCAAGCG AACCGGAGCT 120
 15 CCGGTTTTTA CACCTTCGCA ACAGCTGCCC CCATGOCATA GCACTCTTTG AGTTCTCTTA 180
 20 GTTGCTTTCC ACTAAACACC GCTCCGATGT TTCACAGAAC AGGTTTAATA TCGGCAACCA 240
 25 AAGAGGAGGT TACACTCAGA GAATCACAGT GTCGAAACAC CGGCTATTCA ATGAGGCATT 300
 30 CCCCCAAGTC GGTTCCTTTG GTTTGGATTG CCATTGGCTA GTAATCCACC AAATCCTCCG 360
 35 CTGCTCACCC ATGGGATCGC TAGATGCCCA GGATGAGACT GTTCAGGTTA GGCAGGTGTT 420
 40 GTATGCGCCG CCAGAGGGAA AOCOAATGAC TTTGCATAGA ACAAACCCGC CATCACCCAT 480
 45 GTCTTGCGCT GTATAGAGAC TAAGGTATCT GACGATCCT TAGCGACTCT CTCACCGCT 540
 50 CGACGAGGCC ATTGAAGCTC TTACGAAGTG CACAAACCTA CTCGAAGTCT GTTCCAGAC 600
 55 TTCTTTCTGT TTGCTTCAA CTGCTTTCG ATGAAGTACC CCCCAGGCTA TTTTCTTAC 660
 60 CCGCCTGGTG TTGCTTATA TACCGGTTG TATTTTGTGA TAAAAA 707

(2) INFORMATION FOR SEQ ID NO:594:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 571 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1407UP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

55 GATCGTCGAA TTGGGTATA GGGCGAAAG ACTAATCGAA CCATCTAGTA GCTGGTTCCT 60

EP 0 866 129 A2

5 GCGAAGTTT CCTCAGGAT AGCAGAAGCT CGTATCAGTT TTATGAGGTA AAGCGAATGA 120
 TTAGAGGTAC CCGGGTIGAA ATGACCTTGA CCTATTCTCA AACTTTAAAT ATGTAAGAAG 180
 TCCTTGTTGC TTAATTGAAC GTGGACATAT GAATGAAGAG CTTTITAGTGG GCCATTTTTG 240
 10 GTAAGCAGAA CTGGCGATGC GGGATGAACC GAACTGGAG TTAAGGTGCC AGAATACACG 300
 CTCATCAGAC ACCACAAAAG GTGTTAGTTC ATCTAGACAG CCGGACGGTG GYCATGGAAG 360
 15 TCGAATCCG CTAAGGAGTG TGTAACAACT CACCGGCCGA ATGAACTACC CCTGAAAATG 420
 GATGGCGCTC AAGCGTGTTA CCTATACTCC ACCGTCAGGG CAAATATGAC GCCCTGACGA 480
 20 GTAGGCAGGC GTGGAGGTCA GTGACAAGCC TTAGGCTGTA AAGCTGGGTC GAACGGCCTC 540
 TAGTGCAGAT CTTGGTGGTA GTAGCAAATA T 571

25 (2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 658 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1408RP

40

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

GATCCCGCTT ACCAAGCAAT TACAGGAGAC AGAAAAGAAG GATAATAATT TACCACAGAA 60
 CTCCAAGCCT GACAGAGCAG CGATTACAT TCTGAGTCAC ATGACAGCAG ACTCTCTTTG 120
 50 CTTTGGAGCT TCAATAAGCA CCAATATGAA TATGAATAGT TTTAGATGCT TTGTATAATT 180
 ACCACTATTA ACITTATCTT GATTAAATATT TATTATTTTG TTATTTTATT ATTTTATTAT 240
 55

EP 0 866 129 A2

TTTATTATTT TATTATTTTA TTATTTTATT ATTATTTAT TTTATTATTT ATTTTATTAT 300
5 TTATTTTATT ATTTATTTTA TTATTTTATT TATTATTTAT TTATTTATTA TTTATTTATT 360
TGTTTGTTTG TTTATTATTT TTTATTTAT TACCTTTTTA TTTATGTTA TTTTATTTTA 420
10 TTTTATTTT ACTTAGTATA TAATATTATA TTATATCATA GTATAGTTAT ATTATGGTGA 480
CTTTATTCAT TATATAGATT GTATTTTGIG AACATAATAT ATATGCTATT TCTATTTCTA 540
15 TTTTATTTTA TTTTATTTTA TTTATTTTA TTTTATTTTA TTTTATTTTA TTTTATTTTA 600
TTTATTTTA TTTTATTTTA TTTATTTTA TTTTATTTTA TTTTATTTTA TTTTACT 658

20 (2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 722 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: PAG1408UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

40 GATCCGCCCTT CCATCGAAGA GGGTACTGTT TGATTATGGT GATTTCCTGG TGTGGGTTGG 60
ACATTCAAGT GCATAGTTGG AGGTTACCGA TAACTTAGAT TTCTTTATAA ACGGTTACCC 120
45 TACGTCCTCG CGGTGGGGG ATATACTGAT TAACAGTTGG AGAGCCTTGG CGGATACTG 180
TGAATGCCCTT CTCCTCAACA TTATTTGAAT ATGCCAAAGT TATTAAATT AAGTAACACA 240
50 CTGTGCTTA TATATTCAAT TGTTCGAAGC GGGCATCCA ACATGGGAT TCTCATCTAG 300
TTTGAGAACT TCGTCTATT CTATTCCTGT GTACGGCAAC GGTATTAGGA GAGACTTGA 360
55

EP 0 866 129 A2

GTTTTGGAA CTTCAAAGTC AATACTTCAT CATCGTAAGT AGCAGTTACT TGGCCTAAAC 420
 CAGTCCCCAC CTTTGTAGGG AGCCTGATTG TTGCGCGAAA CTCGGGTTT GTGGGTTCCTC 480
 CAGTAGTCCA CGGGTCTGTA TTCTCATCCG TATTAATGGC TGSCACGACA ATAGAAAGAA 540
 CTGCATCAIT CATGTCTCGA TGCAGGGCAA TATCTATGTG GTCTTGAGAC ATTACGCCAG 600
 GAACTCTGAT GTGGATCTCA TAGGCGTCCG AACGCTCCAA AATTAATAAT GAAGGAAGAA 660
 CGTCAGAATT TCGCGCGAG AGCTTGATT CTGAAGTAGC TGCCACACTC TCAGCTTTGT 720
 GT 722

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1409RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

GATCCTGGCT ATCTACCTGC TGCTGGGCGC GCTGCAAGCC ATACTAGGGG GCACATTCAG 60
 CGGATTAATG TATGTGAAT ATGCGCGAGT AGAAAACGCA CGTKCATGTG ACAACAAGGC 120
 CACCGGACTA ACCAATTAC AGAACCGCG CTATTTACAG GGCTGCCCTG ATCGGATGA 180
 GTACTTGAT TCGCTTGA TCGCAGTGG TACAGGCCCT GTACCTGCTA TGCGCAGCAT 240
 TTGTGGCACA ATCCAAGCTG ATATAGGATA CAGACATCCA GCAAGACGCT GGATGGATCG 300
 GTGTATCCC TCTGCTGCAT CAATACGCTA TCGCGGCGCG GCAGCTTATT GTCAAGTGAT 360

TCGCTATCTT GTGGAGCACC CAGACATATG TTGCTGAGCC TCCCTCAGCT ATATAAGCGT 420

5 CGAAGAAGGG CGCGAGTGA ATACATGTCT CTGGGCGTGT GTGCCTCGTG CAGTCCCTCG 480

CGATGTCTGC AACTCTCATA AACCGTTCCT TGGCAACTAT CGTACAGAG CTTGCCCTTTT 540

10 TGGTGTATTC CGGGGTCAAT ACGGGGCAGC AGTCAGAGCA GATTGAATCT AATCTTCCAA 600

ACCTTAACGA AGCCCTCCGT GCGGCTCCCG CAAATAACGC AGGGCCTGTG GAGTATGTGG 660

15 AGGCACITTTA TCGGTTTCAG GCGCAACAGC CTGGTTGACC TAGACTTCAA 710

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1409UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

GATCGGGGAC CAGAAAACCA CACAACTGGT CCTTGAGGCG GCGGTGGGCG TATACGCTGC 60

40 TACTGTCTCT TCTTGTGTA GCTGTGGCCT ACGGCTCTGC GTGCGTAACC GCTGGCATGT 120

GGTCATCAC CAGAAAATAT GATGTCTCAA CCGAAGTTGC AATATGTGCC TGTTCCCTGG 180

45 TGGTCTCGGG CTACGGTGTG GGACAGCTGG TTTGGGCGCC TCTGTGAGAC CTGTACGGCC 240

GGCGGATAAC GTACTTCACA TCTCTATTCC TTTACGTGGT ATTTAATATT CCATGTGCGG 300

50 TGGCTCCCAA CATCCAGAGC CTTTGTGGTT GCAGGTTTAT TTGGGGGTC CTGTCTGTGT 360

CTGGACTATG CCTAGTCCGC GGCTCTCTCG CCGATATGTT TCCAGCCGAC CTGCGTGGGT 420

55

TGACCATCGC GTTCTTTGCA TTGCAACCAT ATGGAGGTCC GGTATTTGCG CCACTTATAA 480
 ACGGATTCAT CGCTGTCCGC ACAGAGAGGC TTGACCTTAT CTTTGTGGTC AACATGGCGT 540
 TAGCOGGAGC TGTTTGGCTG TTAGTOGCAC TGGTGCCCGA AACATATGCG CCAATTATTT 600
 TGAAACGGCG CGCAGAGAAG CTGAGGAAAC TAACAGGCAA CCAGAATATA ATGACAGAAC 660
 AGGAAGCACA GGGACTCTCC CTGTCCGCAT GGTGCAGACT TGTCTACTGA GACCG 715

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1410RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

GATCAATTGG TCACATTTGG CGTATGCAAT TTCTACCATC TCCTCTTTGG TAGCCTTTAA 60
 TTCCACTCCT GGIGTAACAT CACTAATGCC AATAGAAAAG CCTCTATTTC CCAGATAGCG 120
 CGCACAAAGC TTTGCCATCC TATTCATAGC CTGCGTTGCT TCTGTGGGCC CGAAATCTCT 180
 CAGAATAGTA TAGAATACGG AATGTTTCTT ACCATCACCA AGCACAGACT TATCATGAC 240
 ACCAGACAGA ATATTAGAGC CTCTGATAAC TACATAACCA TCATTAGCAG ACATCTCATT 300
 TGGATAGGCC TTATTCCTAG GCGCAATATA AACCTTATTC TTGCAATCA AATTAAATAAT 360
 AACGGGAGAT TTCTGTGTCG GTTTTATCAA TAGAGAGAAG AGCTGTTTTC CAGTCCATAA 420
 GTAGTGTGGT CGCATAATTG CAGGCGGCGG TATGTCAAAC TGCAGGTTGC CGTCAGACAT 480

CATAGAAAGC ATTGGAACAA AAGTTGCGCG GTGGAAGAAG GAGTCTTTGT GAGAAATCAA 540
 5 ATATGATCCA GTGATGAAAT CCTGGGTAGC TGCAATGATC GGTTCACCGG ATTTCGGAGT 600
 CAATAAATTG TTTTGTACAC CCATAAGGTT GATTGCTTCC GGGCGAGCCT CTTCGGTTTG 660
 10 AGGAACATGC AAGTTCATTT CGTCACCATC AAAATCGGCG TTGTAGGGG 709

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1410UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

35 GATCTGAGCC CTAGCATCTT CGGTTGGAAG CGGGAAGTCT ATTTTCTCTAT CCAAACGACC 60
 GGAAACGAGA AGCGCTGGAT CAAGGACATC GACTCTATTC GTAGCAGCCA AGACTTTTAC 120
 40 CCTATCGTCA GAACCAAGC CATCTAGTTG GTTTAGCAAC TCAAGCATGG TTCTCTGCAC 180
 CTCTCTATCA CCGGACTTCT CCGAGTCAAA ACGCTTAGTT CCAATAGCAT CCAACTCATC 240
 45 GATGAAGATA ATGGTAGGTG CCTTTTCTCT CGCCAAGGCA AAGGCGTCCG GGACCAGCTT 300
 CGCACTTCA CCTATGAACA TCTGGACCAA CTGCGGAGCG GCCAGCTTCA AAAAAGTCGC 360
 50 ATTGGTCTGA GCGGCACAGG CTCTTGCCAG AAGCGTCTTG CCGGTACCCG GTGGACCATA 420
 CATCAGAGCA CCTTTCGGTG CCCTAATACC CATATCCTTG AACTTGTCTG CCTGCTTCAT 480
 55 GGGTAACAAG ATTGCTTCTG CTAGTTCTCT GATCTGCTTG TCTAGCCAC CAAAGTCGGA 540

GTATGTTTCC GTAGGCTTGT CATCCACTTC CATAGCTTTC ACTCTAGAGT CAAACTCOGA 600
 5 AGGAAGCGTA TCCAAGATCA GGTACGAGTC CTTGTTTACA CCCACCAGGT OGTTCGGCTT 660
 CAACTGCTTA AGGGTCCACT AGCCCAACCA TGGGAGAAA AACGGTTTGT CGGACGAAG 720
 10 TTTCACA 727

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1411RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

GATCAAATGC CCTTCCCTTT CAACAATTTC ACGTACTTTT TCACTCTCTT TTCAAAGTTC 60
 35 TTTTCATCTT TCCATCACTG TACTTGTTCG CTATOGGTCT CTGGCCAATA TTTAGCTTTA 120
 GATGGAATTT ACCACCCACT TAGAAGTCCA TTCCCAAACA ACTOGACTCG TCGAAGAAG 180
 40 CTTAGATGGC ACTAGCACCC CCGCCAGACG GGATTCTCAC CCTCTATGAC GTCTGTTC 240
 AAGGAACATA GACAGGGACT AGCAACCAAG GTACTTTCTT CAAATTACAA CTGGACGCC 300
 45 GAAGGCGCCA GATTTCAAAT TTGAGCTTTT GCGCTTCAC TCGCGTTAC TAAGGCAATC 360
 CCGGTGGTT TCTTTTCCTC CGCTTATGA TATGCTTAAG TTCAGCGGT AATCCTACCT 420
 50 GATTGAGGT CAACTTTGG GAATACTATT CGCTGGAAG GCGTTGTTG TGTACGTC 480
 TTCAAGGCGC AGCTCCACTC CACGATCTGG TCGAAACCTA ATAGCAGTG TAGAACTAG 540
 55

CTCAGACCGC AGTCCGGCGA AGTTCGGCCC ATGGCCAGCA TTTTCAAGTT AACCTTGICT 600
 5 TACGACCGAG TATCACTCAT TACCAACCC GAGGGTTTGA GAAGGAAATG ACGCTCAAAC 660
 AGGCATGCCC CTGGAATACC AGAGGACGCA ATGTGCGTTC AAAGATTGGA TGATTACGGA 720

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1411UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GATCGTCAGA TACCTTAGTC TCTATACAGC GCAAGACATG GGATGAGGCG GGTTTGTTCT 60
 35 ATGCAAAGTC ATTGGGTTTC CCTCTGGCGG CGCATACAAC AACTGGCTAA OCTGAACAGT 120
 CTCATCCTGG GCATCTAGCG ATCCCATGGG TGAGCAGCGG AGGATTTCGT GGATTACTAG 180
 40 CCAATGGCAA TCCAAACCAA AGAAACCGAC TTGGGGGAAT GCTCATTTGA ATAGCCCGTG 240
 TTTGACACT GTGATTCTCT GAGTGTAAAC TCCTCTTTGG TTGCCGATAT TAAACCTGTT 300
 45 CTGTGAAACA TCGGAGCGGT GTTAGTGA AAGCAACTAG AGGAACTCAA AGAGTGCTAT 360
 GGCATGGGGG CAGCTGTTGC GAAGGTGTAA AAACCCGAGC TCCGGTTGCG TTGACACAGA 420
 50 AGTTACTTTC TGTATCTCTA TCAGTCTATC ACCGAAGGAC CGTGGTGTGC TTGCGCATT 480
 TTGGGTTGT TCTTTAAGAT AGTTATCTGG TTGATCCTGC CAGTAGTCAT ATGCTTGICT 540
 55 CAAAGATTAA GCCATGCATG TCTAAGTATA AGCAATTAT ACAGTGAAC TCCGAATGGC 600

TCATTAAATC AGTTATCGTT TATTTGATAG TTCTTTTACT ACATGGATAT CTGTGGTAAT 660

5 TCTAGAGCTA ATACATGCTT AAAATCTCAC CTTTGGGAAG AGATGTATTA TAGAATA 717

(2) INFORMATION FOR SEQ ID NO:603:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 710 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1412RP

25 (vii) SEQUENCE DESCRIPTION: SEQ ID NO:603:

30 GATCTGGAAC CAGGATGACT GTCTGGCAGT TAACTCGGCG GACCAGATTC GCTTCTTACA 60
 CAACTTCTGC TCCGGTGGCC ACGGTATTTT CATCGGGTCT GTTGGCCACA AGAAGGGCGA 120
 CTCAGTCACC AACTTCTCTG CACAGGACAA CCAGGTCTGC GAGTGGGACA ACGGTCTAAG 180
 35 AATCAAGACT TTCTGTGGGG CCATTGGCAA GGTGACAAAC ATCAAGTTCA TCAACAACAA 240
 GGTCAAGAAC ATCCGCAAGT TCGCTATCGT CATCCAGGCG GACTACAAGG ACGGCACCAC 300
 40 CACCGGCACC CCAACGGGCG GCTGCCCAAT CACCAACCTA GAGGTCAGAG GCAACACCGG 360
 TAACACCGTC GGCAAGGGCA GCAAGCTCAA GATTCTCGTC AAGAATGCGT CTAAGTGGAC 420
 45 CTTCGCGGAC AACAACATTT TGGGCAAGAC CTTCOCAGGC TGCTCTGGCG CACCTAACGG 480
 CATCAAGTGC TAAGGCGCTT TTTTTTTTTT GGCTGGCGCT CGAAACTATT ACTATGAACA 540
 50 TTGGCGTCCA CCGCCACTAC AAAAGCATCG GGTCTATCCC ATTATAACAT TAAATCTCA 600
 GTTGATATTA TATTTTACAT TCGAATGTCC TTAGGGCTTT TTTATATTAT ATAAACTTTA 660
 55

GATTAAAAAA ACGAGGTACA AGCAGATCAA CGAAGCTTTT CGGCCAGCCA

710

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1412UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GATCGAACGA GATAAACAGA GGTATTTGGTT GTTATCACAA ACATATAATC CTGGGGATAC	60
AACGCTGTCA AACTCTGGGC CTCTCTCTTT GTGTCTAGAT TCCTTTTCCA GGCTTGAGAA	120
TAACTGTAC AATTTTTTGA TGTGGTTAGT AAGAGACCA TCAACGATAT CATGCCACAA	180
AGTTGGTTT CTCTCCCTG CAAGCGGGA TGGCCTTCA TTACTTCCG AATCTTCTCC	240
ATGAGTCGAT GGTCTGGCG TTGAAGCTTG TAGTGTCAA GGTCTATTG TTGGAGAAGG	300
TTCTATCTCT ATTTTTTGTG CCCAGAAAGA ATCATTGAC ATCCAATATC TTGTAACTTC	360
CCTGGGATGT AATCTTTGAA TAGCGGGTT TCGGTACAAG CTGCTAAGT CCAGATTATT	420
ATTTAACGAT TCTTCTGGT CGTGAAGGT ACGTATAAG TGGACGCTAT TGGGTTTCTT	480
TTCCAACATA GGTGTTCAT CAAATGAGAG GTAAAATGGT TCCTGCTGGG AACGGACGA	540
AGGCTCCTTT ACTTTAAGT TTAACAAGG GTCAACATAT TCTTTTGA TGGTTCTAGA	600
AGTGGTTACA AAATCCATAT TGGGCTTAG ATCTGACTCC TGAACGCTT TGTCTAGTTT	660
CTCATCCCC AGTGGTAAAT CTGAACGAGG GACAAAGTAC ATGCAACTGT CCTCATCATT	720

GTAAGTCA

728

5

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 732 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: PAG1413RP

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

GATCTGCTGG GAGTGACTCA GGAAGCTTTG TCAGTACCTG GAATGAAAAA ACAGTCTCTG 60

30

ACAGAGCGGG GAAGCTGGGC CTGATGGTGG TTACAGCGGA CCAGTTCAAA GAATATGAAC 120

AATTGAAGAC TGTACGCCCC AAGGATCAAC TTGCTCAGCA GGCGAAGGAG CTAGATATGG 180

35

TGCTAATTGA TGCTGCTGAA CTATACGAAT TAAGAAGCAA AGTTTCCGAT GGACTGTCTG 240

GCGATTTGAA CTCTGACTTT GTCTTGAGCA AGGAGATCAT TCTTGAGAAT GCTCATAGTT 300

40

ATGGTTTAAC GGTTCCTTCAA ACGGAAGAGT ATCTTCAATT ACAGAGTAGT TTGGAGAGAG 360

AACAGGTAAC GTCTACAAAC ATTGCCGAGA AAGCAACTAC AATTGGCTAC GTTGCACTTC 420

45

CAAGAACCGA GTACGATGAA CTTGTAGCTT CGCAAGCTTC TACGAAAGAA CAGAAATTTG 480

AGGTATACGC GCGGAAAAT GGCAAGGTCA TAGTGATAA ATCTGAGTAT CACGATTTGA 540

50

AGATCAAAGC TATCCAGTG ATTTCACCAT TGCTCAAAT GAGCAAGAG CAGATGGTTG 600

AAAAGGCCAA GGAAGTTGGA ATGGTAGCTT TGCTCAATTG CGAGTATGAG AAGTTAAAGA 660

55

GCCCTATTTT CGATAACGCT TTGAATGCAA CAGCGAAGGG ACCGTGGAAA GGTGTGTTCTC 720

CTAAAGGAGA GT

732

5 (2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 721 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: PAG1413UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GATCCAGTTT TAGGTCCACT TCAAACCTGGA TTTTCGGGTA CTCCCCGCAC ACCACCGTCA	60
AGTCATCGGC ATAGATGGAC TCAAGCACTT CCAGCTCTTG CTTTGTCTCC TCCTGATAGT	120
CCATACCTAT CCGCTCGACC AACTATGAGC CCACCGGCAG CTTAGGGCTA GACCGTTACA	180
GCTGCAGGTG ACCGTCCGGG GGACGATGGC CTATCGCTGG CGAAATTTT CCGCTATACC	240
ACCACTTATG TTACCCGGTC TATAGTGCTG CTCTCGACC TCACTGATGG TGCTGTCCCG	300
CGGGGACTGC TGCCCTGTGC GGCCAAATCC CCACCGCTCT GAACGCTCGT TCCATCTGGC	360
TCACGGGFTG ACCGAACGGG AATTGCGCGC GCGAGAAAT CTTGGCGAAC CATGCTGCAC	420
GTAGCCTTAC TGCCAAAATT AAGCCGTCAA ATGGCTGGCT ATCCTTCCAC GCACGCCCAT	480
AGTCACCTGA AGCTGGCTGG AACAGTGGTC ACCAGCTTT CTGACGCATA CCAGGAACAG	540
GTGGCCGAGC CCGAGGCCAA CCGTGGGTGA TTATGTCAGC GACTTTTGGT GGATTACGTA	600
AATCTGGGTG CATGCTGGC ACGACAGGC GCATGCGACC CCAAGACAAA CGTGCCACAC	660
CCATTCAATA TTAGAGGACT TTGCTGCACA CCCTAATCAT CCGTTGGGTT GTGAGATACG	720

C

721

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1414RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GATCCGTAAT CGAGTTTAGC TTCCGTGTG CATCATCGAC AGGTGAAAT GCTCGCTTGT	60
CGCCGCTCTG AAAACGAGTC AGATGTGCAG AGAGGCTGAA GTCCAACATT TTAACCACCG	120
CTGAAGACCG GGAATAGTAG GGCAACGTAG TTCCGCGAAC TTCAGTTTGT TTTTCTTTTA	180
ATTTAATGGA CTACACCAA AAAAGCTCAA CAACAGTCCC AATTAGTTCT GCTAGAAGAT	240
GCAACACGT TAGTGATCAG TAAGTATGTG TACTCGTGTA CTGTCCTGC ACTGCAAAGT	300
TCGCGTCACA ACTAGCTGTG AACCATGGTT TGAAAAAAAA TAATGATAAT GATTCCGCC	360
AGGATCGAAC TGGGGACGTT CTGCGTGTTA AGCAGATGCC ATAACCGACT AGACCACCGA	420
ACCACTATA AGCCCTTAAT TATACTCAGA TACTAGTGAC CATTTTCTAG TCACATGATG	480
CTAGTTTCCT GAATAAAGA TGCACGTGAT TACCAAATCT GTATTTACTA GGTAAAATGC	540
CTTGGTGAAT AAGTACGTAG ATATTATATA TGTATACATA TGCATTTTAG ATGCAATAAA	600
AGCTCTATTA TGTATGCGCG CGGAGCTTTA AGCCAGTGTG TTTTCCGATT GTTTTGTGGA	660
TGCAATGGTC TTTGCATAAA AGCCTGACTT TCATCTTTTT CGTCTTGA TGTAACTTC	720

CAACTCTGA

729

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 639 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1414UP

(x) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GATCTGGCCC	CGCGGGGGCA	CCGCGGCCAG	GGGCCAAAAA	GGAGAGCGCC	CGCGGTGGCG	60
GCCGCCACTG	CGCGGTTTC	ACAAGACATA	TATGTGGTA	TATAAGACCG	CGGTTGCGC	120
GTGGCTGCGG	TGCAGAACCC	GCGTGGCGG	CGCGGCAGA	GATTTCTAAT	ACTCTGGTT	180
TTCTTTTTC	AGCGCTGGT	ATATAAGTTC	GGCTGTGTC	GCGGGCGTC	GGCGCGTTC	240
GCCAGGGAGA	TAGGGGAGCA	TTCCGCAGCA	GCGTCTGTA	GCGGACCAG	TACGACAGG	300
ACGCAGGACA	CAAAGCAGG	GACGGCGAGT	GCGCGGATC	AGCAGCGCAC	AGCGAGCCAG	360
GGGTATAAGA	GCGCGGTAC	GAGGCGGCTG	GTAGGTATAG	GCCAGATGG	AGGTGGGTGC	420
TAACGGGATT	TTTCTGCACC	AGAACGACTC	TGCGGAGACG	ATCAAGCTGG	AGATGTGCGC	480
TGTCGGCGGT	TGCGGGAGCG	CAGGCAGCGG	CATCGCGATG	GGCAGCGCGG	ACGACGAGCT	540
GACGAAGTGC	ATCAGCGACC	TGAACATCTT	CGATCTGCTG	CACAACAACC	CGCGTGGAG	600
TTGCGACGAC	AACAAGGAGG	GTGGCGCGCG	GCGGCTGC			639

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1415RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GATCGTGGTT CTGTTATCGA AACGTTGGTT GCTAGAACAT TCGGCCAGGT TGAAAGTAGC	60
CAGAGCATGA TACGAATTCT GGGATTATCG GCTACATTAC CTAAGTTCTT CGACGTGCGA	120
GACTTTTTTG GGGTTAACAG ACATGTGGGA ATGTTTTATT TTGATCAATC GTTCGGTCCA	180
AAACCCCTTAG AACAGCAGCT GCTTGGTTGC AGAGGCAAGG CGGGCAGCAA ACAAGGAAGG	240
GAAAATATTG ATAAGGTTTC ATATGAAAAG CTTTATGAAC ATGTCTTAAA TGGCTCCGAG	300
GTCATGGTTT TTGTGCACTC AAGGAAGGAT ACTGTGCGCA CTGCGGGAA TTACATTTCT	360
TTTGCCCAAG CCAACCAACA GTCGATGTT TTCTAAGTA GCGATCAAAG CGTTACCAAG	420
TTTCCCGAG ACATCTCCAA ACATAAGGAT AGAGATATGA AGGAGCTCTT CCAACATGGG	480
TTTGGTATAC ATCATGCTGG TATGTCTCGA TCTGATAGAA ATCTAACAGA AAAGATGTTT	540
AAAGAGGGAG CTATTAATGT GCTTATCTGT ACAGCGACGC TGGCCTGGGG TGTGAACCTA	600
CCGGCTGATG TTGTCTTGAT AAAGGGAAGT CAGATATMTG ACTCTAAAAA AGGTGGTTTT	660
ATAGATTTGG GGATCTGAT GTGATACA	688

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 703 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1415UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

20	GATCATCAGG AGTTGCTCAC CTTGGAAC ACCAATTCCT TCTGAGCCTT	60
	TGGAAATTTG TCACACCAA CTCTGAAAC GTCTTGTAA CTTTCATTAT GCGGAATGC	120
25	TACAAGTGTC AACTTATCAG GGTGATTG GTCTTAAAA TGTACCTTAT CCAGAACAGG	180
	AAGCATGAG GCTTCACGTA TAACTTATC TTTCGGCGCT CCTTGAATGT TATGCACGG	240
30	GCACACTGAG CACAACGCAG CATAGCCCAT CCGACTAGC TTCTCCAACG TCAGCATCTC	300
	GCCACTATAC TCATAGGGAA AGCCATCATC CCCGAATAAT TCGGGGTCTA AGCGTTGTAG	360
35	CGTAATTCGA GCAAAAGCAG TCACCGGGTT GTCTCATAC CATGTTCCCT GCTTAATGCA	420
	CTGCATGGCT TTAATCATAG TCATAACTGT CCTGAGGTAC CCAGATTGCG TTGCAATATC	480
40	GATATAGGCC TGTAAGAATAC GTAGCGCCTG GTCGAGAACT GAGATCGTAT CTTGGTAATA	540
	ATCTGCAATT GCTAAGTCAG CTCTACTTAG GTAGCTTGT AAAAGCAAAA AGGCTTTGAC	600
45	ATGGGGGTCC CATATGGTA ACTCTGTTC TCTGTAAAA GTACTTTCAA CGGAATATCT	660
	AAGAGTTTCT GACATTTCAA CATTATGAT AGTCTGCCC CCC	703

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1416RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

GATCATCATT ATTTCCTGCG TTCTGTCCGA CGATTGGAAG GCGGGGGTGG GTTCTTTGAA	60
GGATTTTCAGG CGTATGAATG TTGCTCTCAC CAGAGCAAAG GCCAGTCTCT GGATCCTGGG	120
TCACCATAAA TCTTTATACA AGAACAAGCT ATGGATGCAT TTGATTTCAG ATGCGAAAGG	180
GCGTGACTGC CTCCAAATGG CATGTCCGGG CTTCTTGAT CCACGGAACA GAGCCGCCCA	240
GGATGCTCTT CATAGGTTCA AAAATCACCA TAATTATATC GAGAAOCAG ATGATTATGG	300
GCCTGAACCG GTGATGACTA AATCAAGAGG ACGCAATAGA TCATCCAGAA AACGCAAACA	360
TATGGAAGAT AATCCAGATG ATAACCTACGA TCCCGTTGCT GAATTCAGA AGGAAAATCA	420
AAGAGAAAGC AACACAGGCA CCGGTGGTTA CCGTGCGGAT ACATCTAACC ACAGATTGGC	480
ACCTGCTAGG AACGATAGCA AGAAGGCCAA GACGTGCTCC AATGCCGCCG GTATTTCCGA	540
GGCTACTTCA GAGGATGGTG ATCGAGGTCA GAAAGGACAT GGAACCTAGA AGAAGTCTTC	600
CATATTCCGG AATTMTATGC CCCAGTTGA TGACCGGACC CCTGCTGCC ATGTGTACGA	660
CCCTAAGGAA CGCAAGCCCA AGAATGCTGC ATCCGCTTAA GCGGCTGGCC TTGGGAAC	718

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

EP 0 866 129 A2

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1416UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

```
GATCTTGGCC GGCAAGACCA GGAAGTGGTT GTACGTCAAC CCGCCCCGGG TCTTGGAGTC    60
CATCAACTGC TCCACGGGAC AGCCCGTCTT TCTCGGGGTA CGTGGCCAGG TGCTCCAGTG    120
CGGTGGCTGC GTCTCTGTAA GTCATTGGGC TTTGTTGGC GTGCTATGAA GAGAAGGAGT    180
CAACACTAAA CCCAAGCTCT CAAGTTGACC CATCCATCA GTAAGTATCC CGAACAGACG    240
COGGTAAACC CAGCTGGGAT TTGGCGCATC TAGAAAACCT ATTATATCTG CAGCTCATCG    300
CTGCAAACTT TTCACGTAAA AGAAACGATG ATCCAGCGGG GGCACAAAAG CAATGGGCGT    360
GGCGCGCAG ATGCGAGCCC TACCGCGGGC CAGCACCAGG TAGGAGCTGT CAGGGGCGCTA    420
GAACGCGGC ACGCTAGACG GGCTCTGGG GGGCGCGGC AGGCGTCGA CCGGCGCGCTC    480
GCAGCAGCAG GCGTGCCAGG CGGAACAAA GACCGACCAG CCAGCGCAGC AGTCTGTAGA    540
CGGCGCGGAG CAGGCGAACG GCCAGGAATA CAGTCCAGAG CACGGCGGAG AGCAGCAGGA    600
AGTTGAACAC GCGTCCATG CCCACGCGCG CACAAACGGG AACAGCGCCA GCGCGCGCTC    660
GCAGAGCGGC TGCAGGAATG CGACGACGGA CAGGAACGGC AGGATAGGAC TA          712
```

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 715 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1417RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GATCCCCCTTG GCGTCGTGCT TGACCAGGTA GCGGCGCTGT AGCCCGAAGA AGCCGGACAT	60
CGGGTCTGAC GCGGTCTGTA GCGGACGGGC CATCATGGGC GCGCTACTGG AGATCAAGCG	120
COGGTACAGG GGCCAGTCTT TTGTGATTTC GACGCGGGC GCGTAGCGCG TGCCACGAC	180
GAACGGATGT GTGCGTAGTG AGTCCAGAAG CAGCGGTACG CTCTCTGGCG GATGCTGCAG	240
GTCGCGCTCC ATGCACACCA GGTACTCGCC CTGGGCTCG TAGAAGCCCT TGAGCACCGC	300
ACTGACAGC CCGCGCTGCT CCGTGGCGAC GATGATCCGC ACGTTGTAGC CCTGCTTGGC	360
CAGGGCTCC ACCTCTTCCA CAGACCGTC CTGGGAGTTG TGTGACAA AGATCAGCTC	420
AGTCTTCTTG GAGTCCGGT TACCGAGGC GGCAAACAGC CGGTGGCAA GGGCTTGAT	480
GTGGGGCTT TCGTGGTAGG CCGGACGAC CACAGAGTCT CGATGCTCAT GCGCTCGTA	540
TGGTCTTAA TGTAGTGAGT AGCGAACGTC GGTAGCTGTT TCGCAAATAA GTGAGGCTG	600
CGCGCTAAT GTGTTGCTT TATCGTTGCT TTTTGGTTG TGTCAAGGG TTACCCGGCC	660
ACCAGGCTAG ACAGCGAGAC CCGCGGTGAG CAGCCACGA CCAAGAAGCG CTGTA	715

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1417UP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

10

GATCTGCGTA GGTAGTAGAT GAATTGAGGG TATAGGGAAA AGTTTGGTGC CAAGCGAAG 60

GAGCGGGGGT CGCCCTTGTT GTAGTCGGCG TACTTCTGGC AAAGCTTGAT CAAAGTTCTA 120

15

TCGATCCACC GGATGACGTC AGCGCCATCA TCGGAATCTG CCTTATCGAC TGCAACACGC 180

GCCATTAGTA CAGCAGCGGC CTCCTGGTCA AAGGAAGCAG CGATTGCOGG GTTACCGAAT 240

20

GGCAACATCT GGTTAGCAAC TGTAGTCACT CTGACACGGT TGGTACCAGA TGCATGCTGG 300

TATGCAGTAA TGAATTGGGT GTATGCCAAT TTGCTCTGT CCCCCATGAG GCTGGCAGTT 360

25

GCAGCGGTAT TTGCAATCTC GAAAAAGATA GCGTAAGAGT GGTGAGGGCT CAAGGACGCC 420

ATTTTCCATG TAGAAGTGCC OCCAATACCG ATTTCTGAAT CGCTCACGTT CTGTGCATCA 480

30

ACGTTAACCG GCGAAGCATG GCCAATCAGT CCTGCGAGCT TTAGATCTGC ACTGGTTTTA 540

ATGCACATGG AAGCATTGAA CGCCATGGTT AGGTACCCCT CTCATCTTTA GAAAACAGTC 600

35

TGATGAAAGA TTGCTTGAAG ATGGCGCTCG AGAATGCGTC AGTCAACAAC AAAACACCAC 660

CAGTGGAGTC GGTCAACTTC TTCATCTCAG ACATACAACC TGGTCGTAGC ATCCA 715

40

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 728 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

55

(A) ORGANISM: PAG1418RP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

5	GATCCGCGAG ATTCATCGTG GACCCGCCAC AGGCAATTAC TATAACAACA TCCTGGGGTG	60
	TTAAAGGACC TAACTCAGC TCAAGTATTT CAGGATGATA TCCTAGATGA AGAGCTGGC	120
10	CACACGCTGG TTCGGTTACA ATATTGCTCT CTTCGCCAAA ATTTAAACAT GTCTGTACTA	180
	CAGCGAGCTG GTCAAGCACA ACAGATTTTG TCCTGTATTT TTGGGGTAA CTCAGAGTAA	240
15	GATCCGTCAC GAAAGATGTG CATAAAGAAG TAGCAACGCT TTTAGGATTC ATCGAAACGT	300
	TCCTGCCCAG CAGCAAAGAT CTGTGCAAAA CCTCGCACCC CTCTGTTTCC ACTGCTACAA	360
20	CAGGGATAGA GTCTGCCAAA CCATGTTTCT CCAGCCCAT TACAATCCCA TTATATAACC	420
	CCCCGOCACC TACGCTGCAG ACGATACCTT TCACGCTCTC CAATTGCACG OCTTGGAGAT	480
25	GCAGTGCTTC TACTACTTCA TCTACCATTG TTGCATGCC TTCCAGATG AGTGGGTTGT	540
	CGAATGGATG TGCATATATC GGAGCGACTT TTCTAAATT CACATTCCCC ATCAACTCGG	600
30	AACGTAAGTA GTCATCGCTC TCTTTCAATA CACTTCCCAT TGATATCACA TCTGCCCCCG	660
	TTGACCGTAT CGCTCTACC ATCCGCGCTC GAGTAGTTTC AGGCACTACC ACTGTGCAAG	720
35	GTATCCTA	728

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1418UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

5 GATCATCTGC GTGCGATACT GGCAAAAAT GAGAGACAGC ATGATGAAAA TATAGTTAAT 60
 10 AAGATATTGC ATGATATAAG CACAGGCGGG TTTCGTCGAA GAGGAAAGGG TGCACTTGAT 120
 CTGGAATGA GTGAAAATGA AGACCAAGAG TTACAACAGT TTAGACAGAA AAGACGAGAA 180
 15 CTTTGTAAAC AAAAGATATT GGAAAATGGT GATACTAGCA AGCTCGTATC TAACCCCAAG 240
 TCATACGCTT TTTTTCAGAC GATGGTGGAC GATGTTACTG AAGCATCATT TGGAAATACA 300
 20 TTTGATGCCA ATATAGATGA AAAACAGAT CCATCTGCTG CAGGTGGGAA AATTGTCATA 360
 TCAGAACAAT TTGTAAAGGA AACCCTGTCA TTCTGTGCGA GCAAGAGTGG CGACTCAGAA 420
 25 ATCCCTGCAG AACTAAATC TATTTTCATCC AGCACAGTTG AACGTGAAGA AATTCAAGAC 480
 CTTCATACA TTGAAGCAAA ATAGTAACAT TAAACATTTG AAAGGAATCT AGAACTTCCT 540
 30 GCTCAGATGG CTGAACTCAG CAGTGGAGAT GAAGGTGATT ACGGCTTTTC TTTAGATAGA 600
 TCGCTCTGC GGCAAAAAGT TTAATAATGG AACTAACGTC GACGATAAGT TTAAAAGTGG 660
 35 CACCAAGGCA GTGCGAATCT TAAAGGCAAT AAGACAATTG GCGGTCAAAA GCC 713

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1419RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

5	GATCTGGGGA GTCTCATOGA AACGTATTGG ATGAGGCTTG GTGGTGGCAG GCGGCTCCTC	60
	GCTCGATTGG CGAGCTGGTG ATGACTTCGC ACTTCTCCGG GCCGGAAAAT TCGTGTGAGA	120
10	CAGTCGGGGT TGGCGTTGAA GCTGCCGCTG TTGCTGCACA CGTGGTGGCG CCCTTAGCTG	180
	AATACGTAAC GCTGGCGCGG TGTCOCGCGC ATCCAGGTAT TCTTCGAGGC TTCTTCTTTC	240
15	GGGATGTCT GAGATATCTG GAGCACCGCG AGCATTCTGA TACAGTGGC CCGAAGATGT	300
	TTGCTTCGCG GTGAAGTCTC CCTCAAACCC GTAGAAGTCA TCGGGTATT CTCCATCCGG	360
20	CATTGTCAAT GTAGTAGTGG TCTCCACATA GGTACGCCA TTGATGTGCT TCACCGTCTG	420
	GCGAGTCAAG GTCGGTGTAC GGCCTGGAG GTCTTCGTT TCCGTGCTCT TCACCGTTAT	480
25	CGTATTGOCA GCTGCGACAG CAGGAGGGCC AAAGCCGTTG TTGCTCGGTA GCGAATGCG	540
	GCGTCGTTGC GAGTCATAC TGTAAGTCCG CGGAGGCGCA CCGAGGTAGC TGGGCGAGC	600
30	AGCTCCTAGC GACCGCGTCC GCGGTACCC AGTCAGTGAC TGAGTCCGCC CCATCCCAAC	660
	CCCTGGTCTT CGGAGTGACG CAACCGAGCG CGCGCAGAC GACAAGCCGC TGCTGTGTA	720
35	ATA	723

(2) INFORMATION FOR SEQ ID NO:618:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 721 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1419UP

55

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

5	GATCGGTCCG CGCCTGGTA CCCATAGGGG CGAGGTGGC GCGGGCCCGC CAGGTCACTG	60
	CGCCCAAACC GCACCTGCAC CTGAACCGAG CCTGCAGCCC ACGAAGGAAC GCCACGCTAC	120
10	ATGTGCCCGT GCAGAGCACC GCGCTGTCT TCGGGGCTG AAGTGA CTGT GGCACGCTCC	180
	GCAGGACATA TCTTTTAAAT GAGCTGTGTC ATGCGCACAT TCTCACCGTC GCGCTACCGT	240
15	AGCGTGGCCC TCTGTCAACG TGTGAGCTGC TGCCAAAACA AACAAATCGG GACGGGCCCCG	300
	CATGCAGTAA TTACCTCCTC CGAAGGCAA CGCCTGGTT TGTTTTACGT TGGCCAGAGA	360
20	TTTTCTCTTT GGGGTGGATT AGCTCAGCG TCATCCCGT GGCAGAGGTG CCTGCOOCTGA	420
	CAGTCTTCG AATATTAGAT GCTGGTATGC GGGCAGCCT AGCGCAACCG ATTGTAGTTT	480
25	ATTGTTTCGT CACACCCGCG TAGAGGGCCG AGCTACAGGA TCGCCGATGT GGCGTGACCG	540
	ACAGCGTCAA CGTTACGATC TCAACGGTCG CTCGTGGGG CCGTCTGTG GTAGGCGTTG	600
30	AGATACGCTT AGGATGAAAG CACGAAAATT AAGTTGTG TAAAAACACA AAGTCAACTG	660
	GGGTTCGGA ATGGGTTAGA GTGCCATGTT AATGGCGGAC GGAGAGTGT CATGGTGCGA	720
35	G	721

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 721 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1420RP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

5	GATCAATTCA AGGTTGCTTT CCCAGACATC TACGCTGTTT TCCAAAAGAT CGCTCAGCAG	60
	CACCCCGACT ACGAAGTGAC TGTCACGGGT CACTCACTGG GTGGCGGTTA TGCTTACTTG	120
10	ATGGGCTTGG AGCTCCAGCT ACTTGGCCAC AAGCCACATG TGATCACTA CGCCGGCCTG	180
	CGTATGGGTA ACGCTGACCT CAACAAATGG TACGACAAGG TGTTCGACAA CGTCAAGAAG	240
15	GTGAGGACT TGAAAAACGG CGGAAACCCA AGAAACGCTT ACATCCGTGT GGTTCAGAGC	300
	CGTGACATTG TTCCTATGGT TCCAACGGC CCTATCTACA CGCACGGGGT TATCTATTTT	360
20	ACCATCACTG ACGTGGACAG CGAAGTACCT CTACAATCGG GCGTCAGACT TGATGGCTGT	420
	AACACCAAGC TAAAGGAGTT GGTCGGGAC ATCTCTTTCA GCGGGAAGTT GCTAAGCTTG	480
25	GTGGGTCTCC TGAACCACAA CAAATTTTTC AGAAGAATGG CTTTGGCATG CACTGATAAT	540
	TCCTTGAAGC TATAATTCCG AGGAAGTAAT GAATTTTAAG TACGGAACGT GCAGTCGCTG	600
30	CAGTCTTCTG CCTCTTCCTT ATGCCCTATA TAGTTAATTT GATGTTCTGT TCTATTTTTT	660
	TACATTTTCC AAACACTGGG AATGCCACCT TGTAGATGTT GTTCCCAAGA TGGATATTTA	720
35	G	721

(2) INFORMATION FOR SEQ ID NO:620:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 626 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
50	(ii) MOLECULE TYPE: DNA (genomic)
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1420UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

5	GATCOGTGCG GAGGCGGCGA CCAAGCGCAA GTGCATGGTG GTTGTGGCCG GCGTGGAGGT	60
	CTTOGAGATT GACATGAAGA AGCTGGOGAA GACCTTCGCG TCCAAGTTCG CGACGGGTTG	120
10	CTCTGTGTCC AAGAAGCTCG AGAAGAAAGA GGAGGTCTGT GTTCAAGGCG ACATCGCGGA	180
	CGAGGTGAG GCGTACATCC ACGCGCTGCT AGAGGAGAAG GGGATGAAG GTGTCAAGGT	240
15	CGAGCAGATA GACGCTGCCA AGAAGAAGAA GAAGACGCCG ACGACGACGA CGCGCGCGCC	300
	GTCGTGAAGA GCGGGTCCG ACATGTGTAT CAGATTCGTA TGTAGTGATT AATGATTGCC	360
20	GCGATTCCA GTGTCTTACC AGTCCAAGAG GACAGGTGTC TGGCATGCTT GCACATTGCT	420
	GGCGTCTCGG TGGGGACCAT GAGCCTGGAG ATGGATCTAA TTGAATGGGC GCTTAACCTG	480
25	CGTGCTGCGG GAGGCGGGGT ATTTGGCAGT GGCAGCGAGG AATTGGACAG AGTGCTAAAA	540
	CTGCACTACC GAGTGACATA CCATGCGTTT GACCGGGCA CCAAGCGGTC GGTGTGGGAA	600
30	GTCGTCTGGC GGAGGCGGAG AAGATC	626

(2) INFORMATION FOR SEQ ID NO:621:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 582 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
40	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1421RP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

55	GATCOCTCAG TTCCCATCT TGCTTCACA GCCAGGATGG ACCATCCGTA ACTGGGAGTT	60
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5 ATGOGGTTTC ATTTGTCITT TTAGTACAGT ATTATCTCTC TGGTTTTACA TCCTACTTGT 120
 TTTATCGTTA CTTGGGTATG TATGGCATCT TAAATTTTAT CGACTCTAGT ATTTTATGA 180
 CTGTGTAAAC TAATGAAAAA TAATGAATCG AAGTCTCGTT TACCTAGAGC TGATTATGCC 240
 10 ACATGCGTAC TATOGGCGTG CCACCGCAAT TATGTATCTA TCCTACAGAT AATCCTTTCT 300
 ATTAGCAGTT CTCACGAAAC GTCTCAGTTG CCACTCGAAG TCAGCATCCT TGTTCCTCAA 360
 15 GGTGCCAGT GTCAGCTCGT AGAGCTTCAT TCGAACCGT GGTCCCACT CCGCCAATTC 420
 AACTCATCT CTCGTCTTGA CGTATACGTG CTGCGGCACA CTAATGAAAT CGCGCGGTT 480
 20 CGCAAATGTG ATGACCTAG GCGTGTCTTT CTTGACTCGG GCGGGGAACA TGTGCTTCAG 540
 TATTTTAACG ACCCGTGGC CCAATGGAGT ATTGAAATTA TC 582

25 (2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: PAG1421UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

45 GATCATCATA CCGTGTCCAA CATCGCCAC GGAACCAACA GTCACTTGAA GTGGAACGCA 60
 GGTAACATAC GCGATGGCCT CCAAGACGAC TTGGCCAGCT TCAAGGAGC AGTGTGCAC 120
 50 TGTCTCAGT TCCGAGCGG CCACTCCGC GACTACCGC ACCAGTCGTC CATGTTCCG 180
 AACGGTTCTG CTGGCAGTGC CAAGTCCGG TCGTGGTTCG GTGGCGGAC TCACTCGGC 240
 55

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	GATGGACTAC TCGAGCGGG GCGCGAGGCC GGGCGGAGG CCGGTGCGA GGCCAGCTCG	300
5	TGTTCCGCG GCGACAGCG CACCGAGGAT TCGGGCGGT CGTGGTTTG GCGCGAGCC	360
	CGCGACCCC GCGACTCG CTCGGACCG TGTGGTTTG GCGCGAGCG ACCGGAGGCC	420
10	CGCAOAGCG GCACCTGGCT CAACGGAGAG CCGGACCGCT CGTGGTTTG TCGGAGAAA	480
	CACGCCACC TCGACGAGTC CGACCGTGT TCGGAATG GCGCGGTCT CCGGTGAC	540
15	ACCACGGCT AGGCGCGAC GCGCGCGCA AGGTGACGA CATCAAGCAG GCAGGTGCG	600
	ACCTGGCGG CTCGCGCAG GCGAAGGTG ACGACTTCAA GCAGGCGCG GCTGACCTCG	660
20	GTCGCTCTG CCAGGACCG CTCGAGCGG GGTGTGCGA CGCCAAGCAG ACGCTCTCAG	720
	GCGCGGCTC CACCGTCTC GCGCGCGCG CTCGCGTGC TGGCGCTCT CCGGAGCGG	780
25	CTCGTTCGC CGCGACAAG ACCAGTCC TCTCAACTG GGGCTACAAC AAGCGGAAA	840
	AGTGAAGGC CATCGCCATC GCGAGTAGG ACAAGGCCAA CAGGACTAC CAGCAGGCCC	900
30	TCGAGCCTA CAACCGCTC AAGCGCTGC TCGCGAGCG CGACCGAC CTTGCAACG	960
	GCCTGAGAG CGCCAGGCC CAGCTGCGT ACTGTGCGA CAAGCTGAC GCATCTCCG	1020
35	CGGAGTTGA CCACTACGC CGCGAGAACA TCTCGACAT CTCCGGCGN CTGGACCAAG	1080
	AGGACCGGA TTCCGCGCT TCGCGCTCT TTAGCTGGT CCGCTTCAAG GCGCGCTGT	1140
40	CGAAATGAC CT	1152

(2) INFORMATION FOR SEQ ID NO:623:

45	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 713 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
50	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

55	(vi) ORIGINAL SOURCE:
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(A) ORGANISM: PAG1422RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

10 GATCCGTGTC CTGGGGCTGG TCGAGAACAT GAGCGGCTTT GTGTGCCCAT CGTGGGAAAA 60
 CGAGTGGACC ATCTTCAAGC CAACAACAGG TGGTGGTGGC GCCTTGTGGC AGGAGCTGGG 120
 15 GATAAAGTTC CTTGGAGCGG TCGCGATTGA TCCGCGAATT GGAAGATGCT GCGACTCTGG 180
 CGAAAGCTTT TTGGAAGGCT ATCCGGACAG TCCAGGCTCG ACGGCCATCA TGCATGTGGT 240
 20 AGAGGCTCTC CGTGACGCG TCGGCGACGT ATAAAGCGCC TAGCAGTTCC TGCCAGTGAC 300
 AGACTGATAC CAGTTTATAC ATACATACAT ATTTGTAAAA AAGACGCTTA GTGTTACGTG 360
 25 GATGCGAGCG CCGTTTCAG GTAGATAGTT TCGGCTGTC CCAGCGCAA TGCAAGTAAT 420
 CTGTCTTTAA AAGACGGGGT CTCCAACGCT TGTCGATAAT TCTCAAGGAT GATATGACAG 480
 30 ACAAGTTTGG ACATGACACA GCAAACGACG GAGAGTTCTC GGTGGGAGCC GAAATCCGTG 540
 GCCAGGACGG GCAGAACCCG GACCAGATCG GAAAGCAGCT CTGGGTGTG GTGTGTGTCA 600
 35 AGTGCTATCT GGAGGTACTT CTCAAATACC CCCAGGCGGT GAGTCCAAGT TTCCATCTGT 660
 TGTGCGGGGA AAGTCTCCAA TAATTGACGC AGTGTCTGCA AGTTAGCAGC TGA 713

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(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 642 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PAG1422UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

5	GATCTCTAG GCGCCAAGTC GACGACTACA GCGGGCTTT TTGGGCCAAA GACCGAACAG	60
	AAGCCCGCAG GCGGCTTTT CGGACAGAGT AGTGCGCTC CCAATGGCAC TGGCGGGGT	120
10	GGTCTCTCG CTAGCACGGG CAACAGCGGC AGCACCCAAT TGGTGGGCT GTTCGGCAAC	180
	AGTGCTCGG GCGGTGGTGG GAGTCTTTT GCGCGGCT CGGCGGGAA CAACAACGA	240
15	TCCACCTCGT TGGGAAATCT CTTTGGGAAA CCTAATGACA CGGCACGGC AGCTGGTGA	300
	GGTCTTTTCA GCAATCGGC GAACACAGCC ACCACAAATA CGTTTCTTC CACTAACAGT	360
20	CTTTTAGCA ATAATCAGG AAATGGTGG CAGAATAATG GGGGCTCTT TGGTGGGAA	420
	CCTACCGGG GGTCTTTGG AACACGACC GTCAGGCAC AGTGCTCGT TTTTGGAGCT	480
25	TCCTCTCAC AGAATAATCA GCAGCAGCAG CAGCAAACAC AGCAACTGTC CCTTCTGGT	540
	TCCAATCCAT ATGGCTGAA TCTGACTGGT GTTCTGTGA CTACCATGCC GGAATCTATA	600
30	ACGGCAGCAA TTACGTCTAA GAAGAAGAC AAGCTACCG CT	642

(2) INFORMATION FOR SEQ ID NO:625:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 719 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1423RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

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GATCGAACAC AAATTCATCT ACGAACACAA ACTTGGAGCG GTTCGTGTTG GTTATATTGG 60
ACAGGAACAT TGACCTACCT TCAATGTTTG CGCATTCGTG GATCTACCAA TGTTTAGTAT 120
TTGACGTATT CAATCTCTCC AGAAATACGA TTTCAGTACC GAATACTGAT GAAAAGGGAC 180
AACCACATA TAAGAAGATG GATATTGAGC CTAAAGACTT CTTTGGACG ACAAATGCGC 240
ACTTGCCGTT CCCAGACGCA GTGGAGAATG TCGAAATGC ATTGGCAGAC TATAAGGCCG 300
AGGCGGAAGC GATAACCAGG AAGACAGGCG TTGACAATAT AGGCGATTTA GATCCTAACT 360
CTCAAAATGA TACTTTGCAA ATTACAGGAGG CAGTGAACAA GTTCCCGGAA CTGACTGCTA 420
GGAAGAATAT CATTGATACA CATATGAATG TTCTGGCTGC GTTGTTGAAA GAGCTAGAAA 480
ATAAAGGGTT GGATTGTTTC TTTGAAATGG AGCAACAAAG TGACTCTGCT AAGGTGAGGC 540
AAGCATTCAT GGACGTTTTG AAAGATGGCA AGACCAATAA CCTCAAGGAC AAGTTAAGGA 600
CATACATAAT CATCTATTG ACTAGTTCGG AGAAGCTTCC CGATCAATTC GTCCAACATG 660
TTGAGAGTTA CTTCCAAGAT AATAATTTCC AAAAGCCAGC GTTGAAGTAC TCTATAAGT 719

(2) INFORMATION FOR SEQ ID NO:626:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 719 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1423UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

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GATCATCTCG TTGAACTGCA TGCTCATGTC GTCOGATGAG TACACATGAT TGAAGTCAAA 60

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CAAATGTTTG CCGACTTGA CCTTGCCGOC ACGCAAOGTC GCAAACAATC CGTCGCTGGA 120
 5 CCGAAAGTCT GGGATGCCTG CAGCCACAGA GATCCCCGCA CCGTGACCA CCAOGATGTC 180
 CCGACTGTGC TGGAGCGCAT ACGAATGAA GTCCGGGTCC CGGGCGCTCA CCAGCTCCGG 240
 10 GTCACTGACG TAATGCGCTA GCTGAAATAC CGAGTTCGTC GCAGGCTGT AGTCAGCCG 300
 CGGCTTCCTC CGCACCGAG CCGGGCGCTT GCGCAGGOC GGTAACAGCT CCTTCGGTGT 360
 15 GACCTCCTCG GACACGCTCG GCGGCTGTC GCAGGCTCT GTCTGCTTCT TTTTGACGCT 420
 CGACGGGGC GTGATCGCA GCTTCACCTT CATCGGOGAC CGGTACCGCT TCACACCGAT 480
 20 ACCACAGTA GCTCCGTC TCCGCAOGT TCACAAACC TCTGCGCTT GTGCACTCG 540
 TGGTTGCCCC GCTGGTGGC GTGTAGCGA CATGAAATGA GTGACGGCGG GCCCAATTTT 600
 25 GCGGGGTTC GCTTTCGACC AATCCGAAA ACTTATCCCC CGTAAAACAA AGGCAGGACT 660
 TCCGTGTGG CGATAGCGC TTTGTGCGA TGGCTCTG GTCCGTTAC GCCTACATT 719

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1424RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GATCTCATCT GTATTTGGAA GGAACGCAC CAGACGGGG TGACTGCAG AAGCTGCCAG 60
 AGGAGAGAGA AAACATAGAA AATATATTTA TATTATCTAT ATTCAGTTTA CATAAGAATG 120

TGTCATAATT TTATTGTTTT TAGATTTTGA CTTCGGAGTG CCTGCATAT GACTATCCTT 180
 5 TTATTCTAGA TTCAGTGCTA GCTAGTCGCA AGGAAATCGA TATCGTAATT CCCATTTAGA 240
 ACAAGATACA AATTAGCGAA TTTCOCGGAA AAACCGTCT TATAATACAG CATCATTGCC 300
 10 GAATCCATAC CAGTCCTTCA ATTAAACTTC CGAATCAAAA AAGGCCCGGC GCGTCTCAA 360
 GAATCTTTTC GCCAGTACTC GAATGGTGAC TATCAGCAAG CGACTCTTCA CTACCCGAAA 420
 15 CGACCAGTAT ATTTGTGTGC AGCAAATGAT TTAAGGCTCT CGAGACACCT CTTATTGGOG 480
 TCCTATGTGT TCTGTGCAGC CCTGGCCCC GATAAGAAT GCAGGTGOC TAATAGTAAT 540
 20 TACTAACCGT TTTTAAATC GCGTCTTGG TTGAGACCTG TGAAACGATA ATCCATTTA 600
 TACCAGATGA ACTCGCCGCA CTATAGTGTG CGTAATTCAG CACTGTGGAT TCCAGTTAG 660
 25 GGTCCGCGAA GTAGCAAATT TGTTATCCT CCATAATAAG GATATCCAAT GCCAGTATAA 720
 TAGT 724

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1424UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

GATCATCGTA TGCACTCAGT TGTATTCTAG CATAGCCCGT GCGATTGCGG TGATTTCGAA 60
 55 CGATGATGAC AGGCAAATCA CCATGAGGAG CCGAGGATTC TCCGCTAAAT TCAGCTGCAT 120

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TTGCAACAAA GATGGOGTGT TTCTATGOGA GCUUCTTCAC ACGGGGTAA AACATGTTG 180
 5 AAATGCTGCT CGCTCTGCCT TGGCTGCGT GTGCCCTCAG CCAGACGGTC TGTTTGCTTC 240
 TAATGTGGGG GAGAGTCGTT CTACTCAAGT GTTCAGCGTG CTGAATAACT TGCTATCCT 300
 10 TACAGCTGCT GACCTGAGGC AATGCAAGTT TCCAAGTCCA ATAGTCTACG GGCCCGAAGG 360
 TTGTGCGGAA TGCACAGTGA TGGTAATCT ATTACTACAG CCCACTGCAA GCGTACAGAC 420
 15 AACCTACAAT GACGGGCGGT TGTACAATAA AATCAATTCC GCTTGCTOGA CCGTTAACC 480
 AAAGCTATAC CGTACCTTGT GTCCCTCCCT GTTCCATTA GCGTTGCAT GTGCTTTTTT 540
 20 ACTGTGATTA CAGAGCCTTT CTGTAGAATG GTTACGTGAA TTAAATACTA GAGAGCTATA 600
 AAGCTCTCTT GTTCTGTAA TGTCTGTTT AGAAGATAAA AGGTAACACC AGAAAACGAG 660
 25 GTACGACCCA ACGGCTATTG GACTACGAAC TGGACAAAAA CTAAGAGTCG TAAGTAAGAA 720

(2) INFORMATION FOR SEQ ID NO:629:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 710 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1425RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

50 GATCAGCTCC CACTTGGTTG CAACAGTATT GCTGAGACTA TCATTCTTGT AGAGCGATTC 60
 TTGTGAAGCA GTTGGCCCGG TGTATGAAAC CGCGTGTTTA CCAAGTGGAG GCCTTTGTTT 120
 55 AGAAATTTTA GTTCCTTCTC GAACGTATTC GTGGTCCTGG AGAATAAAGT TTTGTGCTC 180

GACATAGTCA GGGTCAAAAA CATTCACAGG TGTGTATCA TATGGGGGOC GGCTGCCCGA 240
 5 GGTGTGTGGG TCAGCCTTTC TGTGTGGCTC CGAGTCTCCA ACCITCGAGA TAGCTTTTGA 300
 TAAGTTGTAG AAGTCGTCCA AAATATCGTC TTCGCCGAGA GGAGCAACGC TOGAGCCCCCT 360
 10 GAACAGTGAT CCACTAGAAC TTCTTGCACT AGCCTCGCCG TCAGCATTAT TGCTATTGTG 420
 TGTACTGCTC GAGTTGCGCA GATTAGATAT ATCAAACTGT TTCGATTGTG TGGAACTTT 480
 15 ATATTCATCA TATGCTCCAA AAGAATCTCT GCTTTGCGGA GAGCCTCGCG CTGCATGAGG 540
 AGGAGGAGCC ATAAAAGATG AATCCCTGCC AGGAGAGTTG TGTAACCGCC CAAATGGTGA 600
 20 TGCAGCGTAG TTGTCAATAA TTGAACCAG ATCTGCAAGC GACTTGTACA GGTCCCTGGG 660
 GTTGTATCCT GCCTTGGGGT CGCCAACTTC TTAAATGGAC CGAAGAAGC 710

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1425UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

GATCATAAC GCGCTGCGCA TACAGTTGGC CAGCAACAGC ACCCGCGACA GCTCCAACG 60
 50 GCTAGAGACG GACACCGCAG GCCTTGTGCG CCAAGACCTT TCCCGCTGGG CCGACAGCAC 120
 CAATGCATAC ATAAACGGCA CAGAGCCTC CGTAAATGCC GGCCTCCTCG GCTGGGTTAC 180
 55 CACAGCCACT ACAGCCCTCA ATACCACCGT CGCCGCCCTG CTGGCGGACA TCGATTCCAC 240

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CGTCGACCGC GCGTTGCGAG ACACGCCACT TCACCGCCCC ATGGTGACCG TTGTCTCCTG 300

5 TGTAATCGGG AACAAAGTTGC GCGCCATCGA GGCAGGCGTC ACCTGGACCC ACGACCACGT 360

ACGCATCGCC CTGCCGCGCA TCCATACCGC CCGCCTTCGC GACGCTGTGG CAGAACCAGA 420

10 CCTTCCAACC CATCCCGCCT ACACAGCGGT GCTCCAGTCC CTCAGTGACC GCTTACGTCA 480

TTGGGTGAC CGTGTGCTAC ATCAGTGCTG TGCCGGGGTC CGCATTGAAC TCTACGTATC 540

15 GCTTGCCCTG CTGGGCGCTT GGATTTCTGA GACACCTCTC GGCTTGGCAA TGCTGCTATT 600

CAAGTCGCAC TGCCGTGCGA GGAACTGGG CCGCAGAATG CTTTGAGCCT AATTCTTACA 660

20 TAATCTTAAT TCGCCATTCT GCTGCTCGAA CACGAACCTC GCGTTAGCCG G 711

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1426RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

GATCTTCTCT CCGCTCGAG TCACTGGCGG CATGCACGAC GCCATGAAC TGTGCTGCCG 60

45 CTCCTGATCG CCTCGTGCA CTGCTAGCG CGACTGGCCC TCCAGAAACC GCGCCATCTT 120

GTTCGCATCC TGCAGCAGCA CCACCACATG CCGAACCACC GGCTGCCCTG CTGCTTTGCG 180

TAGCTGAAAC GAAAGAAGAC GCGCTATAGG CCGCTGCGCT AGCATATACA CCCACGGGAC 240

55 ACCCATAACA GCGCTTCTAA CCTCAACCG AGTCACTGAG AACTGGCGTA GTGCGCATCA 300

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	TCGAOCTCGC GATTTTTCAT TCTAGTGAAT AATCCTTACA CCGCCAACAC AAAGGCAGCT	360
5	TCACCACCAT TCTGGCTCAA CTAGGAGGCG TGTOGGGCGA ACCAGGAACG CGTTACTCGG	420
	TAAGCGGGCA TCTAGTCAAG TGGGCACTTG CAGGCGACTT CTTTTGTGT GTTATTCAGG	480
10	GTGTAGGATG CTTGTTATAG GGTGACAGG AGGTATTGCA TGCGGCAAGT CGACGGTGTC	540
	GCGGAGACTG CACGAGCGAT ACOGGATCCC GGTGATCGAT GCGGATGCGA TTGCGCCGGA	600
15	GATTATGCGG CCGGGGGAGC GGGCGTACCA CCGGTGGTGS AACGGTTTGA GCAACGGGTG	660
	CCGCAACTGG TGCAGGCGAA CCGGGAGCTG AACCGCGCGG CGCTGGGGGC GTGGATCTTC	720
20	CA	722

(2) INFORMATION FOR SEQ ID NO:632:

25	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 703 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
30	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1426UP

40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:
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45	GATCTGCTCC AGCGCCTGCT TGAACCAATC TCCAGAAGAG TGTCGGCTC GTCAAGAACC	60
	TTGAAGTCAA CCTCGGTAAA GTACTTTTGA CCGCAAGCCT CGAGCATGTC GATCAACCGG	120
50	CCGGCGTGG CAACCACGAT ATTGGGCTC CTGCGCTCTA GGGATCTGAA AGTTTCAGTC	180
	CGCGAGGAGC CGCCCATCAT GACAACCGCA TTGAAACGGC GAAGCTTCCT GTTGGCGTTG	240
55	CGCATCTCGT TGATCTCGTT GAAGATCTGC GGGGCAAGT CCTTGGTTGG TGCAATCACA	300

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ACAGCCTTGA CATTTTCCGA AGGAGGCCCC TCCAAGAGCC GCTGGAACAG CGGCATCAGA 360
 AACGCAAGTG TCTTACCTGT TCCAGTTTTC GCGCGTGCCA CCACATCGTG CTCGGTCTGC 420
 AGGATCGGCT TCAGCGTCTT CTGCTGCACC GGTGTTAGTT TATCGAAGCC GCGTGACTGC 480
 AGCATCTCGT ACAGCTCGTT GCTGAGCAGC CCTCCTCCA CCAAGGTCCG CGGTGTGCTT 540
 TCGACCCCCG CAGCTTGTG GGCACACGC ACCACCTGG TGTGCGGCC GAGGCTGAAT 600
 CCTCGCGCG CCGCGCGTC TGTACGCGC CGTCTGCOCT GTGGCTTCCG CCACATGCCG 660
 CCGCGGGGAC CAGGCTCACC ATCCTCCCTG TCGCTGCCCC GCT 703

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1427RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GATCTTTCTA TCGGGGAAAG AGTCCATCGA ATACAAGGTG CTTCTAGAAG GCGCCTATGG 60
 AAACACCATT CCGCGGCTTG CTGCTCCTGA CCGCGCTAC GTGGGCGCCA GCGCAGGTCT 120
 TGGCGTAGCA GCGGTCTACC CACACTTCGT CTCTCTGTTG GACAAGGAAA GCCAGTTCAC 180
 CCATTCATTC TACTGGATTA TAAATGACCT TTCATATCTG CATTGGTTTT CCATGAGCT 240
 GAGGTACCTG GCGGACCGGA ACTGCGACAT CAAAATTATT TACACGAGGA GCAATGAGTC 300
 GGCTAAAGAA CTGACCCAG ATGTTGCCGA TTCGCGCTCT GCGAAGTTCG TGGATTGCT 360

GGATATCTGC AGGCTCCTCC TGGGCCCAGA TCTCAAAGAG ATCGTGAAG AGCAGATCCT 420
 5 GCTCTCGTCT AACCAGGCAC AGGACGTCAC GTTTATTAGC AGCGGOCCTT CGACCTTTAA 480
 TGACCATTTT CCTATGCTG TGAAATCTAG CATCACGGC AACTCCAGT GTGATGTGA 540
 10 OCTAGAGGAG GAAAGCTACA CCGGTAGAT AGATACCATC TTATTAGTA ATTGTACTTA 600
 TTTATCCTC TTCCTGTATC TTAAGCAAAT CCGCCATGT CTCAACCAGC TTCTGCATGC 660
 15 TTTGCGGATT GAGCCCTGCC TCGACCACTT CCAGAGGTAC CTGGTTTTC G 711

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1427UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

GATCATCTTG TCCATGCCCT TGGGGCCCAG CGACGTCCTG ATCGCATCCG CGACTGCTCT 60
 40 GGCAGCAATA ATGTTGCCCT TTCTCACTTC CTGGGGCTTC TCGGGTTTT TGAACTGCGC 120
 ATTGCTGGCA CTGACCTTGG GTGGCATCTT AATATACTTC CTGATTCGGC GCCCCAGAAG 180
 45 CCTTACTTGC TGCTAGAGAA GTTAAGGTTG TTTGTTTATG CTGACAACGC CTAAGTTACC 240
 GTCAAACGAT CAGATTTTTG CCACTGGAAT TTCCCTTGTG ACAAACGGAT ACTTGATCCT 300
 50 TTGATCTCCA AGAGCTGTTT CATCGGGATG GCGTCTGAG TAGTCCCGGG TTGAAGGGAA 360
 AATCGGGGCT CGACAACCTG GGAAATGTCT ACGGAGGACG CGCGGTTAAC AGGGATCGCG 420
 55

GTGACGGCAG AGCTCAAAAA AAAATGCGCG TTTTCCAGCT GGTATGAGGC GTTCAAGGGC 480
 5 CAACTCCGC GGGCCGAGGT GATTCCGCCG CTGCCCGAGG AGTTGTGAG CTACGTGGAT 540
 CAGCGCGGGA TCAGGCTGGC GCGCAAGAA GGCTCGAAGT ATTTCTACCG CCAGGAATGG 600
 10 AGOCTACGAC GGACGGAGAG TACAGCGACT GGGAAGGCGG CGACAGCGCG AGTGAGCGGT 660
 CGTTGTGCC GCTGGACCGG TGGCGGACTT CCGGAAGTG CACGCGCGGG TGAAGCAG 718

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1428RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GATCATACAC GCATTGCAGG TATACATTAT AGTGCTCATA ATTATCGGAT TGCAAATAGA 60
 40 ATGGGGCCCT TACCGTAGTA CTGTCTTGGT AATGCAGCGA CGCTCAGGCT TAAGAAGCTT 120
 TTGTCTTCC GTGTATTACT AACAAAATAA TTCTCTGAG CACAGGGAGT AGAGATGAAT 180
 45 TACATAATCC ATATGGACAC CTGTCACCT TCCAGCGACA TTAACATTTC CTTATGAATG 240
 CCCAATAATG GTGCCTAAAT GATGTGCTTG GTGTAATGCG CATTATAAAA TGTATGTGGA 300
 50 TTATATATTG TTGTAGCAT CTAGTAGAAC CATGCTAGCG AGGTCTTTGG CCATACCCCTT 360
 CTGAAGAGAG ACATAGCAAC AGTGTCTTGT GCAGACAGTC TGCCGTGAA TGTGCTTG 420
 55 AAGTAACCAT GAGTACCAAG ACTCTCCTTA ATGAAGCCAG AGCGTCCAGA TTTCGTGAAT 480

AGTGGGATCG ACTTGAACCA CTCGACATCT TCTGGCCTAA AGAACATATA GGGCACTGTG 540
 5 ACGACGGGCT TGTTGAACTT GAATGGATGG CCAGTTAATA TGATTCTCTT GGCCAATATC 600
 CGTGTGTGGT CTGGGTTTCAG GAAAGTGGCG TGGGCCACGA ACGTCAGGCG CTTTGGATCA 660
 10 GAGGGGTTTT CTTTGAAGTA GATGGCCGGT GACTGGGTCA GGTCCAAGGG AAGCATGCAT 720
 GTC 723

15 (2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 726 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: PAG1428UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

35 GATCAAACCA GAGTGGAAG CGCACACGG GCACTGGCG GAGCCCTTAC CGTAGTTTCT 60
 TGGGTGGGAG AACCAAAGT TTTCGTGAGC CATCTTGCT GCAATGGGT AGTACTCTGT 120
 40 CTGACCGCTT GGAAGCGCTC CGGCCCTGCT GAGCTGCCA CAGCTGGC GTCTGGCGCG 180
 TCCTCATTGC CGCACCGTA TTCTGCTGC ACGACAGCT CTAGACCACA CTTGGCCCA 240
 45 TCCTGTGCAC ATACGATTAT GCTTTGCTC TTGGTATTAT CCTTAGATT CTTAGACTTC 300
 GACACTATGG TTATCACCAC TGTGAAGTC TGCTTCGGT GGCACCCAA GTCTGGGAC 360
 50 TGTAGTTGGA AAGCGAGTT CGCGCAAAT CAAGCATCTC ATAATGTGTG GTTCAACCG 420
 TTGAATGTGT GGTGCAACA GTCAATTGTA ATTCTTTTT TTGATGAGA GATGGGATGC 480
 55

5 GATGAGCTAG TTGAAAAATT TTAGTATGGC AAAACTGGCA TGCATATCTG AGATGGGCCA 540
 TCAATTGCGG CAGCTTAGTG TTAGACGACC AATCCAGAGG TGGTAATTGG GCTATGGCAG 600
 GTCACCTGCA CAGGTGCTCG GTAAAAAAGG GCCACAAAAC GTTCAAGTGG AAGCATGCCA 660
 10 GCAAGGGGCG GTTGAAACGG CTGCACAAGG GCAAAGTGGG ACAGGAGACC GCTGCTGGGG 720
 TGAAGG 726

15 (2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 712 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: PAG1429RP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

40 GATCAAAGTT TAGCATGTAA ATGTGCAACA AACTATTTAT TACCTCTGCA CTGCCCATGT 60
 CGCTTGAAAC CGCGAGGAT CCAAACCACT GCTTTCATAA TGGAAITGCA AAATTGAGTG 120
 CAGTAATTGA TAAGTATCTT GAGAAAAGCC CTCGCGACTT TACCTAGAT GATTGCTTAA 180
 45 TATGTTCAAA AGCCTCCGAG TTAATAAAAA GGCTTGCTAC ATCCAAGGTG CATATAGATG 240
 TGATAGATGA GACTAACAGC ACCATTCATA AAAAGCGGAA GCGCAATTTT CGAATCACAT 300
 CACCCAGAGC AGTATACACA TCATTITGA ATGTGCTATT AAGAAAGTTG GATAGCGTTG 360
 50 TCGACCAAGG AAAGGTAGAA ACGTCCAAT CCTTTGATCA GATACITGAG AATTTCTTTA 420
 55 TTAAGTIGAA AGAAGTCGAC TTTACTCTAT CTGGGGTTGC TCTGATGTAT AGCACTATTG 480

ACTACTGGAA CCCCCACATG ATCCCAGGCT ACGGCAAAGT TAOGACTGTA GAGCATTTCC 540
 5 TGGTGCAGTA TATCTTACAT CGATATGAGG TATTATATGT GCGCGCGAT GAAAGCCTAC 600
 TAGATAGTCT GGTGGTGCC ACTATTGGGA AGCTATTTGA ATGCATGCAG TCACAGCATG 660
 10 ACCACCAGAG CCTGGTAGCG AATAGCCAGG CTGATACCGC ACGAAGAGAT AT 712

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1429UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

GATCAACCGA TAGCGGAAGG CGGACGAGCC TCGGAAATAG TACTAGGCAG TGGTGGCTT 60
 TTGTTTTTAG CTGTGTTTCA AGATGTCAGC GAGAACAAGC AGGGAGGCAG GCGCCTCCAG 120
 40 GGTGATGGGA GGTGGGAGTA GTATGGATGG AAAGTCCGGG ACAGGAACAG GGTATTTGGA 180
 ACAGCTGAAC TCGCCAAGCA TTCAGAAGCT CATGCACTCG GACGCTTCCA CGACAGCACT 240
 45 ATTGGAGAGG TTGAAGATGT CCTAGTGAC TTGGGTGGAG TTCACGAAGT TCATAAGAAA 300
 GAAATACTTG CTAGAAGAGG GCCATGCGCA GGAGATGGGC AAGGCTTATA AGAACTTCTT 360
 50 TCCGAGGGC GGTGAGTGCA GCTTGCAGAA TAGCATACAT AAGGTTTTGG AGTATGACGG 420
 AAAACTTGCG CAGGTGAAAC TTTCATATGT TGCTGGTTG CAGAAGATGT ACGATGAGTT 480
 55 AACGTGGCTT CTTGCATCCA TGAATAAAT GCGCAAATCC CTCAGGAGA GCAGTCGGCG 540

GTTCGAAAAA GAAGTCGCAG ATGCTATACA TAGCGCCGAA AAGGCAAAGG CAAGATATAT 600
5 GTCCITGTGC ATGGATTGGG AGAAGCTCAA GCTTGTAGAT CCTGCAAAGA CGAAGTTGAC 660
ATTGCGGGGC TCAAAGACCA CTCGAGAGCA GGAAGAGGAC TTATTAGAAA GATTGATA 718

10 (2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 730 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: PAG1430RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

30 GATCGCAGAG AGACACAATG TCCTGTGGC CACTTTGTCT ATGCTTTATC ATTTATTGAT 60
TCTTGTGCAG GGGAAACTG AAGGCCCAAC AGGGAATTGT CAACCATGTT TAAACTTTTC 120
35 CATGTGCATG GAGCTCGTA TGTAGCAATA TATTCTCATA GCTAGAGATC TCACTATATA 180
TTAGCTTGGC ACATTATATG CATATCGAGC TTGTTTTTTG TACACCTTTG TGTCAGGTAG 240
40 CAGGGGCGGC ACATAACTAG TTATAAAAAC GATGCCGCGG GAGAACGAGA TCTACTATCT 300
CTCTGAGTAG GCACAGTTTC CAACGTATTA GTCTTAATG AGCAAGCGAA TCATTCAACT 360
45 CATACTTCTC TCTGCCTTTG CGCGAGCTAA TTACGTGGAG CCTTCAAAT CAAATCCATA 420
CATTGCTTGC TCAGAGGCAA GCCATTGCC AAAGGAATGG CCATGCTGCT CGCAATATGG 480
50 ACAATGCGGG AGTGGGCGGC TATGCATTAG TGGCTGCAAC CCAAAATTCT CGCATAGCCC 540
TGAGAGCTGC GTGCCAGTGC CGCGCTACT ACCGCAATTG GAGATAGTGG CCAGCGATGA 600
55

TAAAGGAGTA TACCTAGAGA TGTCGGGTCA GCGTGCCCTTG GTCACAAAGT TCCAGCGCAA 660
 5 GAGCTCGGCG CAGTTGTGTGG AGGTACATCA CGAGGAACAG CAGTATGGTG TGTCGGCATT 720
 AGAGCAGGAC 730

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1430UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

GATCGATTTG GTTACCTTGT TGCCAACCC ACGTACTTCA AGAGATTCCG ACCCAGAGTT 60
 GTAGACAGCG TACCTATTCC GAGCGACAAA AGTCGCAAAG CTTCCTTTAT CCTCAACTAT 120
 ATTTGTGGCA TCAACAGCAC CGCTAGCCTG TTTTGGGAAG AGGCAAAGAG CATACTATC 180
 GCCATCCCTG CTACTTGAGT TCACGAGGAG AGAGTGTTGC GAGGGATTAT AAGAGATGGA 240
 CTTGAACACG TTATATGGCT TTCCAAAGTT TTTTAGAGAA ACAAATGGCA GAGAGGACAC 300
 CTTCTTTTCA TAGTCAAACA TTGGACCTG CTTCTCTTTG TTGACAAAGT AAAGCTGGTT 360
 CTGGTTCACA GCCACAGGTG GTCTCTCAGG GTCCAGTTTA AAGACCATGA TACCGAGTC 420
 ATGCGCGCGG CCAAAGAGGT TCACATTAGG GTGCGCCCTA ATCGACCAGA ATCTGTCTG 480
 TTCTCTTTTG AACTGTTTTA CAGGAGTGGC CTGTCTAGA TCCAGACCC TAATGGTAGA 540
 ATCTCGCCG ACAGAGATAA TTAGGTTTTG AAATGGGIGA AATATTACAC TGTCGACGTT 600

GTTCGTATGA CCTGCACTT GTCGACCTCC CACGCTTTGG TGGAGCTCAT ACGCCACAAC 660

5 TTGACCTGTC TGCTTCAGA ACCGGAGACA ATCAAGGGCA GAATGGGATG GAACGAAGG 719

(2) INFORMATION FOR SEQ ID NO:641:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 730 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1431RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

30 GATCATGTTA TACAGACCTT CAAAGTTGAT ACCAAAACCC TCAATGGACT CGCTGACCAT 60

ACTTGGTACT TCCTGTTTAG AGGCCCTGGG GCACACTTAC TGCCCTCTACA AGAAAAAACT 120

35 GTTGCCCTCTG AATTGGATCA CCCTTTTTCG GACACTAACC ATTGCAATA CAATGCTATA 180

TTGCCCTCTAT CAATGGTCTA TTGACCTTGT TGAATCCAAG CTCGAAATCC AGCAATGTGT 240

40 AGAGATACTG CAGCATTTTG GTGAGAAATG GGTTTTGGCC AAGGAGTGTG CGGTGCTCTT 300

TCAAAATATT GGAAATGCGA TACTAGATAT AAGTCTCTCC CGAGGACAGG TAGAAAACGT 360

45 TGATAAATTG ACTAGGGAGC TATTTGGAGC TAGCAATGAA TACCAAGATA TATTGGACGA 420

AAATAACGTA GATATATCCT GGATTGACCT GCCTATCTAA TTTCTGAAAC CATTGAGAAC 480

50 CTGTTTAAAC TATTTGGCAG TAATTCATAA TGTATTGGTT GTTCATAGC TGAATTGCTA 540

TTGCCGCTAT GGAGTTGCTT ATGCAATACA CCGGTTAGTG GGTGATTGTC GTGTTCTTAT 600

55 ACCCAAACCTA ACCGAATCCG GTCTTAATCG ACTCCGGTAG ACTTTGTCAT CCAGTAAGAC 660

ATGTCTTACA CGCCCGAATTA ATGGTTGTAA TCTTTAATCG ATGAATGAGA AATGGTATAT 720

GTATGTGACT 730

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1431UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

GATCTCTGT ACCATCATGA AAGTCTTTT ATCACGGGAA AACCGTTTC TCAGGCACAT 60

CTGACGCACT GCTTGTGCA CATCAAAGT CAAGTTCGA TCCCTTGTA GCGCTTCCAA 120

CTCCAGAAC TCCTTCGCA GATTTTATAC TGGGCGCGC ACAACTTCTG CCTGCCCTCTG 180

GGGCACATAT TTCTTTAACA CCTCCTTCGG AATCTTAAAG TCCTTCACAT TATAGCGACT 240

TACGAGACCT TCGAATAAGA AGAGGCACCT TATATATAAG TTGACATAT CCAGTTTCAT 300

CTCGCACCCC CGCAGCATCA GGTCCCGTA GTCCAAGTGC GCCTTCTTC TTGAATTCGT 360

AGAGCTCGCC CCCGAGGATG AGCCTCGCTG ATCAGAGGTG CCTGTCTTCA GCGAGAGCTG 420

TGGCATACTC GGCTGTGTGG CAAGCTCCAC CTTCACCTGC TTGGCAAAGT TCACATTTAG 480

GCCCTGGCCA AACGGTCCA GTGAGCGAA GATATGGTTC ACCAGCTCGA GTGGCATGCC 540

CATCTTGTTC ACGTCCAGTG ACACGTTCCC TTGGCCTAGC TGGTGCACTA GGGCCGGCT 600

CTGTGTGAGT TGTCCCTGCC ACACAGAGTC CAATTCACCT CGCATCATGC GCATCGCGTG 660

CTTCAACGCA CGCTCACTGA TCTCCCTCG CTCAGGCATC TGTGGAGCCT CTTCTGGCT 720

5 TC 722

(2) INFORMATION FOR SEQ ID NO:643:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 724 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1432RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

30 GATCCAGGAC TCCCGTGCCT GGTGCGCTC AAGGAGACT TAGAAATGAG GTGTGGGOC 60
 GCATTCTGGG CTGCAGATAG AAACGAAGAC AAGATGCCAC CGTTACCCAA TTCTCAGOC 120
 35 CCAGAGAAA AATTCCCGTA CCGGTGCTTC CCAGTACCAT CCTGGTCAA GGGTGTGATA 180
 TCCGAAATT TATCTCAGT GTCTCTCTG TATCTGCAT CCGAGCGGT GCTTTGGOC 240
 40 GCGCGCGGG GCTCGCGGC CGCGCCAGAC CGCACATGG AGTGCGGCG GCTCATCTCA 300
 ATTGGCATGC TGAGCGACGA CGAATTGCTG TCGCGCGGC TATGCCAGT GCGGCGTCC 360
 45 CGGCCACCC ACCCCAGGG GAGCGACGAG TTTGTCTGT TCGGTAAAC CACCGTGGC 420
 GACATGAGC ACGATTCTG TCTGACAC CGGCTCTCA CATCCGAGC CTCCCCGOC 480
 50 GCCACCTGA CATCACCGC CTCGCGCCC GTCCGCGCT CCGATTCCG CGTCGCTACC 540
 CGTCTTTGG CACTGCTGC GCGCCCTTC CGCGCCCT CCGCGTATG CTTCTTGAAA 600
 55 AGTGCGGCG GCTCTCTG AGCGACCGG ACGCTTCG CTCTCTGCC ATCTTGCTA 660

GCCTCTGCCT GAGAAGAGCA TCTACCTCTC CTCCTGTGTT ATTCCGCGGC CTTTGTGGA 720

5 AACA 724

(2) INFORMATION FOR SEQ ID NO:644:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 615 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1432UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GATCCCGGTC GCGCGCTCCT CCTGGAACAT GTCTGTACC CCGCGCAGCG GCTGGAACAT 60
 30 CCGCGCCACC CCACGTAAT GCGCGGGA GAAGTGTGTG TCACCAAGCT GTTCGTGGCG 120
 CGCTGGTCC GCGCGCGCA TATTCTCTC CTCCTGGTAA GCTCTCTCT GCAGAGACTC 180
 35 GCGCAACTTC TGTGTGTGT ACTCCGCGC CCGCGCGCG CTTGCAGGC CACTGGGTGC 240
 GCGAGCTGC GTGTGCGCG CGTGCTGAA GTACAGCGAG ATTGCGGTT CCACGTGCG 300
 40 AACTGCATA TCAGGAACT GCGCGCCAG CTCGCGTGC GCCACCGC AGATGCTTTG 360
 GAATACGCG AGCTGCTTGT CTGAATCAT GCTCTACTT TCTGGCGCTG CCGTGTGTG 420
 45 TGGCACACTC AGGAGTTTGT CTGAGTTGT CGCTGGCTCC AGCTTTTAT ACCGGCGGT 480
 GCCACACATG CCGCGGCGC AAACGCTTAT ACATATACAT GCTACTTAGT CCGCGCTTG 540
 50 GTACCCGCC CGTCTGAA GCGGTGTGC GTGCGCTGGA AGTGCACCG CTGATGCGG 600
 CCGCTGGG CGCG 615
 55

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1433RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

GATOGATGCG GACCACCGTG CGGAGGAGGC CGCAGGTGGA TATGCAGTTT GCGGCGCTGA	60
GCGGCGCGAT TTGAGAGCT CGCGCGTCCG CTGGGTGCC CGCTTCGCGC AGCCACGGAA	120
CCAGCTGACG CGAGGTGTCT CCCCCGGGC TGGCGTTTG CCGACAGTG CTGCGCGCT	180
GGTAGTTCTG TAGCCACGC GCGCGTTAA TCTCGGCAT TAGTAGCGC AGCATCTGCA	240
CGAGCAGCG CGACTCGCGC ATCTTCTGTA TTTTGAGCAG CTGCGCTCG ACCTTCTCGT	300
CTGGGTGCC CATGTCCCG CCCAGCCGT ACTGTTCTG CAGTCCAGC TCTGTCACT	360
ACCGTGCTAT TTGCGCTCG TTCAGCACTT CGTCATTCTC AGCCACCGGT ATTCCAGGA	420
GCTTGCAAT TCGCGCGCT TTCTGTAGGA GAACGTGGTA GCGCGGATG ACCTTACGTG	480
CTTTGGATGG TTTGATTGCC GCGTATGTT TGACGGCGCT CTTGCGCGTA ATGCTTCTTC	540
GCTTCTGGC CAGCATGTAT GAAAGTTAAA CGCAGTTAC TACTGGTACT AGATATGCCC	600
TGGGAATGCC ACCCGATGAC CTGCTGGTGT ACCTTGCTTT TGTATCACG ATGCTTCGAG	660
CTGAATCGTT GAAGAATTTT GAGTGAAA	688

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1433UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

GATCAOOGAA GAAGGCAAGG TCAAGAAGGT TACATTTGAT ATOGAGCOGT ACAAGCCCAT	60
CAACACTAAG CTATACAAGT GTGACAATAA GTTCOOGACG GAGGTGCTCT CGGAGCTGCT	120
GGAGGCTGAC GAGAAGTTCG GGTTCATTGT GATGGATGGT CAGGGGTGTC TTTTCGGTAT	180
GTGTTCGGT AACACCCGGA CTGTCTTACA AAAGTTCACT GTGGACTTGC CGAAGAAGCA	240
CGGTAGAGGT GGTCAATCCG CGGTGCGTTT CGCCCGTTTG AGAGAGGAGA AGAGACACAA	300
CTATGTGCGC AAGGTGCTG AGGTGGCAGT GCAGAACTTC ATCACAAAGC ACAAAGTTAA	360
TGTTAAGGGG CTAATTTTGG CTGGTTCTGC GGAATTCAAG ACGGACTTGG CCAAGTCTGA	420
ACTGTTTGAC CTGAGGTTCG CAGCCAAGAT TGTGAAGATT GTAGATGTAT CGTACGGTAG	480
TGAAAATGGT TTCAACCAGG CTATTGAGCT GTCCCGCGAG GCGCTGGCCA ACGTTAAGTT	540
CATTCAGGAG AAGAAGTTGC TCACCGAGTA CTTTGATGAA ATTTCCGAGG ATTCCGGCAA	600
ATTCTGCTAC GGCTGTGACG ATACTCTGAA AGCGCTAGAT TGGGTGCGGT GGAGAAATTG	660
ATTGTGTTTG AAAATCTAGA GATTGTTCG GTACGTGTTT AAGACTTCTG AA	712

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:

EP 0 866 129 A2

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1434RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

GATCAGATGC TTCTGTGGTC CTAGAGAAGA CTGCTATTCT TAACCCCTTCG TCAACGAATA	60
TAGCCGAGGA CGAGTTTGTC GATGCCATAG CGGAACCTCC ATCGGCGTCC GTGGATAGTA	120
CGOCTTATGT GACCGCGGCG CGGATTATT OCTCGAAGA CACCGGGGA CGTTCTGAAC	180
CTACAATAAC GGAATACAAA ACTGCAATTG AATCACCATC CACCTTTGGC GACGATAACG	240
AGAGTGTATT TCTGTAACT TCTCGGACC TGCATCCATC GGTGTCTCT GCGAGTCAA	300
CATTACAAC GGAAGAGCTT CAAGCCGTG CGACAGCCA CCAATATAAG ACCGAGGTGC	360
AGATTGTAAA ACAAGACGAA GATGAAGTAG AGGATGTTCT AGAATTGGAC TCGCACCAG	420
CATCTCTGTA TGATGGTGAT GTTTTGAAG AGGCAGAGAA AAATGATAGT AGCAATGTTA	480
TTCCTGATGA TTCCATAGAT ATCGATGAAT ACCTCGATGA AACTTTGGTT AAAAATTCA	540
CATTGGAAAA CGCTCTTCT TTAGATGAAA TCTTCGACGA TGATAATGTA GTTTTGGAG	600
AAGAGAAGCT GCTTGTGGAT CCAGACCTAG AATCCCGGA ATTAACTGGA ATGGAACAAG	660
ATATGGAATC TGAATATCTG CCGCTGATTG AAAATGGTAC GGAGGCTGTT CTACAA	716

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1434UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

GATCAGGTTT TCCGGTACGT GAGAACGTAT CTAAGGCACA AAGGGCTTTG GGCGACTGTG	60
CGGACGCTTG AGTTGCGAGA TACAGGACAA AGCTGTTACG GCGGCAACTG GTGCAGCAGG	120
AGCAGCCGAG GAGCGATTCT GCGCGAAGCG ACGGTGAATT CGAGCCAGCT GGTAGCAGGA	180
GTCCCGGATC GTCTATTTAG TTGGGACGGG CGTGGGACA GGATGCAGT AAACGTTGCG	240
GTAACACGCG ACGCTGACG GACGGCTGCT ACGCGATAG CACGGGAGCG CAAACGAAGG	300
CAGCCGCTGT CGCCAGAGAT GTCTTCACCA CTGCGCGGTA GCAAGCTGCA GCGGCGAAG	360
CAGACACTTG AGGCGCGTCC GGGTGGCGCC AGTGGGACAC ACACGGTGGA CGAGCTGGCC	420
GCGCAGCTGG AGCGGGCTG CGAGCAGCGG TCGGAGCGGA AGCGCGGTA CTCGTATGCG	480
GTGCTGATCG GCGTTGCGAT CCTACAGTCG CAGGAGGGCA AGCTGACCTG TCGCAGATAT	540
ACCGGTGGAT CTCGTCTTTC TTCCCTTACT ACGGCTGTG TGACGCGGGG TGGCAGAACA	600
GCATCCGGCA CAACTTGTG CTGAACGAAG CGTTTGTCAA GGGCGGCAAA TCGCTCGATG	660
GCAAGGGCCA CTTCTGGGAG ATCAAGGCAC TGTAAGGCG CTTCTCGCG ATGGG	715

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

EP 0 866 129 A2

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1435UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

GATCCGATGC TACCCGTCGC CCTGCCAACC CGTTGCGCTA GCGTTGACGC CTAGGTCTGA	60
AACTGAACAA CAGGTGGCAT TGTTGGGGGG CCAGCAGGCC CTGGGGGAC CATGCCGCCA	120
TGGGGGGGA ATAATACCAC CAGTTGTGAA GCCCAGGTGT CTGTAATCTG CACCGAACAT	180
CTTTATCTAC CAAGGAGGAG CCTTGAAAAT TATATATCTA CCCCCTCCCC TAATATATTT	240
GACCAATTGC CTCTCCGGA ACCGAATGAT CGAAGAGGCC ATCAGGGCAG CGGACAGCAC	300
AGGAAGTGAG GAGTGATCTC GCAGGTACGA TGGGAAGACA GTCTATACAG TCTATTGGT	360
CGAACCAAAG CGTACGGAGC ATCSOGAGCA CGAGCGGAAC CGCAGACGAG TCGCTAATCT	420
TTGAACGGAG CGTTGAGGAT CGTTTGGCCC CGTGAAGGAC GCGAAGGGTT GCAGCCTGTG	480
TGGTGTCTCC CAGGCAGGCT CTCTGCACGC CCGGCTATCG GCGACTGGGG GCGCGTCT	538

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1436RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

5	GATCAACCTC GGAAACGTAT TTAAAAGCTT GTACTCGACA TCATTAAGTC TTCTCCTCGT	60
	TTCTTTTGGT AAAGTATWAG CATCCAGTAA AGTAACAACG AAATGCAATG CTGAAAGATC	120
10	GTATACCCTA GACGACCTAA ATGGGGTATT TTGATCATCC ATACTAGCTT GAAGATCAAT	180
	GAAGTCAATA ATAGTGTGTA CAGACTCAGG GGAGAGTTTG GACTTGATGT ATTCTCAAA	240
15	GCCAGTCCAT CCCAOCCTTC TAGCACTAGG AGTAATCTTC AGCGATTCTT TAAACGGAAT	300
	ACTTCTGATA AAATCCTCCA GCTTTTTTTC CTGTAAGG ATCTGTACAA AATTAGCAAG	360
20	CGGGGTGGTA TCCTTGTTAA TTATGATTCT TCCAACCTCA ATGACCTTGT GGTGGGGAT	420
	TTTCTTGATA AGCTCACCAA ATACCATCGG AGATTTTTCA AATACTTGA OCATTAGAGT	480
25	GACCAATAGT TCGTTAATAA TCGCCTTATT TTCAACCATA AGACTGAAAT GCTTCGTTTC	540
	TGAGATCAAA GTCAAGGCCA AATATTCGGG AACAAATATG TAATCATCGA AGAAACAATC	600
30	ATGGAATAAT TGAACATAG GACTGGAGOC AAACCTCTCT CTTGATAAGA ACAGTTCAT	660
	ATCGAGCTTC GATACCGATG TGAGATATAA CAAGGAGTTC TTTGAGTTTG GGAGTACTTT	720
35	AGAGACTT	728

(2) INFORMATION FOR SEQ ID NO:651:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs

(B) TYPE: nucleic acid

45

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1436UP

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

5	GATCCAGAAG ATTATCCGAC AATATTAGTG ATATCAAGGC ACAGATCGCT GCCAACACTA	60
	GAGGTATTCA ATTGCTTAAC CAACTGGTTG ACGTTTTCGG TCTAGGGACT GTTACAAGGT	120
10	ACATGGACGC AATTCAGGAA AATGCAGCTC TTACTGTAAA GAATGTCTTG CGAAAGATTA	180
	CCAAGCATTT TGGCAAAACC GTCTATTGGG COGAGGATTA TATGGATGAT GGCTCTGTTA	240
15	TAAAACTTAG GGTGGAGCTA AATGCTAAGG AAGATAAGTA TATTTTTGAT TTTACGGGGA	300
	CTTCTCCACA GGTCCACGGT AACCTCAATG CACCTGTTC TATTACCAAC TCTGCCATCT	360
20	TATACTGCTT ACGTTGTTTT GTAGACGAAG AGATTCCGCT CAACCAGGGC TGCTTAAAGC	420
	CCATTACTGT TATTATTCCA GAGAGCTCTA TCCTATGGCC GACCAAGGGT GTGGGGTAG	480
25	TGGGAGGTAA TGTATGAAG TCTCAGCGTG TAACTGACGT AATTCTCAA ACTTTTAAAG	540
	TCATGGGGGA CTCCAAGGA GACTGCAATA ACTTTACTTT TGGGACAGGT GGGAACGACG	600
30	CTTCTACCGG TGAATATACT CAGGGTTTTG GATATTATGA AACCATATGT GGGGGGCATG	660
	GTGCAGGTGG AGATCATGGC GTGGTCCGGG GTGGCATGGA ACACATCTTG TTC	713

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1437RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

EP 0 866 129 A2

5 GATCGCGCGC GAGCTATCGC TTCCGCCGGT CAAGCTGCAC TGTAGTATGC TCGCGGAGGA 60
 CGCCATCAAG GCCGCCATCA AGGACTACCG CAGCAAGCGC AAGGCGACCG AGCTGGGCTG 120
 AGCGCAGGCC GCCGCAGCCT GTGGGGGGCC GGCCGGGGCC AGCCGCAGAG GGAAGTCCGC 180
 10 GGGCCGGCGA GAGCCGCCCG TTTTCTATGT AGCGACTCKA GCATCTAATA GACATGGTAA 240
 TAGCTTCTCG TTTTCTACGT TTGCACACAG TATACAAAAT TTTCACGCAG CTCATCGCCA 300
 15 CTTCCACTTG CTGAAGCGCA GGTACGGCAC CAAGACCTCG GCTATGTCCT CGACTCTCTT 360
 TGACGACATC TTCAAGATCC AGGAAGTGA CCAGGGACCG TACAATAAGG TATCGCGGAT 420
 20 TGAGGCCATC TCCAGTCCG AGGACACGTG CAAGCTGACG CTGGATGTGA ACACAGAGCT 480
 CTTCCCGCTG CAACCACAAC AGCAGCTAAC GGTGATGCTG GCGACGACAC TCAACCTCGA 540
 25 CGGAACGGAG GACAGCCACG GGTCTTGGGG GCTCCGGGCC CCTGGGG 587

(2) INFORMATION FOR SEQ ID NO:653:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1437UP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

50 GATCCGGCGG GACCGCTACA ATATTCCCAT ATGTATTAYA GGCAACTTTA TACCCATCTC 60
 CTAAGTGCAG TAGTACTGT TTGTACTCT AGGCTCTCC TCGGGTGAG CCCGTGTGTG 120
 55 CGGTCCACCA GCGCGCGGAC CGCGCGGCCG GGCCCGACGT GCAGCGCGGC CGTGGCGCCC 180

GCCTGCACCG CCGTGGCGCA GGCTGCGACG AACTCGACCA CGTTGTGTCT CGAGCGCACG 240

AACTTCTCCA CGGCCACGTC 260

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1438RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

GATCTCTTTT TAACGGCTGT TACCAATAAC GATACGGCAG CTACATCTGG AGAATAGTCT 60

GCATCCCATG CCTCCAAGTT CCTGIGAACA TACTCTGGG GATOGACCTC GAAGCTCTCC 120

AAGGTCTCTT CGCTAGGACA AAGAAGCGG AAGATAACAT GTTCCAAAAT GGTTCATATA 180

TGTGGGTCAA CTATGGGCA AGTAGACTTT TGGACCACTG TTGTTCATAT GAACTCCAAT 240

ATGTAATATA GCGACTCCTT GCTTAACCAC AATTGGGCTG CACCCACCTT TTCAATCTGC 300

TGGAAATGCA ACTGCAATAG TTGGGGCAGA AACTGCTCCA CATAACCAT TTTAAATTC 360

GTGTACTCAA ACTTTTGTCT GAGAGATTCT GAGGCATAAC GTTGAATAA TCGATACATG 420

TTAGCATATG CCACTTTTGT GGTCTGACC CATGGATGG CCGGCTATC ATGACCGGC 480

AGCGCCATCA CATGCTCCG CAGCTGGCTT TGTATCACAG AAACATGGAA GTTGGCCAC 540

GGAATGAAGT TTTCGACCG TTGGAGAGTG AACGGCAGT CATTATATGT CACAACTTG 600

TAGATCTTCA GCACAAGCTT CAACATATTC CCCACGATCT CGTTGTGCTT TCCTGCTGT 660

EP 0 866 129 A2

ACAAAAGCGC GTTTGGGTAG TGCAGCAAGT CTGGGAAATA TCTCATGATC AGCATCTCCA 720

GCTCCTGA 728

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1438UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

GATCGGCAAA CCTAATGCGT CTGGACGTAA TGTAATCCAA CAGCGACTGT AGAGCTGCTT 60

GCGGTTCCTC GACAGAAATC AGCTCATCTG CCGGCTTCAA GGCGTTTTC A GCGCGCAAAA 120

CAGGTGGAGC CATGCTGAAT TAGAGCTATT TGGTGACCTG TTTGAGTAGT GTGGACTTCC 180

TTTGAATGTG GTGAACTTTG AAGTAGGTTA TTCAACTAGA AAATTTTTC A CCCAGAAGGA 240

TGCCCTCTAT CAGCGGCGGT GTCTGACGAT GATCTCAACC GCGTAAAGGA CGAGAAGTCG 300

TAGGTGAGT CTAATCTACT ATTGGTACTG ATGAACGGGA CTGGCCAGCT AACGTGAAGG 360

CACTGTCTGC GGGATGAGGC CCCAGGGCCA GCGCACGGGC CCTGCGATGA GCACAGGTTG 420

CCTCGAGAGC ATTGCGATCG GCTGACGGGA AGCCAGGTTT CCACAGGTTT GGCGGACTCG 480

CGTCGTCAGG CTGGAAGTGT AGAAGGGTTG TCTTGAGCTC CCGCGACGCC GCAAGCTGCC 540

CAGGTAGCTG GCGGGCGGTG TTCATGGGCG ACAGCGGTGG GCTGCTGTGC ACGTGGCATC 600

GAATATGTCA CGTGATTACA CGCAGCAGGG CATGCGAGAC AATGCGCAAG CAGCAACAGG 660

AGGAGGGTGT GATCGGTGGT GTGCGTTTAA GAGTATGTGA GCTGTGCAGC TGGCTCCCCA 720

5 TCTCTGGGTT TACTCGTACC TGTGCGCTTA TATAGGCATT GCCAAAAGGT TTCC 774

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1439RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

30 GATCCTGTGTG GACGCTCTGC AAAGTCGTGG TCACCCCGAC CAACCTCTCC TCTGTAATAC 60

CGCTGTACTT CGTTAAGTAG TCCACAATGG GCTCATCTGG CTTGACAAAC TTGTCATAAA 120

35 CTAAGTTACA ATCAAAATCG ACGACGCTCA CACGGGTCAA CACGTATCCG TTTTTTGAAA 180

GGCACATCTC ACAGTCGATG GCAAACGTGT GAGAACCGTC GTGTTGGAAA CTGACAGTGT 240

40 CCACCCACCC ACTGTACTTC TCCTTATTCT GATACTTTAG CAACAAAGCC TTTTGGTACT 300

CCTCCGATAA GGCAGGTGTG TTTAGATGGA TGGGGTACTC ATTATGCAAT AAGTCATCAA 360

45 CGGTCATTAG CAAATCAAGC AAAGTGATTT CCTTTTGTGT CAATTGTTC ACCTTTGCGA 420

TCTTCTCCTT TTTTGACAAG CCTACATTGA CAAAAGAATT GTATGCAGAA AATAGGGAAT 480

50 TCTTTGATCC CGGCGCTGAT AACGGCAAGA TACACATTTG CTTCACATC TGTTCATTTT 540

CACTAATCGA GTTTAGATGT GCGTCTTGCA ATTTCGGAAT ATTTTATGA AACAAATGAAT 600

55 CCTTCGGTAG ACTGAAGTCC TCGGGTAAAA GGCCTGGAGT GAATAAGAGC ACCACCTTCT 660

TCAAAGAGGC CTATTTTCTA TCGTAATCCA GTTGGGAGAG TTGTTCTGTAT CGTGGGAATAT 720
 GTACTGGA 728

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1440RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

GATCTATTCT TCATTCAGCA ATCAACAAGA GCTGGTGAAA CTTGGGCAAG AAGCTGAGCA 60
 AAGCGGTAAA TACAACCTGG CATTCAATGC ATACTGGATT GCAGGAGATA TCAACAAGGC 120
 CAGGGACGTG CTTTGAAGA GCGGACGCA TTCCGAGGCT GTGCTTCTGG CATCCACATA 180
 CACCTCAGAC AATGACGCCA TCAACGCTGC TGTAGAAAAA TGGAAGGAAC AACTGAACTC 240
 AGCTGGAAGA GTATCTATCG CAGAAAGAAT TATACTTTCC GGAGAAGACG ACTTCCCTGC 300
 AGCTCCCCAG ACTTTGGTCG AAATGGATGA CGGATCAGAG TCCGGTCTA AATAAACTAT 360
 AATTTTAAAG ATAACAGCAG GAATAAATTA ATTACCACGA AGGAAATTG TATGTACATT 420
 CTAAC TAGAC CCAATGGTAG AATTTCAATTG CGTAAACACG GCAACCTTAT CAATATCTTT 480
 CCGTTTGTCC AGTCCGACAA AGTAAAGTTC TTTGGATTCA GATCGGCATG CTTCCGGCTT 540
 AAAACGCCGC ACTTTGGTGA ATACCTTTTCG CAGACGCCGT TCTAATAGCT GGTCTTCCTT 600
 GCCAGTGTAT AACTTGCAAA CGAATGAGCC ACOGGGCTC AACAAATGCAA TTGCACATAG 660

CAGTGTCTGGC TTCACACAAG TCATCGACA TGTA

694

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1440UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

GATCCTACAG AAATAATCCA GTACAAGGTA CCTCTAATCT ACTGTGTTAA CATGGAAAAC	60
ATTTCGCCCTT TAGGCTTTTT CTTTTCACCG AAAAGGTAAC GTGTTCGAAA CATATATCAC	120
GGGTTCGAAA CTGACTAAGG TTGCTCATGC CTAAACCAGA TAGGCAGCAA TGGCAAGGGG	180
CTTGAGGTGG TACCAGAAAA GCTGCCAAGT CCTGCTGGGT GCTTACTCTC GCAAACGGTG	240
TATACTATTA GTGTGGAGT ATTTATTGCT TATTAAATAA CCGAATTGTG GGCTTAGAAG	300
TGGCGATTAT CACTGAGCAG CAGCGGCTGG CAGCGCAGAC TGCTCGGAA GCGAGCAGG	360
TGCGTTTGAG GCAGCGTTTA GAGCTGCAGC CGTGACCATC AAACCTCGC CGCGGAGGAC	420
GAGTATGAGG GCTAGCTCGA GGCGCATCAA GAGCTTCTTC GATATGCCGC AGACCTTGCT	480
GAAATACTCG TGGGAGTGCA CGGTGCTCTC CACAATCTTG GTTGAGACAC GTATCAAGGC	540
CACTATGAAG CGATGCACAT AACTCTCGGC GATGGGCCAG CGGATCTGCA CCGGACCGGT	600
TTCCGAAGGA GGCCATTTTA GCGTGAGGCG GAGTAACAAG CAGCCCGCGG TCTGGTAGAC	660
TATGGGCGCA AACATGCATT TGGCGTTGAT GCGTCTAGG TACTCGGTAT AC	712

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1441RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

GATCGTTAAT TGTAGCAAGC GACGACCAGA GATGGTCTAC CAAGGCGGTC TACGACAGAG	60
CACGCAAGCA GTCGGTCCOC AGGAGCAAGC CCCCAGGAC AGACCACAAG CACACTTGCC	120
GCGTCTGACC AAGGCCCTCA CTACCCGATC CTTAGAGCCA ATCCTTATCC CGAAGTTACG	180
GATCTATTTT GCGGACTTCC CTTATCTACA TTATCTATC AACTAGAGGC TGTTCACCTT	240
GGAGACCTGC TCGGTTTATC AGTACGACCT GGCATGAAAA CTATTCCTTC CTGTGGATT	300
TCAAGGGGCG TCGTAAGGCG ACCCGACCCA GCATAGATGC TGGGCTCTTC CAGCCATAAG	360
ACCCCATCTC CGGATAAACC AATTCGGGG TGATAAGCTG TTAACAAGAA AAGATAACTC	420
CTCCAGGGC TCACGCCGAC GTCTCCACAC TCAGTTAAGT TCGCGTGAAG AATCCATATC	480
CAGGTTCGG AATATTAACC GGATTCCCTT TGATGGTGG CCTGGAAAT CAGGCTTTG	540
AAACGGACTT CCCCATCTCT TAGGATCGAC TAACCCACGT CCAACTGCTG TTGACGTGGA	600
ACCTTTCCCC ACTTCAGTCT TCAAAGTTCT CATTGAATA TTTGCTACTA CCACCAAGAT	660
CTGCACTAGA GGCGGTTGCA CCCAGCTTTA CAGCCTAGGG CTTGCTCACT GA	712

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1441UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

GATCCAACCG AACCTTTCCT TCTGGCTAAC CTAGGTTACT TGTACTCTAG GCGAACCAGG	60
ACTTTTACTT TGAAAAAATT AGAGTGTTC AAGCAGGGC AAGCTCGAAT ATATTAGCAT	120
CGAATAATGG AATAGGACGT TTGGTTCAT TTTGTGGTT TCTAGGACCA TCGTAATGAT	180
TAATAGGGAC GGTCGGGGC ATCAGTATTC AATTGTCAGA GGTGAAATTC TTGGATTAT	240
TGAAGACTAA CTA CTGCGAA AGCATTTGCC AAGGACGTT TCATTAACTA AGAACGAAAG	300
TTAGGGGATC GAAGATGATC AGATACCGTC GTAGTCTTAA CCATAAACTA TGCCGACTAG	360
GGATCGGGTG GTGTTTTCIT ATGACCCACT CGGCACCTA CGAAAAATCA AAGTCTTTGG	420
GTTCTGGGGG GAGTATGGTC GCAAGGCTGA AACTTAAAGG AATTGACGGA AGGGCACCAC	480
CAGGAGTGA GCTGCGGCT TAATTTGACT CAACACGGG AACTCACCA GGTCAGACA	540
CAATAAGGAT TGACAGATTG AGAGCTCTTT CTGATTTTG TGGGTGGTGG TGCATGGCCG	600
TTCTTAGTTG GTGGAGTGAT TTGCTGCTT AATTGCGATA ACGAACGAGA CCTTAACCTA	660
CTAAATAGTG CTGCTAGCAT TTGCTGGTTG CGCACTTCTT AGAAGGACTA TGGGTTTC	718

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

EP 0 866 129 A2

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1442RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

GATCAATTGC GTCTTCATCC GATGAGACAT TTTGAAAATT GTTGAATAT TGGGCAACAT	60
CAGGGTATGG TAACACCTCC GGTTCCTAAC TTCTAATGG TAGCCTCGTC GCGGTGTAA	120
CGCATGGATC ATCAATGGAC GGTGCTGGGG GCGATCTAGA CACGCCCGAA TTGGGGCTTG	180
GTGTGAGGTT TTGTCGGGA CTCTCACTT TATCAGGTAT GACTATCACT TGATGATTCA	240
TTAGATTCCG TGTATCCACA ACATGGACGT GGCTTTGGTG TTCGAGATA AATAGTAGGT	300
CATCAAACGA GCGGCTAAC TTGCACACC TAAAGGACC GTTCTGTGCA TGTCTTGAG	360
TTGAAGGTAT CTCGCAAGA GCGGTGTCCA TTTTCTCAT ATGTACACC AGACAGAGGC	420
CGTTTTGGAA TATGTTAGC ATGTGACGT CGTTTTGCT ATAGCTTG TG TAAAGCCGT	480
TATCACCACC AGGCGAATCG TAAATAAGAT CTAGGACTTC GGATCTATCG ACCGGGCAT	540
ACCTTGGAAC GCACCTTG TG CGGACCAAT TTGAACCCA CTCAGGAGG GCGTCATATT	600
GTAATGAAAA ACAACCGCTT AGTTCATCTG TCTATAGACC GCAAACCTGC TGGAACTCC	660
CGAAACCACC ATCGTCTTCC CATGCTGTGA TATTGCGAG CAGTTTAAAG CAAATTTTAA	720
GT	722

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1442UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

GATCAAGGCT GGGAAATTGG CGTTGACTGG CTTGGGCTGC GCAGGCTCTC TGTTGCGGCT	60
CTTGCGCGCT CTGTTGCGGC CCTTGCGGCGC TCTTTTGTG TCTCTCTGGT CGCGAGACTT	120
AGGAGCAAAG GACTCGGTGC CATCAAATC TAGGAATGC TTGGCCTTCA AGTGCTTGGT	180
CTTGACGTTC TTGACCTTGG TAGCCTCCAT GAAGACCTCC TGCTTCTTAA CGAACAACTC	240
AGCGTCGTGC AACTTCTCGA CCTTTCTGGC GACAGGGGCC TTGTTCAAGT CGGAGTCTG	300
CTGCTCCAAG TAGCCTCCA AGGTGACGGC AGCTGCAGTG GCCTGCTCCT CCTCGGCAGC	360
GTCGGCGGCC AACTCGGCT CGGCAACAGC GGCACCAGCC TCCTCATGGC CCTGCTCCTT	420
CTCGTTGTGC CCCACGGCT GCTTGATCTT CTTGGCAGAG TCAGTCTTGC CGGTTCTCGA	480
GTGGCGGTCA AAGGTCTTTC TGCTGTCTT GCGTGGCTTG CCTGGCGCAA GAGCGTCTT	540
GGACTTGTTC TCGAAGGCC CGGCTGCTT GTCTCTGAAC GCAGCCTCGT TGCCGGTTGG	600
CTTTGGTCTG TTGTTCTTGG CACCGGATGG GTGGCAGAT GGAGGAGGCA CGTCCGCTT	660
CTTGAAGAG GTGGTCTTCT TCACAAGCTC CTTTGGAGGA GACACAACAA CGGTGGCGTC	720

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1443RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

GATCTATGCG	GTCCTGTGCG	CGTGCATCGA	CCAGCACAAG	AGCTTCGAAT	TCGATAGCGG	60
GAGCTTCTTC	TTTCAGTACG	TCGAAGGCAT	CTACTCGTAC	AGGACTCGCA	GCCTTCTTGC	120
GGGCTATCTG	CGGACGCACT	CCGTGCGGAC	GGCCAGCCAG	TACGCCAAGG	TCTTCTCTAGA	180
CCGCGCGCCC	TCGCCACGTC	AGGCGGAGGT	GCTGCTGCTG	GGCATAGTTG	CGGATGCGCA	240
CGCCATGCAG	CGGCTAGTGC	AGGAGTGCAA	AACGAGTGGA	GGCGTGACAT	CTGCGAGCTT	300
CTCGCTTCTC	ACAGAGTGCC	TCGACATATA	CCTGTGCTAT	GTGAACGATA	CGTTTTTGCT	360
GGGGCCCAAG	AGCAACTTCC	CGCTTGAAGA	TCTGTGGTGG	TTTTGCAACT	TGGTGGGTGA	420
CGGATATCT	CAGGCTTTTC	GTGCTGAGCA	TGATTATGAG	GTGAACAAGA	TGGCGCGGCG	480
GCTCTCTTA	CTCCAAAAGC	TGTATATTAG	GGATAGAAGG	ACCAATTTC	TCTCGCGGCG	540
CAAGGGGGAC	GACTTCTGGG	TCATTGCGGA	TACCACGGTG	AAAAACTGCG	ACATTACATC	600
TCTCCTTCTT	TACTTTGATG	AGTCTTACAG	AGAACAGTTG	GATTGTGTTCC	TGGGCGAGGG	660
CCGTGCTCGG	CACGAGGTCC	CAGCGGCGAT	CTCGTAGCGT	GGGAAAACGA	TATAAA	716

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 711 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1443UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

GATCCGGCAT TTACATCTGA CATGTAACCG GGTGGTTCIG TAGGTAGGGT GTTCAATGTA	60
AACTGGTCGC AGTTCGAAGT TGGGGTAGTA CTAAATTGCA ACCCCGGTGG CCGTGGTAGA	120
AGATGGCCAT CGTGAAGGIG TTCCACAAA CTATTGGTTT CACCCTCGGA TACTTCATCT	180
TCATAACTGC TTCTAACAA TACATCTCGG TCATAGTCTT CGTAGGCTGG TGGAGGCAGC	240
TTCATGCCGT TCAGCTTTCG ATATCCCCAT TTCTTTACGT TTGCTTCAAT GTAGACGAAT	300
CCGTAGGTCC CGAAATTAAC GTGTATCTTG CATGGGACAT TCGACCAAC AATCGGGTAA	360
AGATACTTAA TTTTCCAGCC CTTTATGTGG CCACCAATGC GTTCTTCATT TAACTTCTTG	420
CCATTGGCGG TGAAGAAAAC TGTGCGGCTC CGAGTTCIGT AGCCAATCCC GATGACGTGG	480
CCCTTTTCGC AGCGGGGGAA TAGTGAAGAG AGTTCCTGCG GGAGCTTAAA CGAGTTGTTT	540
AACCTACGTG CTCCATTAGA GTCATATGCA ACTGAGTGAT GGTGCTGCC GGAAGCCTA	600
AAATAGGGAT ACGCGATGT AGCAAGACCA AAGGAACTA TTTGGTTTTC TGAGAGATGG	660
CTGACCGGCG GGCCAAGCCT GTCACAGAGT CGAAGATCTT GCACTCGAAG T	711

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 736 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1444RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

10 GATCTGGTTT TATAGGTTCA CGAAGGGACT CTGGACGGG ACCCTGCTGA AGTGTGCCAA 60
 CATGCTGTAC TTCTGGCCG TGATGCATTT CTACGACGAC TACGAGCAG CGCCGGTACT 120
 15 GAAGAACATT GGGTACTCGA TCTTTATTTCT GAGCATTTGG ATGAATCAGG CACTGCATCA 180
 CGCCGGCCG CTATTCAGGG GGGACGGG GGGCGGTCC TGGTGGTGGC GGTCCGACAC 240
 20 ATTTGTGCTG CAGCCCGCAC TATATATCAG CCAGTTCTAC CTGCTGCTAC TGAATGTACA 300
 GAACCCGAGC TTTCATTCTA CGCCGAAGCT TGACATAATT AATCGCACGG TGCTGGTGGC 360
 25 CTACGTGCCC CTGGCGCTTC AGTGCTTTCT TCGGCAGCTG ACGAGCTAAG TCACTCGGGC 420
 AGGAGCTGCT CGTGAGCTC GTGTGCTATG CGTGCGCGT ATTCTGACG GGCATGAACA 480
 30 TCTGTTATCT CTAAATAGCG TTCTCTAGCT TGCTTAATCC TGGTTACCAC ACTGTGAGC 540
 GGTATATCTG CCTGCAAGGG ATCCAGCTCT GCGAAGGCTG CAGCGGTCTA CGGTGCATA 600
 35 CGCAGCATAC GCTGCTCCA GGGATGGAT ATCCAGCAGC TCGGCACAC TTCCCGCCCC 660
 TGCTGTTCCC CCAGCTCGTT TGTCCCGGC TCGCGCATC TGAGAAGCGC ACGTGTGCA 720
 40 CTTCGAGGGC ACGCTC 736

(2) INFORMATION FOR SEQ ID NO:666:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 709 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1444UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

GATCCAAATA CATCCGGTAT ATATGCTACT TGTGCCAGAA GACATGAAAA GCAAGCATCA	60
AGGGAGCTAA TGAGCATTCT ACAGGAAAAG GCGGAAGAAT ACTACGTTGA TGAATCAAA	120
GCTATGCCAG AGACTGAACT CTTGAGGAC AAAGAAGATG AAGAAGAACT ATCTGTGGAA	180
GAGCAGGTGC AGAAAGAGCT AGAGCAATTG AAGAAAGGCA GTGGTCTGT GGATACCAA	240
AAGAAACCGG TCCTGCAAGA GATTCAGTTG GGATGTGAAT GTATGGTCTT CATCAAGACT	300
AGAAGACCAA TCAAGCCGGA ATGCTTTGTC AAACGCCTAG TACAGGAACT TGCATGCTCA	360
GAAAATACTA CCAAGGTTTC GCGGTACGTC CAGAGATTGA CACCCATCAC TGATTCTGTC	420
AATGCTAGTC TAACAGAATT GGAAAACTC TGCAGAAGGG TGCTTGCTOC TCATTTCAT	480
ACTGACAAAG AGATAAAGTA CAAGTTCGGG GTCGAGGTGG TAAAACGTAA CTTCAACACG	540
ATAGACAAAA TGGATATCAT TAACTTGTG GCGAAGCAGG TGGTAAAGAG TGGGGATTGG	600
GGGCACTCTG TGGACCTAAA GGACTACGAC AAGCTGGTCA TCGTGCAGTG CTATAAGAAC	660
AATATCGGCA TGTCTGTGGT GGACAAGGAT TACTCTGTGG CTCTTAAAA	709

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1445RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

10 GATCATCTTC CGAACATACT CGAGGGAGTT CGGGTTCGGG AAGTTCTTGT ATCGTTGCAT 60
 GTAGTGAAT TGCTCGTAAT CGTCTGTAAA TAGAAAATTG GCGTCAATCA TGTGTGCCCC 120
 15 GTTGGACGGG CCGGAAATGA ACATGAACGG TGGCAGCCCG TAGCGCACCT TCTGGCCCCG 180
 GCACGCGCGC AGAATGCGAT CGTTGGTGGG CAAAATATCG CTGTACGGGA CCGGCATCTT 240
 20 CTCTTCTTGG ATGGGCTCCA ACACCGCCAT CTTCAACAAC TCGCGCCCAT AGCTCATCTC 300
 CATCTCCCGC GAGAGGAGAT TGTAGTGGC CTGCGGGGGC CGACTCGTC CCGACTGCTC 360
 25 CGAACGCAGC AACGTGACG TGCTATTCAA GCTAGTGTTC GAAAAGTGA CATGCTCGTC 420
 ATACGAGGAA CAGCTGAGCG CCATCTCGGT CACGCTGAGA AGGTACTGTT CTCCCGCGT 480
 30 GTACAAAGAC CCCGCTTGT ATGTCGAGCC TCTGGTGCAT TCCATTGGTG TCGCCATTGC 540
 TCTGGGCGAG CCTGATACAC TCGCCGTGA AATACTACCG CACCACGCA CGAACGACCT 600
 35 TTCCGCCATT CTTTGGTTC ATAAACCGG ACTACGATA TATTTCATCC TGCTCTGGCA 660
 TGTCGCGATG CCGTCTCCG TGTGACATAG CTGCTTATTC ATCTGGGGG TTCATTT 717

40

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

55

(A) ORGANISM: PAG1445UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

5 GATCCTTACT GACGAGGAAG AATCGAGCAA TAAAGTTGAC GCGGCTTCGA GCTCTAATAG 60
 CGSTAAGAGC ACCGCTAGTA AACGTCCAGC CAAAAC TAGG AAGCCTAAGG CTGACACTGC 120
 10 GGCTACGAAA AKCGGAACCA CCTCCCGGAT GCGCAAGACT GCTGCTTTGC AGGCGCTGCT 180
 GAACAAGAAA AGGGGGGGCTT CGGCAGAATA GACTACTGGT AAACGTAAGT AATAGTATAA 240
 15 ACTTGGTTTT TTAATCCCTG GCTATCTCAG ACTGCTAAAG CATGGCCGTT TAGGTGTGGC 300
 CTCCTCGGTA GATGGTTTGC ACCACGCAAG GTGAAAAAAA GATCACCAC CCTGAAAAAC 360
 20 GTTTAACTACT TGTCAATCTC TAAAGGCGCT GCAATCAAGG CATATTACCA TTGTGGAGCC 420
 ATGAATCTTG CCAATGAACC GAAGTTCCAA ATACAAGTTG ATGAAACAGA GGATACAGAG 480
 25 TGGAACGATA TTTTGAGGCA GCATGGTGTG ATCCGAGAAC GGCCACCTTC ACGACCGCA 540
 CAGCTOGAGG AAGCGCTOGA GGAAGTGCTA CNGAGACCAC ACGAGAATAG ATTAGAGAAC 600
 30 AAAGACTCTC TGAAGTGGAG GACTGGAAGA TGAAGAAGAT GATGAATTTT TGGAGTTTTA 660
 CCAACGTAAG AGAATGGCAG AAATCGAGAA GCAACAAAGA AGCGCAAGTA TGGGGAC 717
 35

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 775 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: PAG1446RP
 55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

5	GATCTGCAGG CTGCTACGGA GGAAGTGGTT TCGAGGTTG CTCGCTGAG TAAAGACCCA	60
	AACTTTCTTA GCATTTTTCG GCAGGAGCTA CAGAAGCTTA CTGGTGAGCC CCATATAGGC	120
10	GGCAAGGTGG ATGATATAAC GGTAGTGATG GTGAAGGTAG ACTAGTAGAT TGCACATATG	180
	TAGAATTACT AATATCATTC GAATTTCTGG CTTAAGACAA TGTTCCTAAT CCGCTCTCTC	240
15	TCGCTCTTCA ATCTCTGCTC GCGTCTAGT ACGTCATGAA CAAACTTGAC GTGGGTGGCC	300
	AGGCATATCG GCGGAGTTG AGTCCGCTTT CTGATTTCG TGAGAAAGT AAAGGGCACC	360
20	TTACCCGCTT CGACTTTTGA TGACAGATTG CTGTTGACCT GTGTGCTGGT CCCAGATCCA	420
	ACGATAGGAA TGTGTTCAT GGGGATTTTC TCATTCTTGC GGGATTTCTAA AGATTGTTGC	480
25	ATCACAGCTT GGTACATCTT TTCCATTTC TCTTCTGCTC TCCGCTCTC CTCCGACTTT	540
	AGCTTTCCTT CGTATCTTTC GTTATCTTTT TTGGCTCTA GATCTCTGTC AATAGTAAAC	600
30	ACGTCTGTGT CGTGTGAGT ATCTTCTTCA CTTTCACTGC TTGACGGGGA ATCACTATCG	660
	TGTTCATCTT CATGTTATC TTCTCTGAT AAGTGTATT AACGCTTCTT TCTTCTAAGT	720
35	CGCTGGAGTC GGCAGTGTCT CCACTACTAG ACTCGTAGCC ACTATCTTTC TCTCTC	775

(2) INFORMATION FOR SEQ ID NO:670:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 631 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
45	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1446UP

55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

5	GATCAATTAC ACTACTAGCA ATCTACTTTT CAACAATCTG ACTGTCCGGG AGGTAAACT	60
	CTACCGTGAA CAGCTGATGG TACTCAAAGA GCAGAGGTTT ATAGTGGAGG GCATGCTCGA	120
10	GAACGCCAAG AAACAGCGGC GTTTTGAAGA GGTTAATACG TTAAAGGAAA ATACCAAAGA	180
	GCTAGACAAT CAGATAGCCC AGCTCGAAGA AACCTAGGC GACCAGGGTT TTGTTTAGTA	240
15	TCTAGCATGG AGTTTTTTGC TTAATAATAA TTACTGTGTA GATGCCGCAG ATAGCATGTC	300
	GTAGCATAAT TGCGAATTTT CACCAACATG AAAAAGTGTA TGTGTATAAG GCATCCAGTG	360
20	AACTCCTAAC ATGCTGATGA GGTTTAAGT AAAGATATCA CTAGCAATGA ACGTAAGTGC	420
	AGTTTTTGAG CTTTATGTCC TCTGTAGAAC ATAATATTAA CGACAGGGGG ATAGGATGAA	480
25	AGAAGACAGC AGTTATTGTA GCTGAACAGT GAAGCCTGGT CTGGAATTGA TCGGTTCCCG	540
	AATAAAACCA GCAAGCTTGA CTCAAGCATC AAGAGAAACA CAGGTTTTAT CAAAAAGCTG	600
30	AAACAGGGTA TCACGAAAGA CTCGAAAGAT C	631

(2) INFORMATION FOR SEQ ID NO:671:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 703 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

45	(ii) MOLECULE TYPE: DNA (genomic)
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	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1447RP

50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:	
55	GATCCAGGAT GATGAATTTG ACGAGGAGGG GGGTGCAGAA GAGAATGACG ACTACTCAGC	60

GTTTAAAAGA TCCTGCATGT CCTCCACGT CCCC GGTTG TAGTAGGCAT AGCGCTCGTG 120
 5 GTACGGGCGG TCGCCATGG CCGCGCCAT GGGCGGGG CCATGGGCC ACCCGTGGC 180
 GTACATGTG TACATCGGC GCGCGAAGC GTCCGAAAGC AGCGGTAGG CCTCGTTAAC 240
 10 CAGCTTGAAG CGCGCAGG GTTCGTGCTC ACCCAGCCCC TGTGGGCAG CCCCCCGGT 300
 GTCCGGGTGG TACAGCTTCG CGAGCTCGTG GTACCGCTTC TTTAGCTGC GTGCATGAC 360
 15 GCGGTCTTC ACCAGTCCA GTACCTCGTA GGGCGTGGC TCCTTGCCCT GGGGCCACGA 420
 TAGCCCCCCC TGCCACCGG CGACGGTGCT AGCGCACCGC ACGTACTCC GACCTGACG 480
 20 TGTAAGCGAG ACCGCCAAG TCGCCAGTC CTGAGCAGTG CAGTGGGAG CGACAACATA 540
 ACACCTAAGC TCCTAGTTAA CGCTTTGGG ATGGAGATCT TGTGGTGCA TGACATATC 600
 25 CAGGACCGG CTCGGCTCC GCTGACTGC TGGCGTCCA GCTCCAGTT GCGCGCTTA 660
 GCCATATCGG CGAAAAATA AAGTCTGCT CGAGCGCGA TGA 703

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1447UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

GATCCAGCAG ACGCTCCGC TGGCTGTTG AGATGCACTG GCTCTTGGG GCGAGTGGC 60
 55 GGCAACGGC CCGCGGGC AGACGGGCC GCGCGGCGC CGTGGGGTA CATCGCACC 120

AGGTTCTGCA GCTCAAACCTC CAAGGCCAGC TTGTTTCTGT TCTTCTTGCG CTTCGGCTTG 180
 5 TACTTGTAGC CCGGGTACTT CTTCGGCTGC TCTGCTKCT CCAGTTCCGC CTGTGCTGC 240
 CACTCCTTCT TCTCCTCCGC CGTCAGTTTT TTCCACTGGT AGCTGATGAT CTTGCTCACC 300
 10 TCGCAGTTGT GCGGGATGTC CTGGCCGGAC TECTTCCAGT AGTCTGTCAG CAGCTTCTGC 360
 TGGTGGGACC GGAACAGGAT GAACGGGTG CCGGGCCCGG GGATGTGCTG CTTCTGCTTG 420
 15 TAACCAGCGC GCGCGCGCGG GCCTCGCCCG CCTGCGCGTC CTGTTCCGCC ATCCTGGTGC 480
 GCTGCCACTC CTGCGCGCGG GGGGGCTGGT GCGAGAAAAA CTTCTGTGCG AGAGGCGCTG 540
 20 CCGCGCTGCC GCTGGCTGCG CGGCTCGTCC GCGCGCGCTG CGGTTGCCT GCGTTGGTCA 600
 AAGGCAACAA TTGCCCCGAT CTCCCGCCGC TGCTGGCGCT GGTGTACGAT CCGTGTGATG 660
 25 GTCAGCTTCT GCTCCAATCA CAGA 684

(2) INFORMATION FOR SEQ ID NO:673:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 718 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1448RP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

50 GATCCGCTAC GTATACAACG ACATATTGCT ACGTATCGAA TGTGATGTGA CAACATGCAA 60
 GATTCTCAAC AACAAGCGCA AGTGGTTTAG TGGTAAATC CATCGTTGCC ATCGATGGGC 120
 55 CCGCGGTTGG ATTCCGGGCT TCGCATATT TTTCACAACA TGACACACT GTGTGGCTAT 180

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CGAGACGGAG TCCACTACGA GCATCGTCAT TTTTGTCTAT AATTTCACAAG CATATTGTAA 240
 5 CTATTGTGTC ATTGATCTAA ATGTGAGTC GATAGAATCC TTCAGCTCCT TGTAGCTAAT 300
 GATAATGCAG TTCATCTCGT CCGGTGTCAC CAAGATTATC TTTTCAGATA CGCCGGTGTC 360
 10 GAGTTTGTTC AGGCACCGGA GTACGTGGGT GAGGTCCATC ACGGATTTCG CGTTCTCGTC 420
 CACCTGGTGG AACACGTAAT CGTAGAACAG AATGATGGGG AACTTGTCCG CCGCCTCAGA 480
 15 CCAGTGGATG TCCATGCTGG ATTCCATCCT ACCAAAGATG AAATTAGCT TGCACATGAG 540
 CCTGAAGAGC CTGCCATTCT CTAACGCCG CGACAAGTGC TGCTCGATGT TCTCCAGTA 600
 20 GGTCTGCGAC GAACTGATTA TGCTAACAT CTTGTGGCTG AACAGGGCGG TGAACGCCG 660
 AATCGTCTTC TTCTGTCGG ACAAAGGTA CGCCAGCACC CGCTTGAACA GCGGGTCG 718

25 (2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 724 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1448UP
 40

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GATCTCGCCA GCGCTGGCAT CCGCAGCGCC GCAGGCGCCG CGCGCGCGCG CGCGGCGCGG 60
 GCCACTGGCG CACAATGCTG TCCCATAGCC CTCAACATCC CAACTAGCTA GTCACCTTGT 120
 50 GCAATCGGTC TACCGATGGT GTGTGCGGCG GGGACAAAGC CGTGGTGAAA CGGACACTTT 180
 TCAAAATGGG CTGATCTGCA GCAGTACAG ACCGATGAGC TGCGGCGACG GCGACAGCAG 240
 55

TCGCGGTTCG GCGCCTGGCT GCGCATAGGG AACTTACGTA TAGTATAGAA GGGCGTCTA 300
 5 CTTGGCGTAG GCAGCGAGGA TGTCGTCTGT GTAGCGGAGG TATTTCGCGT TCGCGCAGTC 360
 CCGGATGCGT CTCAGCGCCA GGTTCGGCGAA GATGGTGGCC GGGATCTGCG GGTCCAGCAG 420
 10 CTGCTGTTC TTCTTGAGCT CCGTGAAGCG GCGCAGTGCC TCGCGCGCCA TGCGATGCGC 480
 GAACTTGTTC CGGATGTGCT TCTGCATCTG CGTGTGAGCC ACCCGCGCGC CCACGGCGAC 540
 15 CCGCGCGACC GCAGGCTCTT CCGCGGCCAG CGTCATCGCA AAGTGGTTCG GCGCGGCTT 600
 CGACGAGCGG TAGCGCGCCC ACCCGGACTG TCTCGAGTT AGTAGCTGCC CCTGCGCTGC 660
 20 TCTGCGTGT ACATACATAT GCGTCTGTGC TCGCGCCCGA GCTCAGAAC ACCACACTGC 720
 CGCC 724

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1449RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

45 GATCCAAAGA CCGCGTGCTC GCACTTCCAC ATGTCTCCAA GCTGGACGG AACAACGATA 60
 TCTTACTGGC GGTGAAAGAA AGCCCGAATC ACAAATGCC ACATGCTGG AAGCAAGCAT 120
 50 CTCCCGAGGC CGACGCTCTA TGTAAATGCT GCGCCAGAGT CCTCCAGTAA GCCAAACCTG 180
 AATTTTTCAG AAATTGAAAA CTTCACCATG GCTCAGATG TGACTGCTTT AATATCCTGT 240

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AAATACAACC GGACTCTGCA GGTGATGCT CCCTCACTG GGGCCCCAAC TCTCCCTTGT 300
5 ACCGGGTGCG GGGTGGCTG CCTCATTCOG CTGCACTTC GCTTCCAGAG GGGGGCTTC 360
TGGGGTGGCG GGGGGCTGC CGGCATTCAT CGGGGGGGC TACGGCAGCC CACGGGGCGA 420
10 CGCGAGGCAG ACCCGCGGT GGACGTACCT CGCGGGCTCG CGGCTCTTCC AGCGCCTTTA 480
CGCGGGCCCT TCGTTCGCG CGTACATCGA CGTCTGCTG GCCAACGGG CGGTGCCAAC 540
15 ACTGCGCGCC TTCTGCTGC TCCATGAGG CACCGCCATC GCTCCTCTGG CGTGTCTGTG 600
GTGGGGGGTC TACAGCTGG AGTGGTGGC GCTGTTCGG CAGGGCTGC TTGACTAACC 660
20 GGCCGAAGCA CGCATCTGC CGTCRAGAG TTCTGG 697

(2) INFORMATION FOR SEQ ID NO:676:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 715 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1449UP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

45 GATCGGCTCA ATGGGTGCT GAAGCGTGT CTTTGTAAAG ATGACCTCAA CTAAAGGCA 60
GGCTCTGAT ATCTGTTTC TTTTMTAAC AGGTGAGCTT TGGAAAATT TTGGTTCTCA 120
50 GCTCATCTCA TCTACAATAG TATGTCTAGC AGCCAGCAA AGCTTGCGTA ACGCTCTAT 180
TCAATATGAG TAAGCAGGTA AATGATACTA GCAAGAATGG TCTTGACCTA AAGACCTGT 240
55 TTGTCCGAA TATTCGTTT GATGCTACGG ATGCAGAGCT GACAGACTTC TTCTCGAGT 300

TTGCACCTAT TAAGCATGCT GTGATCGTAA AAGATAATGC GGGCTCGAGC AGAGGGTTTG 360
 5 GGTITGTGTC GTTGTCTGTG GAAAGTGATA CACAGGCTGC ATTGGACAAG GGACGGAAAA 420
 CACAGTTCAA GGGCGTCTT CTGAGGGTGG ATGTTGCCAA AAGAAGAGAA CGTTGAAAA 480
 10 AAGGCGATGA GGCCGAGGCA CAGACCTCCG CGGAGGACGC GGAGAAGCCG ACTACTGCTC 540
 CCGAGGGTGA CGAGGCGCTC ATCGGGGCA AGCCCAAGCT GATCATTAGG AACATGCOGT 600
 15 GGTCTGCGG CGACCCGACC AAGCTGAAAA AGATCTTCGG TAAGTTCGGA GTGGTTGCGG 660
 AGGCTCCATC CCGCGCAAAG CGGATGAAA GCTGTGTGGG TTGCATTTGT CACGA 715

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1450RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

GATCAATTCT GTCTTGAAGT AGGTATTAAT CAATGGGTCA GGCTGGGTGG AATTGCTTAC 60
 45 AAAAATACCA ACCCAATCAT CTGTAAAGTT GGTGAGCGAT ACGTAGACAA TTTGCTCAC 120
 ATCAATCTTA TAATCGACAG CATAGGTGAG TTGATTATTA ACCAGTGTCT TTCCGATAAT 180
 50 GTAGAAATGG GATGGCGTAA GTATAAAGGT TTTGGGTAGC CTTTGGGCGG ACCTACCAAA 240
 TTTTGAATGT AGCGCTTGCC CATTGATAGA GAATACGACA TGATCATTAA TTCCAGCTTT 300
 55 CTTTTTGACA AACGCACCOCT TCGATTTTCTG CTCATTACAA GAAAGGTAGT CTCCCAGGAA 360

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TGCCTGTAA CCTAACAAAG ACATTGCACG CCTCTCCTTT CTGCCACCA ACAACTTGTT 420
 5 ACOGTAATCC CGGAGTTGTT CGAATTGGTT CCCATGTTTC ATCTACGGA TAGCAGCTG 480
 GATACGAATC GCAGAATCGA TACGCGTTG TAAAAACGC CGCCAGGCTC TCTGAATGCG 540
 10 AGATGCCATA TTATGCCAAT ACTTATCCCT CATGTTTTTC AAAGCAAACA AGGTCTCAGG 600
 TGTTTTAATA AATACCTTCG TTACACCCAA CTGATATTCA GTCACAGGAA TTGAAGTATC 660
 15 TCTCAAAATT AAATTGACAG CATCTAAGGT ATTACCTTGC CATGT 705

(2) INFORMATION FOR SEQ ID NO:678:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 699 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1450UP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

40 GATCGCAAGT TGAAGAGCG AGTATCCATA TGATTACTCG CGGAGACGC CCGGCTCGCG 60
 CATCAAGCCT CAGACAGTTA TCACTGGGCT CTCGAAATC GCAAACGCCA CCGGAAAGGA 120
 45 GGTCATCGTG ACGACCGGTG TAGGTCAGCA CCAAATGTGG GCGGCCAGC ATTGGACGTG 180
 GAAGAAACCA CGCACATTTA TCACATCAGG CGGCTCGGT ACCATGGGCT TTGGTCTACC 240
 50 GCGGOCATT GGTGCCAGG TAGCCAAACC CGATGOGATT GTCATGACA TCGATGGCGA 300
 CGGCTCGCTC AACATGACCT TGATGGAGAT GTCCAGCGG GTCCAGGCG GCGGCCAGT 360
 55 AAAGATATTG TTGTTGAACA ACGAAGAGCA GGAATGGTC ACTCAATGGC AGTCTCTATT 420

CTACGAGCAT CGTTATTCTC ACACCCATCA GCTAAATCCG GACTTCGTCA AGTTGGCTGA 480
 5 TGCAATGGGG TTCAAAGCAA TGCGCCTAGA GCGCGAGTCG GACATGGAGC CCATGCTGCA 540
 GGAGTTTATT AATTGCAAGG AGCCCGTGTG ACTCGAAGTG GCGTCGAGA AGAAGGTTCC 600
 10 CGTCTCTCCG ATGGTCCCTG CCGTAAAGGC CTGCATGAGT TTATCTACTT CGACCCAGAG 660
 GTCAGCGACA GCAAGCGGAG CTTGCGAGCA GCGGTACCG 699

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1451RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

GATCTTGGTG GTAGTAGCAA ATATTCAAAT GAGAACTTTG AAGACTGAAG TGGGAAAGG 60
 40 TTCCACGTCA ACAGCAGTTG GACGTGGGTT AGTCGATCCT AAGAGATGGG GAAGCTCCGT 120
 TTCAAAGGCC TGATTTTCCA GGCCACCATC GAAAGGGAAT CCGGTTAATA TTCCGGAACC 180
 45 TGGATATGGA TTCTTCACGG CAACGTAAC T GAGTGTGGAG ACGTGGCGT GAGCCCTGGG 240
 AGGAGTTATC TTTTCTCTT AACAGCTTAT CACCCCGGAA TTGGTTTATC CGGAGATGGG 300
 50 GTCTTATGGC TGGAAGAGCC CAGCATCTAT GCTGGGTCCG GTGCGCTTAC GACGCCCCCT 360
 GAAAATCCAC AGGAAGGAAT AGTTTTCATG CCAGGTGTA CTGATAACCG CAGCAGGTCT 420
 55 CCAAGGTGAA CAGCCTCTAG TTGATAGAAT AATGTAGATA AGGGAAGTCG GCAAAATAGA 480

TCGGTAACTT CGGGATAAGG ATTGGCTCTA AGGATCGGGT AGTGAGGGOC TTGGTCAGAC 540
 5 GCGGCAAGTG TGCTTGTTGGT CTGTCTCTGG GGGCTTGCTC CTGGGGACGG ACTGCTTGCG 600
 TGCTCTGTGG TAGACGGCCT TGGTAGACCA TCTCTGGTGG TOGCTTGCTA CAATTAAOGA 660
 10 TCAACTTAGA ACTGGTACGG ACAAGGGGAA TCTGACTGTC TAATTAAA 708

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1451UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

GATCCCTTAG CGACTCTCTC CACCGCTCGA CGAGGCCATT GAGCTCTTAC GAACTGCACA 60
 35 AACCTACTOG AACTCTGTTT CCAGACTTCT TTCTGTTTGT CTTCAACTGC TTTOGCATGA 120
 AGTACCCCCC AGGCTATTTT TCTTACCGC CTGGTGTITG TCTATATACC CGTTGTATT 180
 40 TTTGATAAAA AACTCAGCTC TTCTCTACG GCAGAAATAT ATATCCAGTC CTTAGCGCCA 240
 TCGGAAAATC TGCTTTTTTA CCGCTGTTTC TCCAGTCTT AGCACTGGCA GAAAAAGAT 300
 45 GTATGGCGTA TAGGCGCTGG CCCCOCGGAA AAAAAAAAAA AATAGAAAAA TAGAAAAATA 360
 AAAAGACGTG GCGCGCCCOG CCGGCAGACG AAGAAAAAAT AGGCGCCAC CCTTCCAAGC 420
 50 AGACGACAGG CGAGACATAA TAAATCCCA CACCAAGGGA AGAAAGTCTT GTGCACGCTC 480
 COGGCTCAT AGGCTGCCAT TCTGTTCCAT CCGGCTTGCA AACCCAGTAG TGGCATGTCA 540
 55

AAGCATTTGCT CCGACGCTCC GCTGCTTGC AGTGGACATC CTCTTCTTAA CCCCAGCCAG 600
 5 ACTTCCCATTA CTTTGCACCTT CACATAGCAT ATCACTTTTC AGATCACTAC GTGACATTTC 660
 GTACGGAATG GCACTCCAAT GCGACAAAC CTCTTCTTAC CCGTGACTT ACCCCGATGT 720
 10 GC 722

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1452RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GATCAAATGT GGCTCTACAA GGGCGAAGT GCGAGAGAAT ATTAATGAAT CAGTTCCGCT 60
 35 GACATATTTG TATTGTCAAG GTATTCCACA TTCTTTGAG TACGTATGTC CGTCTAGGAA 120
 TGGCTGGCTT AGTAAGGCTT AATATTAAC TAAAAGCGCA GCAGTGTAAAT CCATCTAGTA 180
 40 ACTAACACAT ATCATTAGC ACATGTTTCG TTCAGTACTA CGTCATTCTT ACGCCGTCCC 240
 TACTGTGAAT TACACATGGT CCTCGAGAAG CCTCATAAGA TTCTTCACTA GCGATGAGAA 300
 45 GCGAGCTCCT CCATCGCTTC CGAGAGAAGA GCAGAAAGAG TTCGAACGGC TTCAGAAGAT 360
 TGCACAGTCA CAAGCTGCCA TCGACGAGTA CAACAGACAG TTGAGAATG ACCATAAGAA 420
 GGAGTCAGCG AACTCTCCCA TTCTCAAGAC AGAAATAGGC TCGTTCTCAC CGGAATTCAG 480
 50 CAAGACGTTG CCAGAGTTTG AGGCGGACAA GAATCCCGAG ACAGGGGAGA TTGGCGGGCC 540
 55

GCGCAAGAC CCACTGCGGT ACGGGGACTA CTCATACAAC GGCGGCGTGA CGGACTTCTG 600

AGGTATAACT TGTTGTTTATA TGTTTGCAGG TTGGTTAAAT ACATAGCTTG CGCTCCAAC 660

CTCTGCGAGC TGCAGACAGG TTGTGCGTGC ACTCCGTGAT GAATTTGAG TCCAGCTTT 719

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1452UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

GATCAACCAAC TCTACAGCAA GAAATCCTAC GCGCAGCAA AGCTGTCTC GATGTTCTTC 60

TATTCTGTAA ACAGTTTGTT ACTTCTGGTC GCTTGTATCT GCATGCGCTA TCATCTTTTC 120

ATCTGGAGCG TTTTCAGCCC GAAGTTGTGC TACCTTCTGG GCTGGAACAT CCTCATCCAC 180

TTTCTCACTG AGACGGTGCT TGAACCTTTC TTGCTCATGG TGGGGGCTG ACTGTCTCTA 240

GTTCCACTTG TATAATATTC CTTCATCAGT GAGAATCTCA TAGTATTGTC ATATATTAGA 300

TATTATCTAG GTCATGTTTT AGAGAATAGG TCTCTTCCGA AAAAATTGGC TACCACTGCC 360

AATCATTACA TGTCAGAACC GACCATCTCC AAGTGTGAA CCGTCCCCAC TGCAAATGCT 420

CTCACTTAGA TCCAGCTTCA GACGCTTATT TTCTGTTTCC TGCAGGGTTT ATGACCAGCA 480

GGCGCAGAAG GCGTGTCTT CTGCCCCGC TGGCACCCG CTGAATCTGC TTATAAAGAA 540

GGGGGGAAG GAGCGTTGG CTCTCGAAGA TCCGACTACC CGAGTGGTTA TGGAGGTGC 600

TTGACCTGAG GCGCAAGCOG CAAAGCTGGC AGAGGACCCA TTAAAGCOG GAAGAAGGCT 660

5 CTGCGGCGGA TGAACAGAGA ACACATCCAG CAGCAGAACT TCCTGGGAA GATGTGAA 718

(2) INFORMATION FOR SEQ ID NO:683:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 724 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1453RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

30 GATCTTAATT TAAAATTTTA ATTAAGTATT TATAATTTAG AAATATATAA TCTAGAGATA 60

TATAATCTTA AAATCATAGG TAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAATA 120

35 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA 180

ATTTTATTA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAA ATGTTATATA 240

40 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTTAATATT 300

AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTA TTAATATTAA GTGATATATA 360

45 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420

TTTCATAATA TTTATTTTTA TTAGTCTAGT AATATTTCTA TTTAATAGTC TACCCTTTAA 480

50 TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC 540

TAATAATTTA TTATCTAAAG TATATAAATT AATTAAATCT TTTTATTAT TATTTAAATT 600

55 ATTATTAATT AGTAAATTAT ATTTATTTAT TTTATTAACA TAATTTTTTG ATAATAATAT 660

ATCATAATTA AATGGTAATT TATTATAAT TATCTTTAAT GAATTTAATG ATAAACCATT 720

5 ATTA 724

(2) INFORMATION FOR SEQ ID NO:684:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 732 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1453UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

30 GATCAAAATT TCAACAATTT CCATTTCATT TAGTACTACC ATCACCATGG ACCAATTGTT 60
 ACATCATTTA GTTTATTAGG TTTACTATTA ACTTTAGCTT TTACTATACA TGGTATTATT 120
 35 GGTAATATTT ATCCTTTATT ATTATCTTTA TTAGTAGTTT TATTACTAAT AACTTTATGA 180
 TTTAGAGATA TTGTAGCTGA ACTTACTTAT TTAGGIGATC ATACTTTAGC TGTAAGAAAA 240
 40 GGTATTAAC TTAGGTTTCTT ATTATTGTT GTATCTGAAG TATTAATTTT TGCTTCTTTA 300
 TTTTGAGCTT ACTTCATT C AGCTATAAGT CCTGATATTC TATTAGGTAA TGTGTGACCA 360
 45 CCAGTAGGTA TTGAAGCAGT TCAACCAACA GAATTACCAT TATTAAATAC TATTATTTTA 420
 TTAGCATCAG GTCTAACTAT TACATATAGT CATCATGGTT TAATTGAAGG TAATAGAAAA 480
 50 CAIGCTTTAT CAGGTTTACT TATTACTTTC TGATTAATIG TTACATTTGT ATTATGTCAA 540
 TATATTGAAT ATAGTAATAC ATCATTTACA ATTACAGATG GTATTTATGG TTCAGTATTT 600
 55 TTGCTGGTA CTGGTTTACA TTTCTTACAT ATGGTTATGT TACTAATTAT GTTAGGTATT 660

AATTATTGAA GAATAAGAAA TTATCATTTA ACATCAACAC TCATGTAGGA TATGAGACTA 720

5 CTACTATTTA TT 732

(2) INFORMATION FOR SEQ ID NO:685:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 714 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1454RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

30 GATCATGCGT CACGGGCGTG GAACATGCAG GTGAGGGGTA TGTACCCCAT GTTGCCCTAT 60
 TTTTTCACCT GAAGCGGATT GGCTCTTGTT TATACAGACT TTCTGCATC CCTTGGGGGC 120
 35 CAGAGCTAGG GCTAGAATC CGTGTGTAA GCGTTGGGCA CTGATTCAAC ACGAGCACAA 180
 TTCCAGTGCT GCTGTAGAA ACGAGGCCCC TGAAGTATAT GGIGATATCC ACATTGCOGG 240
 40 AGTATAGTTC TCTGTGGGGG CGACTTCATG CCATGTGCAT CTCGGGCTTA CTCCACAGCC 300
 GCACACGCTG CATTTGTTTG GGAACATCAT GTGAAATACT GGTATAGAGC GCATTTCATA 360
 45 GGGGTGCCAG CAGCTGTAAT AGGGCGGCAT ACCCGCTCT ATTTTCATGIG TTCATGTGCT 420
 AGTTTAGAGG TATTTTGTAG GTGCATGGGT TATGGCTTAC TTTCATATG GAGATCTCAT 480
 50 TCGCTGTAA CGTATATAAC TGAGGTAGCC GTAAACTTGC ACTGGTTCCC ATTGCCAGAG 540
 CGAAGCTACA ATAGCACCAT CTGGCTGCAA GTTGTGAACA ATGCATTGGA ATCGCATACT 600
 55 CTTTGGGGC TGTGCGCTTT TGCTGCAACA ATTAACAAAT GCCTTTGATG AAGGAGTGCT 660

AAGGAAATGT TATGAATCTG GTGTATGCCA CCGGAACAGG CATTACGGAG AGAA

714

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1454UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

GATCAAGCGC TGTATGGTTC CCGGAGCGCC AGTAACAGCG GTCTGTACG ATTTCACGA 60
 TTCCAACATG GACGATGATG GCTCCAAAGT TATGTTCCG ACCACGCTTG AACTCAAAAA 120
 GGTTTTTCAG GCTATTCTGT TTGAGGCCAT CAAACGGGG CTGCAAGTGT TTCCATTAG 180
 GAATATTGCT CCTATCTTCC GACAGGTGG ATTCAAGAAC GTAAAATATA CGTTCGTGAC 240
 ATTCAAGCGC GCGATTTCG TGAATGAAAT GGGTTCTGT AAGAGCTAC TTGCAACGTT 300
 TCACTACGAT TTTCTAGTGC GAACCTTTTT AACTGATCGT AGTAAGTATC CAGTTGGAAC 360
 TGACCCACAG ACACTGCCGA GGAGGTACAT TGATGAGCAC ATGGGCCAAA TAGATGACAA 420
 TGCAGGATGC TTGCGTCTTA TTGCAATCAC GGCGGAAAA CCAGAGTAGG TTTCCACCGT 480
 TGCTATTGCT ACCCGGGGCA ATTCTCCGG TCATTATATA TGTTAGCAGG TGTCAATACC 540
 TCCTTACAAC CTAATATTTT AAAACCTAAT ATCTTCTGCT CCTTAGAAAG AGCCACTTCC 600
 TTATATGTTA ATATCTACCG CTAGTTCTAT CTAATAATTT TATAATTTTG ATAAATCTTG 660
 ACGTACATCT TATCACTAAG GAAGATCTCA TCACAAACTC CGCAAAGTGT TTCATATATA 720

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1455RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

GATCTCTTCG ACATAGTGTC TTAATAGGCC TGCTGAGGAC TTCACTGAGA AAGCTTCAAT 60
 AGCGGGCAAT GGCCCATCTC ATCAACACTT AAAATTTTTC GTGGCAAAG AAACAACACT 120
 GGAATCACGT GACCACACAA AACTCAAGAT TTA CTGTGTA AGGGGAGCAG GCTACGACGA 180
 CTCTCTTCG CATGGTAACT CGCTGCTGTC CACTTGCCGC TTGCGAGCCT TCTTTGCTGA 240
 CGCTGCTCTT TTCTCTCTT CTAAACAGCCT CTCCCGGTTA GCTGTGATGT AGTGGATGAA 300
 GAAGTGGCCA TCCTTGCTGC GTTTCGCATC ACGCAGGAGC GTCTCGACAT CGTCGTATAT 360
 ATCAATGGGT CGCTTTCGCA GTTGGTTTAG CAGCTTGTTA TCACGCCCTG CACATTGCAA 420
 CTTCGGATG GCTTTGGTGC ACTTGAACGA CACCTCGCCC GGTTTCATAT ATCCAGATTT 480
 GCGCAGGTTG TGCCAGGGCG TGCTCACAAT GCTACATTGT GCGTCTTGT TCCCTTGTTAC 540
 AGACTCTGAC TTGCACAACCT GCAGGCAGGC ATGCAGCACA TCCCGGGCA CGTCGCTGGA 600
 GCTCTGCTGC TTTGCATGTA ACTTGAGATA GACATGTGGC CTGCCATACT TGTCTACGTT 660
 GGAACCAGAA GTAGTTTAAT CCGGTACCC GTGCTTGAAC AAAAGGTGCT TC 712

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1455UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GATCCCATCA CATGAAATGT CTAGAACTCC CTGCATGACG CGAATGAGGC CAAGAATGTC	60
TGGTGGGCTT GGCTAACCGA TGTTOGCAAC TGCAACAAGG GGTACCTGGT GTTTATAGCC	120
GTATGTGTC ATCCGGGATT CGTGCAACAG GAGAGAAGAA CCGGACCACA AGGAAACGGC	180
GTAAAGCATC TAGAATCAGC AACCTAGAG AACGTTTGTT CGTCGTTGGC GCAAGAGCAC	240
GGAGCGTAGG GGCTGGGAGT TCGGTGGCT ATTCAATCGT GGGCAGCCCG GGTATATAAG	300
TAGGGTATGC GTCCGTTGAA CAGAATGGAT CCGTCTCAGA ACAATACCAA AATCGCATTT	360
GGAAAAACAA CCACTAATAT GAAGTACACC TCCGCTATTG TACTCGCTCA AGTCGCTTTT	420
GTTGCAGCAC AGTCATCCTC GGGGTCTGTT ACCGGCAGCG CTGCCCCCGC TCCGGGTGCG	480
GGGTGGGGCG CAAGCATTTT TAGCACCAGC ACAGTCACCG CCTCAGGTTC TGGACCAGGC	540
GCGAGTCCG GTGCTAGCTC CGGTGCAGCA GCGGGGGCG CTGGGGGGGC CGCAGGTGGC	600
GCCGCATGTG GCGCCGAGG TGGCGCCGCC GGTTCCTAACT CCGGCAACTC TGGCTCCAAT	660
GGATCTGGCT CCGGGCCAGA AACTCTGGA ACAGAACACT CCGGCCAGA AACTCTGGA	720

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1456RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

GATCCACGCC	GCGCTGCTGA	CCAACGTGGT	CATCATGGGC	GGGACCTCCC	TGCTCCAGGG	60
CCTGGAGCAG	CGCTCGTCA	ACGACCTCAG	CCTGCAGTTC	CGCAGTACA	AGCTCTCTAC	120
CTACGCCACG	CCGCCCCACG	TGACCCGCCA	GCTGCAGAGC	TGGCAGGGCG	GCGTCAACAT	180
GTGCCACCTC	CGGACTGGA	AGCTCGGCTC	CTGGGTCACC	AAGCAGGAGT	ACCTGGAGTC	240
CCTCGACAAG	TAGCTGTGTA	GTATGTAACC	GTATGCCGCG	ACCTTGCGGT	TTCTTTCCCG	300
CTCCCCCACC	CCCATGAGC	CCCCCGCCCG	CTTCGCCGCG	TCCCACGCGC	TGGCGCCCCG	360
CGCGCCCCGC	CGGACACCG	TGAGCTCTA	CCTGACTAC	TGCTGCCCCCT	TCTCGCGCCG	420
CCTCTTCTCT	GCTTGGCAG	ACGCCCTTTT	CCCCCGCGCG	CGCGCCGACT	CGGCTTTCCA	480
GATCGTCTTC	AACCACTCA	TCCAGCCCTG	GCACCCCGCC	TCCCAGTACA	TGCACGAGGC	540
CGCCCTCGCC	GTGCCCCGCC	TGACCCCGC	CGCCTTCTCT	CCCTTCTCGC	GCGAGCTCTT	600
CCTCCACCAG	GACCGCTGGT	TGACACGCG	CACCGCCGAC	AAGTCGGCGC	ACGCCGTGTA	660
CCGCAAGCTC	CGGACTTCGC	GCGCGACGCC	GCGCGC			696

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs

EP 0 866 129 A2

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1456UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GATCTGGAAT ATTACCGCA CAACTTGGC GCTGTGCTTC CACACCAGCC TCCGGTACCG	60
CTTCACGGCC ACCAGCTCCT GCAGCAAGCG AATGCACACG TATGCCAGCT CCATGCGCTC	120
CAGATTAGTC AGAACCCGCA GGTAGTTGGG GTTCGACACC AGCGCCTCCA CCAGCTCCTC	180
GCTCTGCAGC CCTCCTGGA TCAGCAGCGA GACAAAGTTG AAGCAAGACA GCAGCAAGAA	240
CTGGTCGTCC GCGCGCTGT CCGTCAGTGT CGACTCGTAC AGCTTGCGCA CAAGCTCCGG	300
GCCCTTCCTG AAGTACCGCA GCACCTCGTG CAGTACTTGT TCGCTCGTGA ACAGCTCCGA	360
CAGCAGGTTT AGCACCGGCC GCTTCGCATC CAGGTTGTTT GACGTGCGCA GCAGGTGCAC	420
CAGCGCCTGC ACGCCCTGTT CCAGCGGCAG ATCCAGCGCG CCGCCGCGCG CGTGTTCCTAA	480
CAACGTCGAC TCGAGCTTCT TGGCAATCC CCGTCAAAC TCGCTCAGCT CCGGCGAAGC	540
CACCAGCGCG TCCAAGCCA CATGCCTCGA GCTGATCGTA TTGCGGATAT CGTTGAAGTG	600
CGTGCTATCA AGCAGAATCT TTTGAACCCC CTGAGCCACG GGCATCGTCA CAGCTAAGAT	660
CTACGCTTCC ACGCCACCGT ACTGCCCACT TTGAACCCG TGGGACTAGT CAATATCTGG	720
CGTGGTCTGG CGGACTCCC	739

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 688 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1457RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

GATCAATATC GGGACGAAAT CTGTTGTATC TACTACGGC ACGGCGACTG CGCCCAGCGC	60
ACCAGGATCT CAGGCTTGGT CAGCGAGTCC GGATTGTGCA GCTAAACAAA AGAAAGATTTC	120
ATCTCCACTA CCTCTTGACT TACCTCCACC GAAGGATTTT AGCAAAGAAA TCGAGGAGAT	180
TATAGAACAC GATTTGACTA AATTGGCCTT TCAGAATCCT CTTTTTAAAG ATGAACTTCC	240
ATATTGGTTA CAGGCCAAGA GGCCTATGAT CCAACCGTAC AGCACTATGT CTGAAAGAAT	300
GTTGAAACAG CTGGAATCCT CATTACTTAA CTGCCAGAT TCGCTTGACG CTGACACACC	360
ACATCTCTAT CAACACCCGC TCTCTTTACC GCATCCACC TCCATTTTCT TCCCTAGTGA	420
ACCGATCAGG TTCGTGGCTG CTGGCTGGAA TAACGATAAT ACGTCCACTA AAGATATCTA	480
TGGAAAACT TCTATGGTTC AGATAATGAC CAAGTTCGAT TTGGATACCC TGTTTTTTAT	540
CTTTTATCAT TATCAGGGAA CGTACGACCA ATTCTAGCT GCCAGGGGAA CTAATCATCC	600
GTGGGTGGAT ATTAAATAGA GTCAATCGGT GCTGGTTTGA CAAAGAAGTT GAAAAGCTGC	660
CCCTTGAAT GGATCAAAAA GAAGAGGT	688

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 711 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

EP 0 866 129 A2

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1457UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

GATCGAGGAC TTGAAGCAGT TCCGGCAGGT CCGGTCCAAG ACCCCTGGGC ACCCTGAGTA	60
CGAGCTTCCC GCGGTGGAGG TGACCACCGG CCTCTAGGC CAGGGTATCT CCAACGCGGT	120
TGGCTTGGGG ATCGGCGAGG CGAACTTGGC TGCCACTTAC AACAGCGCG GTTACGAGTT	180
GTOGGACAAC TATACGTACG TGTCTTTGGG CGACGGCTGT TTACAGGAGG GTGTGTCTTC	240
CGAGGCTTCC TCGCTTGCAG GCCATCTAAA GTTGGGCAAT TTGATTGCGT TCTATGACGA	300
CAACAAGATC ACCATCGATG GCCACACTGA GGTGTCTTTC GACGAGGATG TCTTGAAGAG	360
ATAAGAAGCA TACGGGTGGG AGGTGTTGAA CGTTGCCAAC GGTGACGAGA ACTAGAAGAC	420
ATTGCCAGTG CCTTGGAGCA GGCCAAGAAG AACAGGACA AGCCAACTTT GATCAAGTTG	480
ACGACCACTA TTGGGTTTGG CTCTTTGAAT GCGGGCTCCC ACACTGTGCA CGGCGGCGCA	540
TTGAAGCGGA TGATGTCAAA CAGTTGAAGA CGAAGTTGGG CTTTAACCCA GATGAGTCTT	600
TCATTGTGCC TCAGGAGGTT TATGACCTCT ACCACAACAG CACTATCCAG CCAGGTGCGG	660
AGTCCGAAAA GGAGTGGAAC GCTCTACTCG AGAAGTATGC GGGTGAGTAC C	711

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 688 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1458RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

GATCCGCAGT AGCTGATTGT TCGGGTGGCC AGGCGAATAT TGCTGGAAGC GGTTCAGGCG	60
CGTATATTTC CTCTGGGAC CGCCAAAGTA CCGGCGAGG TTAATCTTTC TGGTCGTAAT	120
AGAGAAGTTG CGCACTGCCC TAGCAAGTGC GGTGCTAGGT ACGGGATTTA GCTTCGCCAG	180
TAATGGTGTG AAGACGTTGC GAAATGGCAC AGACGCTGT ACTGGTCGCA CTTGCAAGTG	240
GATAGCGTTG CTAAGAAAGA AACACCGCCC ATACGAGCGC GTGAACGTAG ATAAGCTCAT	300
GGTCAGCAAT CAACAAGCCT AATGATGATC TTCCTTACAA AATGAGGTTT TAAAGCGACG	360
TTAAAAAGGG ATGCCCAACG CTATGTTTGA CACCTATGCA ATATCCGTAT GAATGACTGT	420
GTATCATTAA CGACGGTACT TCCTTACAGG GCAATGGCAG GATGGTAAAG CCGAGTAATG	480
TCCAATAATC ATCATATATA CTCTAGTTAT ACGCTATGAG GGTTCATTTC ATGTATTGTT	540
CGTTGGCTTA TGGCTATGC TTCAAATTGC ATGAGGTTGG GCAGCTGCC ATTGTTAAGT	600
GCGGGTGGCA TGTTCACTTT CTCTAGTCTC TTTTGTGGGC GGTGTCTTC GCTTGGTCC	660
ATGTCAAGGT CCAAGAGATC ACAGAAA	688

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 724 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1458UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

GATCTGTTGC ACCTGCTATT TCAGGCAGAT TTGTGCTGC AGCAGCGCAT GGCCATACTA 60
TCTGCTTTGG CGCTGCTGC GCGGAGTTG CGGGGGCTGG AAGACAAATA CGTGCTCAAA 120
CCCGTCCTTG ATTTCCCCAC ACGCGGCTG CCCAGAAATG ACGCACCATC AAGAGCCCTT 180
GAAAGCGCG AATCOGGTAC AAGCTCCGAG GGGACCATCT CTGCACACCA CACCGTCTGG 240
CGGTGCGSCA AACTTGACTC AGCGCCAGCA CCAGAACGTC CGAACGCCCTT TOGGAAGCAT 300
GCACCTGCGT TTTTCTTCCC GCTGCGGCAC CGGTGGCTGA ATGCCATCGA CCTGGGCACT 360
TTTGACGCCC TGTTCAAAAA GCACTACCTA AGCACCCCTG GCCTTATTCT TGCAGCCGCC 420
AACCCGCATG CAGAATTGTA CCGATGTCC GAACTCATGA GCTACGTTTT GCAGGACGCT 480
GAGGCGCAG ATATCAGCAT TGAGTAGCCC GTGCGGCATG TGTACGCGCA TCTGTGGACA 540
ACTCCTGCTT GCAAACGTGA TCCCGACCAC TACCATGCAT TAGTATGAGA TCTATAGAGC 600
GCCAATGCA CGCCTAGAGA GATGTGAACC TCGCAATGCA TCTCTTGGGA GTCTCTGTGG 660
COGGCAGTAT CTGCTAGTAC ATACTCTTTG TAACTCTACA GAGATGTGAA GTCTGTGTAC 720
COGG 724

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1459RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

GATCATGCTG GGGCATATCT GAATGCTCTT GAACAACCGA CTAGATTAAT GGAGCCTTGC 60
 ACTCAGAGGC TTGGGCAGGA TGCAGCTTAT GCGGGAGCGG CTGTTGGAGC TTTACAATAC 120
 CAAGCAATAT GTGGTGCTGC CCCCAGATGA GACAGTAAAA CTGCAGCGAG AGGTGACGGC 180
 GAGCCTGAAC TCAGCAGATC CAGGACTCAA CGACGTTGAC CGCATGGCCC TAATGGAGAT 240
 GAACTTCTAT TTGTTGGTGT ACATTGGCGA AGAAATAGAA GCAGACGTGC TCTACCGCAC 300
 ACTTGTGGA CGTATAGGTG AGAACTCGCC CCGGATGCAC CTCATGAAGG CTACGTTACT 360
 GCAGGTTACA GAAGGTGATC CCGCTGCCGC GAAGTACCTG AAGAACTGC TTGAAAAGCA 420
 GCTTGAATAC GATACAGATT CCGTGGATTA CCTGCAGGTG GGCAAGAAGC TAATTGCGCT 480
 GGAACGGCCC GCGTTGTCCA CCGAGCTGTG GATGAAAAAG CTGCTGTGCG CTGCTAGAGA 540
 AGTTTCCACT GGACGCCGAA CTATGGTGG 569

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 572 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1459UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

EP 0 866 129 A2

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GATCACGTGC CTGCGACATG GCGACTTCAT CCACTGGGCG CCAGCTAAGT GGTATATGAC 60
 ATTATGGCCG AGAGGTTAAG GCGTGAGACT CGAACTAAAT TGAGGGATCT CTTGGGCTCT 120
 GCGCGGCAG GTTCGAATCC TGCTGATGTC GTTATTTTTT GCTTGCGCGG CCTACGGGG 180
 GCTGTATTTT GCTTGTTGCT ATTTAGATAA ACGAGATAGC TAAACTATGG GTAGAAGTCG 240
 CGTACTTCC CGTAGTAGTA GGCTGTGCGG AAGCCGCGA GGGCGGTGAG CACCAGCGGG 300
 ACGGGTTTGG CGAAACGCGA TGGCACGCTT CTGATGAGGC CGGTCAACAG CATCAAGGAG 360
 CTCGGGCCAA GGGCGAGCTC GAGGCGGCCC TCTGGGTTCT TCCGAGCAA GTACCGTCT 420
 ACAGCGTAGG TGCTACCAA AACGAGACCT GCAGCCAGCG AGGCACAGA CCTTTTACGC 480
 CAGTAGCCCA TCGAGCCACC GATGACGGTG AGCGCGGCGA GAGTGAAAGA GGGATGTTCC 540
 CTTGGGGTGG TGGTGGGTGG TGCTGTGGGG AA 572

(2) INFORMATION FOR SEQ ID NO:697:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 688 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1460RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

50
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GATCCGGGTG GAGACACGAA AGTAGACAGA CACGGACGGC TGTTGGGTGG AAGGAAGTAC 60
 CTGTTGGATA CATTCAGCT GCGCCAAAAG ACACATAATT TCTATGTGCT TGTCAGCAG 120
 CTGATAGAGA TTTTGCAATT CGAGGGGAGC GGCTCTGACT TTTTGCACTT GCATAATCAG 180

CTGTACCCGC TGGAGCTCAA AGACAACGAG CGGGCCTTGC TTGCAGAGGC TGGGTTGATC 240
 5 AAAGGCGAGC TGGGCTCCCC ATACTACGTT ACTGCACTCT CTTCATACAT CATTTTGTGT 300
 GCTGCTATTG TGGGAGGGG CTGTAGGATA ATAGATGACT ACTGGGAGCA GGCCTTAAAG 360
 10 GAGCAGGGAT TCACCATGCA CCACCGTGTA TTCTCTCTGA ACGGCACGCA ACTTTCATTG 420
 CTACGCCTGC TGAAACCCCC GCGTCCAGAA TCGCATCAGC AGGGTGAGAA GCTGGATACC 480
 15 AACTGGCTAC AGAAGTGGGA GGATCCATAC CCAACGATCC AGGAACAACC AAATGCTGAA 540
 GCACGGGGG AATAAGCTAG AGAACAGGC AGAGGTGAGC ACATAAGAT GATTGTTCCA 600
 20 GGTCAAAGTA TTAGCGGCAG TATAGAACTG AGCCTAAATT ATAAACTTCC TAAGTACCAC 660
 TACAAAAACT CATTTGCTAA TGGGTTGA 688

25 (2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 649 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: PAG1460UP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

GATCCAACAA TTCCGCGAGC GCGCTCCAG CGTCGTCTC CGTCGCATCA AATGAGTCCA 60
 50 CGCGTGTCTC AATCCGCGAC AGCTGCGGTC CATGCGCCAC CTCGAAGTGC ATCCGCGAGC 120
 CAAACAGCTG GATAAACAGC CGTTCTGTCT CGCACCCCGG CCGCAGCTGT CCAAAGAGCG 180
 55 CCTCCGCACC AGCTGCTATA TCATCGCCCC AGAAACTCTC TACGAATGCC CCATCGCGG 240

TGTACCTCGT CGTAGTTGTG CATGTGCTG CCTCTTCCG CTGAATTTTG ACAGTCTGGC 300
 5 CCCCCACCCC AGCTCCGGAA CGCTACGTAA TACAACACAC AACCAAATGC OCTACCCGAA 360
 GGTGCAATC GTCTTCTGCA CCGCTGCCG CTGGGGCTTG CGCGCAAGCT GGTATGCTCA 420
 10 AGAGTTGCTA CAGACTTTTG GCGACTCCCT AGCGAGATT GCCCTGTAC CGGTCCGTC 480
 CGGTCAATTC CAAGTCTCT GTTACGCAAG CCAAGAACAA GAGGCCACGG GACAGCGCA 540
 15 ACACCATCTG GGATCGGCC CCGACAATG GTTTTCTGA TAGTAAATAT CTGAAGCAGG 600
 CTGTCAAGCC ACTCTTTTGT CAGACAGCG AACCGCCTGG GCGCCACAT 649

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1461RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

GATCAAACCA CCACGGCACA TCATCATAGT TGATTAAATC AATTAGGTAA GGCAACCATA 60
 GTTCAGACT TTGTTTCTGT ACCATTTTCT TGGGATTAAA GAAGTAGGGA GTCACGAGGA 120
 45 AATGCACCGC ACATGCTTTG AGATTGGTGT TTTGGGATTT TAGAAGGCCA GTAAOGAAGA 180
 CGGTGAACGA GCTGTCCAGC CATAGATTAT TTTTAACTGG ATGAACCTTG TAGCACTOGA 240
 50 TGTATAGGAC AATCGCCAAC CAGAGCAATG TCTGTGCAA CCGGTTCCTG ATGACAAGCG 300
 CACGCGGGGT GCTGTGAAT GGTAGGAGTT GGTTCCTTCC TATCCACGG TTGCTAAATG 360
 55

CCATGTACTC TTGGTCCTTG GGGTTCGGCG CGACGCTGAC CTTTAAAATG TATTTGAGGT 420
 5 CCAACTGGTG ACCATAGGGG TCCACTAGTG ATAGCATGAG TGCTCTAAC GGCAGAAGAA 480
 GCCCTGCGG AAGCGAAACC ACCTCCCGGC ATTTGAGCAC GCGAGACATT AACTCCAAAA 540
 10 GCGTGTGGC CCAGGAGATC TCTGCTCGG AGTCATCTGC TTCTCATTC TCCCGAGGA 600
 AGTGTATCAA AAGCCCGGC AAACCCACGG GCACAGCCCG CCGCACATCC GCGTCCCAT 660
 15 TACAGTAGTC TATCCACAG TTGTTCAA 688

(2) INFORMATION FOR SEQ ID NO:700:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 728 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1461UP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

GATCGGCAG TTAAACTTA AAGTTGATAG AGTCCCGTC GTGCTCTCTG GATACAATAG 60
 40 AGGCCACCGA GTGAGGTGG CCTGCAAGT AGTGCCCGC GTAGCGCTG TGTCCGAGA 120
 TGGCCCTTTC TAGGTTGATC TTGGAGCCAG CTTCCAGCT GCTGACTTCC GTCCGATAAA 180
 45 CTGTTTCTGG TGCGATCCG ACCTTGAAGC TATCGCCGT GAACTCCGTC ACCGTCAGGC 240
 AGATACCAAT GCATGCAATC GAGTCACCGA TGTGGCAATC CGCCAGTATC GGAGCCCAT 300
 50 CCTTGATAAG GACTGACACA CGTTGCGC CTGCTCGCT GGCATGTTT TCCAAGTACT 360
 CAGCAACAGT GCCAATGTGT TCCACTATAC CGGTAAACAT CCTATCAACT TCTATGGCG 420
 55

ATATAGGCTT CGGTATGCCA TCTATGCATC TTCTTTTCTG CTACCGGAG CTTTTTAAAC 480
5 TOGTAAGACA TGCATAAGGA AATGGCGGTT CGCCATGTAG CTGACTAATA AACTAGAAG 540
ATACGACTAA CTATCTGATT ATACTTTAGG ACTATCTCTC CTGCGCTGG TCACAGAAAC 600
10 ATCGTTGAGC AAGTCGGTC TATCGGGAAA ATCACTTGGT TCCTTTGTGG TAGACTAAC 660
TGCTGAGAA GCTGGAAAGC GCTCTTTTAA AGTCTACTTC GAATGGTGGT GTACGTCTGG 720
15 GTGCTGGC 728

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1462RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

GATCTTAATT TAAAATTTTA ATTAAGTATT TATAATTTAG AAATATATAA TCTAGAGATA 60
TATAATCTTA AAATCATAGG TAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120
45 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA 180
ATTTTATTA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATATAA 240
50 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTAAATTTAA TTTAATATT 300
AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTTA TTAATATTAA GIGATATATA 360
55 ATTTAATTA TATAAATTAT TTAATTACT TCATTGATAT ATATAATTAT TAAATGTACC 420

TTTCATAATA TTTATTTTAA TTAGTCTAGT AATATTTCTA TTTAATAGTC TACCCTTTAA 480
 5 TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC 540
 TAATAATTTA TTATCTAAAG TATATAAAAT AATTAAACTT TTTTATTATT ATTAAATTA 600
 10 TTATTAATTA GTAAATTATA TTTATTTATT TTATTAACAT AATTTTTTGG ATAATAATAT 660
 ATCATTATTA AATGGTAATT TATTAATAAT TATCTTAATG A 701

15 (2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 728 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: PAG1462UP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GATCAATTAA TAAATGGTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA 60
 40 CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT 120
 ATTGAGTTTA TATTAAATTC ACCACCTCTT ATTCATTCAT TTAATACTCC TCTAATTCAA 180
 45 TCTTAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAATTG 240
 GTAAACATA TGTTTTAGGG ACATATATCT TCAGTICAAA ACTGAATATC TACATATTAT 300
 50 ATCATTAAATA TAATAACTCT TTAATTAGAG TGGTACCACA AGAATGCTGA AAGCATTAGG 360
 GGIGTGTAAC TTAGCTCTCT AATTAAAGTT ATAAATTTAT CTTAACATAT AAAAATAATT 420
 55 AATTAAATAA ATAAATAATT AATTAAATTT AAAATGTTTA AAAAAAGAAA TAAATAATAT 480

GTTATATTTA AATAGATCAA AATTTCAACA ATTTCATTT CATTAGTAC TACCATCACC 540
 5 ATGACCAATT GTTACATCAT TTAGTTTATT AGGTTTACTA TTAACTTTAG CTTTACTAT 600
 ACATGGTATT ATTGGTAATA TTTATCCTTT ATTATTATCT TTATTAGTAG TTTTATTACT 660
 10 AATAACTTTA TGATTTAGAG ATATGGTAGC TGAACCTACT TATTTAGGTG ATCATACTTT 720
 AGCTGTAA 728

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1463RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GATCCCTGAG TCTGCTACCA AGGAGGTGGA GGAGGAGGAC ATCGATATCG AGCAATTGAA 60
 40 GCAGGAGATG AAAGGCAACA AGGAGGCTC TGCTTTGTAA GCTTGCTGTT TGCCGCTTGT 120
 GCTAGCCAAT CGTTGCTGAG ACTATCTAAC TTGTATACAT GCGCTATCG CGGCACGCGA 180
 45 AGCGAACACT ATAATGTATA TGTCAAGTGA AATACATCAT ATATTATCTT GTGCCTCAAG 240
 GGTCTTAAAG ATGTCATAGG ACAGTCGGT GCTCAGACAC ACGAATATAA TCATAATAAT 300
 50 AAATATATGG CGGTCAGCTT CATGACCAGG TCAAGCCTTG ATACCAGAAG ACACTTCTAG 360
 GAATTCTCA ACGGAGAGA AAACACTAGG GTGTAGGTG TCATTGCTCA AGGACATCTG 420
 55 CTCTGGGTC CACAAGTTGG CCTCTGGTAC ATAGTCTGGT TCACCGACAC CCAATAAGCC 480

ACCGTGCGCA GCCCAATCGC TGACACGTGG AAGCTGTAGT GTCTTCCAGA CGTCATCCAT 540
 5 GCGGTCCAAT AGGACATCCG ACAGGTGGTT CGTGTGGCCT GGAGTAGGAA TGATACGGAG 600
 TCTCTCGGTC CCGGTGGAA CCGTAGGAGT TGAAGGGCCT GTACGTAGAT GCGATGCTCT 660
 10 CCATCAAAAT GTCGGAAGCA CGCTTGGC 688

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1463UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

GATCAACAG TAGAAGTATT AGAGCTGCTT GCAAAGGGCG TCATAACAA GAGAGCTGTA 60
 ATGTGACAA ATTAAACAGA AAAATATCAT TATTAGTGA TAAATAACCA ACTTGCACTG 120
 40 AGAGTATAGT TCTACATGTT TATTCGTAA CAGAATTTCT ATCCAAATAG TTTAATTCCG 180
 TTTTACTTAT CTACGGAGTA GCAGTGCAAG AACCTTGTAT CCCAAATGC TAGAGGGACA 240
 45 TGCAGATGTA TAGTAAAGCA ACGTCTGTTT CTTTGGATTT AGCAGGTCA GGCGAACAAA 300
 AAAAATAGAA AGTCAACAGG GATTGGGAAG TTATGAGAGT TGATATGTTT GTCCATTAGT 360
 50 AAGTCATTCA GTTGATATGA GGTGCTTAAA TGTTTGTAAG AAGCAAGAAC GAAGAGAGAT 420
 ACAAATGTG CAGTTGTGAA TCGTGAAATT GACACCAGAG GACGTCACCTT CCGTTGCCA 480
 55 CTGTTTGCCA ATTGCTTCTC GAGCTGCTCA ACCTTGGCCT GTAAATCTCT ATTGACTTTC 540

TTTAGTAGTT CCAATTCAAT ATGCGTTTCC TTGATCTTC CATAGCTGAG CAGTTTGGCC 600

5 ATCTCTGGT TCTCTTTTGT CAACATTTTC AGTCGGACAA TCATCTTGTG AGCGAGGGCT 660

TCTTGTCAT AACGGCCGAA TCGGTAAAC GAATTAGAGG GATT 704

10 (2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 699 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: PAG1464RP

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GATCGAAATA ACTTCGCTG AAAACGCAGC AGAGGCAGCC AATGGTCAAA TGGAGGAGA 60

35 ATATCCACGA TATTTCTAGG GTACTGTTC TTGCCAGTTG GTGCTCGAA ACATAACCCT 120

CAATGGGGCC CAGTGTGTG TACATACCC ACACCGGAAA CAGACCCATG AATGACCGGA 180

40 AAACCACCAG CCACGCGGT AAGCCGCCAT CCGGGTATTC GTTGGAGTTA TCGAGATATG 240

CGGTCTCTC TTCTCTACC TTTTCGTGC TGAGAGGGAC AGTCTGCTGA GGCACGTGG 300

45 TCGTTGGGCC ATGCCAAAA AGCTCTTTGT CGCCACAGC TGTGGCTCTG CCGCTGTGAG 360

ACGATGGGCT GACGTCTAGG GCTACGGGCT CATGCCATG CCGTACTTGA ACGCTGTCTT 420

50 TGTGATGAC CACCATCGTT CCTAGCACGT ATGGGAGATG CTCCGAACCG CGTCAGCGCC 480

ACCACAGACC ATCTATCTAC TTAAATACCT AATTATCTGG TGTCCAGCTA AAAATCCGAG 540

55 TATCAGTCAT CCTGTGGCGG CCTTATCACC CATTAGGGTC CGCTTTGCGG TAGTCATTA 600

CCGTCGGCGG GATTTCATCT CCAAAATGTC TCAAGCGATG CCTTGATTCC GAGTGTACAA 660

5 GGGCCAGATT CCAACGGGCC AGGAGGCAAC TAATAGAGG 699

(2) INFORMATION FOR SEQ ID NO:706:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 710 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1464UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

30 GATCTTGGGC TTTTCTTCA GACCGGGTG GGTGTAGTAT TGTTCCTCT TAATGTTGGA 60
 GTTGAGGGCG GACGAAGAGG GGCAGAGGG GTCTGGGAG GCAACGGTGG AAAGGGGCT 120
 35 GTGGGGCGGT TGCAGGGCA GCGCGCGTC GTGTGGTGG TAGTGGTAT GTTGGGGCGC 180
 GGGGGGGCC GACTGTGGT CCAGCGGGTG GCGTGGAC GCGAGCGCG AGAAGTGGC 240
 40 GTGGCGGAAC TCGTACTCT TCTGCGGTC CTGCGGGCG CGCTTGGCG GCGGTCCAC 300
 GGACGGGCG GGGACCTTGA GCGCGTTGA GATAATGAAC TTGTGTTGA CCGAGCCCTT 360
 45 CGGATGCTTC TTTCCGCCAT TGCGTTTGG GCGCGGCTC TCGCGTGG GCACGGGGC 420
 GGCGGGCGG GCATGCAATT CGTTCCTGTC TGGCGAGACT GGGGGGGAT AAAGTGGCC 480
 50 AGGATCGGT CCACGTTAGT GAGGTGCGG TTGCGCTCT CTGCGCTGC GTGGTGGTG 540
 TTGGCGCGGT GAGCGCGTG CACCGGTCC TCTCGTGGG GCTTGGGCTC CTGCTCGGC 600
 55 ATGCCCCGTT CGGCTGCATG CCTCCAATCG ACTTGCAGT CGTACGATC CATCCAACGA 660

ACCCCGTAAC TTATCTOGAA GTATGCCTGC ATACCTATAC TGGTCGTTCA

710

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 703 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1465RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

GATCACTTC TTGCGGACA AGACATTCGA GGGCGGCAAC GACTGGGAAA TCTACAACGA	60
CCCGGCGACC ATCGGOCACA GCGTCGGCTC CCGCGAGGAC ACGGTGAGGA TCCTCAGAGA	120
GCTGTTCGAC CTGTAGGCGC CGCGCTAGC TAGTTCCTTG TAATTGCTCG ACATTTACAA	180
TGCATATTCC TATATACACC GCGCGCAGCG CTCAGCTGAG CAGCGGTACG TACGCCAGCA	240
CGAGCGCAAA CGTACCGGTG CACACGCGGA TCAGCCACTG CATGACCTGC GTCTTGACCG	300
AGTCGATTTG CATCTTCATA TTAGTGACCT CCTGGTCAAT TCGGTGTCA ATCTCCTTGA	360
TCTGCAGATT GTGGTTGCTG GACTCCTCCC GGATGCGTCC CTTTTCGAAC GAGAGATCCA	420
GCTTGAACCC TCGTTTCGCC TTCGTGATCT CCTCTCGGAG CCGGTTCGCG AGCTGCTCTA	480
GGTCGTTTCG AATCCGCTCC TGTTCGTTCT GGATGGAGTG GATCTGCTG CCGTCGCGCG	540
TCAGCAGTTG GTCCCGCAGT TTTGCAAAAT CCACCGCTG CTGGTACGTC AGCTTCGTAA	600
GCTTCTGCGG GGACGCTAGG TCCTGCGAGA CATGCGTCAC GCGCGCGCG AGTGCGTCCG	660
ACATGATATC CACGATCGCA TTCGCTGCT GGCTTGCTGA AGT	703

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1465UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

25	GATCCCGCAA TAGCTTGATT CGATCGTCTG GTGCGGTACC TGCTCGACTT CTCITGCTCT	60
	TCCTATGTT CGTTGCTCAC GCGCGGAAAA CCACTACAGC ACAAAAAATT CACAAGGTCC	120
30	GCGCACCAG CCTTTTAAAT TAGCGCAATG GCAGCGAGTC CTGGTATATA AGGCAAAAGA	180
	CGGGAGGGGG ACAGCTACTA CAGGCTCATC GAGGCATGGT ATGTTGGGGG ACAGTGGGGG	240
35	CAGGGGGCAG GACTAACCTT GATGTTGAT AGAATGGGTT GTACAACCAC GCGGTGAAAC	300
	AGAAAAAGTT GCTGGAGCAG GAGCTGAATC GATTTGAGCT CGGGGTGGGG GCGCCGGTGG	360
40	GGCTGCAGGG TTCCATATCG ACGGCACTGG TGGGACTGGA GCGCACAATT GAGCAGTATC	420
	AGGCGCAGGT GCGCAAAAG GGCAGCGGGG CGGAAGCCGG CAAGCATGGG CAGCGCGTGG	480
45	GCGAACTGAC GGAGTGGGCA ACGAACGGGC GCGGGGGGTT CGAGGGGGCTG CCGGCGCGCA	540
	GCATGCAGCC GGTGGCGTTC CAGAGCGGGG CGGCAGCGCC GGAGGGGGCC GTGAACCAGC	600
50	CGGCGGGGGG GCGCGGCAC	619

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1466RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

20	GATCTCTTAC TTTTCTACT CACCAATGTC TTAAACAGAC AACCAGAGTC ACGGCGGCA	60
	GCTTATCTGC CGTGCTGGCG CCATGCCCCG CCGCTGGTAC TGGCCCGCTC GTGCTCGCGG	120
25	TAGTCTCACA GCAACGGAGC TTGCTCCAAT TGGGCTGCAT TCTCCCGACC ACAGTCTGTT	180
	TGTCAAGTGA CTCTCAGCCG TCCCGAATGT ACATTTCTAT TTATCTACTT CTGCGCGCCT	240
30	TGCGCGCAC ACCATCCGGTG CCGGCGACGA CACCGACCGC GCATCGCGGC CCTCGCGTTC	300
	GTAGAACTGC GCACAGCACG TGTACAGTGC CTCCTCTGCC GCGCGCAAC GGCCCTCTCT	360
35	GTACCGTGTG CGTTTCAGAC ATGCTTGAT GGCACATGCC TGGGCTTGC ATGGGGCTG	420
	TCCCTCTGG CGTGGCGGCC TATTGTCCAT GTTTTGTTT CTATCTGTTG GCGGTACCA	480
40	CGTTGTTGTA CCAGAGTACA TTGTGCGGT GACCCGTGT AATGTCACC CGTGGGCCAC	540
	AGATGACCTT GCCACATGCC TCATTTCTTT GACCGCACCG TGCCGCGAGA CCGCCACAT	600
45	GGGCGGTGG CACTCCGACG ACACCCACGG GCGGCACTG CAAGGTCGC AGGTGGGAT	660
	GAGTCAAAAC AAACCAGGTG TGGGCTGGG CCGGTGAAA TCGACTCATA GAGAC	715

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1466UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

GAICTTATTA ATTTTGATGG TGCTATATTC TAAATCAAG TAATGATAGC GCGTGATGCG	60
GTACGTACCT ATACATATAA CGCACAGTTC ACCATCGTCT ATGCGTGTAT GAAAATCACT	120
CCAGCCGTGC GACACGCCAC GTGTAATCTA GTGAGTTTCA AGTTCTTCTT CCTCATGGGC	180
AGAAAGTTGG CCGCGGGGGG TGAGGTTCTT GAGCGCTCC TTGAGCTGCG CGATAAGGCT	240
ATTCTCCCTT TGAGCATGCA TCGGATACC CTCTAGAGAC ATATGAGCCG AATCTGCACC	300
ATCTAAACCA TGTTCGTGT TCGTCCAGT GCGAGCTGCC AGTTGGGAC TGGACAGACC	360
TGTCGTCCA TCTTTGTAAG AATCTCGGT CGTTGCCGAG TTGGAATICA TGGTTCCCAT	420
AGTGTCGCAAG ATTTTCTCTT CTTCIGTTAG TTCCAGATGG GTACCTGTCA GATTGATCAA	480
GGACCTGCCG CTTTACGGC GCGAGCTT GGGCAGAAGA GAGTGCCCGG TTGGCGTGGC	540
TTCAACCAAGG TTTGTAATGG AGGTGTGAGA TCTGGAGTC CTGGTAGTC TCAGACACGA	600
AGCACCGGCA TCATGTATCC ACTTCGCAAC AAGCGAAGTC CAGCCACACT GGTGTGATGC	660
GCCCAAGCCC CTACCAGTGT CACCATOGAA GTAT	694

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 690 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1467RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

GATCGCAGAC	TCCGCCGGAG	AGACTTTTCG	ACCTCGGCA	CAGGTCTTGA	AAGAGAGCTC	60
CGGCCGTTCC	GTGCCAGACT	CTGTGTTATC	ATGTCCGTAA	GAGCAGCGTT	CGTGCCAGGT	120
ACGCCCTTCT	TGTTCTGTGT	TCCACCAATT	GATGGAATTT	GAGACGTGAA	CCTCTGCGGA	180
TTCTRRKCTAT	TGAGCACACC	ATTGGCACCA	CTTGAGCCCC	TTGCTCTGTC	CATCCCTAAT	240
CGTCTATCC	TACGGCCGGC	TAATAAGTTA	CTACCAGACT	CTGGCCCTCA	TCTGGGACTG	300
ATGTTATCGT	CTGCAGCCAG	ATCTGTTTG	TGACCCGATC	GAAATCATCG	AGTACGAATA	360
ACCACGTGAC	CATTATTCAC	GTGATGAATT	TGGCGGTCCC	TGTTGCCGAC	TCTTACTCCA	420
GGTTAACCAT	GACTAGATGG	GCATACCTCA	GATACGTTAT	TCATGGGATC	CGGAGTTGCC	480
GCGTGGCCCG	AACCGCCCGG	TGAATCTGTG	CTGACGACCT	AAAAAATAGT	GTGGCAAGC	540
TTCTTAATC	TGTGAGATGC	AACTGACAA	ACTTGAAGGC	TGAACCATCA	AAGCGATAAG	600
CCTCATGCAC	GTGCTCAATA	AGGTCCAGGA	AGTCTCGCAA	TGGGGCAAGC	AGACGGTAGA	660
TTGCAAGACA	CAGACGATTG	GGTGTGCCA				690

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 700 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1467UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

GATCGTCCGA GTGCAAATCC ATACCAAAAA TGTGGACCCA GGTACGGGAT TCGAACTTCT	60
CGAAGAAAAA TAGCCTCAGT GAAGTGCCCA ATTGCCTTAT AGTCGTTTTC CAGAGCATAT	120
AGAAATGTGG GACAAGGCGG TGGGGGGGCT TGTGGAGCGC GACGGAAGAA GGGATCTGGG	180
CGGGAATTAC GCGGTGAGA GGCAGGGGTG CGGAAGAGAA AAAGGTGAAG CGAGTTGTTG	240
CCATGAGCGA GATGCAGCAG CCAATACCTA TCCCAATGGT AAACGAGGCG GTCCAGATGG	300
CCCAATGGCG GAGGGCAACA GGGCCCGGCT CCTTTTTCGG CGGTCTGGGG TGCTGTTTCT	360
TGGACTTGAC GGTGAGCTCG GTTTCATAGC CGGACTGGGA CTCGTTGCAA AGTTTGTGCA	420
GGTGCTTGAG CAGGCGGTGC TTCTCGTGGT GGTGACAT GATTATAGGG CTGCAGTATA	480
CTCGGATGCA TTGCGGTGCG GTGTAGCGCT TCAGGAGAGC CGCCAGCGTG CTCTTCTGGC	540
CCTTCTGGCA CACGGGAATC ACGGTGGGGC AGGGGGCCTT CTCGCACAGG CCGTCCAAGA	600
GCTCTGGGCG CTGCGCTATG TGTGGAAGA CCACCATAAC CGGAGGTAC CGCTGGCCCA	660
CGTCCAGCG CGTGACCATG CCGAGGTCT TCAAGTCAA	700

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1468RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

10 GATCTCGTCG CTCATTGTCTG ACCTGCAAAA AGTGTTCAGA AGGAAGGCAA CATGTGTTTT 60

TAATCCTACG GCGTGGCCT CAGAGATTGT TCACTCAATG TCGTTCATCA TTATGAATGG 120

15 GTGGCCGGCG CCTGCCGGCC TCGAACCCGC GCCACACGGC CTCGCGCGCG CGCTGCCCCG 180

CTGGGCCACG CAGGGTCCAA AACCACCCCA AACTCACCGC GCCCACCCCG CTACACCGCC 240

20 GCCAGCACGT CAGTGGCGGT TACCGGCCCT GCGGCACTG AAAATTTTTT CCGCCAACA 300

CTATCGCGCC CGAAAAGCA ATTTGCGGC CAACCACACA ACGATCTGTT ACGAACAGG 360

25 ACAGGACTCA TGCCCCGTC CCTTCTTTAT TTATTTACTA GCTCCACATA GATATTTTTG 420

ATATTTATAT GGTGTGTTTT CTCCGCAAG CGCAACCCA GCACTTAGCA GACCACGGG 480

30 GCAGGGACTG ACACCCAGC AGAACAGAAC AACACAGGC GACCTTACAA TGAGCATGGA 540

AACGCCCCCT GTAGATATCG ACAACATCAT CGACCGCTTG CTGGAGGTGC GGGGCTOGAA 600

35 GCGGGGCAG CAGGTGGACC TCGAAGAGCA CGAGATCCG TACCTGTGCT CCAAGGGCG 660

CAGCATCTTT ATCAAGCAGC CCATTCCTC 689

40

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

55

(A) ORGANISM: PAG1468UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

5	GATCTCAGAA TTATCGGCTA GCAATTGATA TTAGCATACT TAATTOGTGC TAAATACTTT	60
	GGCATGCGAT CTAGACATAG GAAGTAACCT CAAAAAAGCT ACGCAGATAG TAAACCTGGA	120
10	AGAGAGATTG CGCAACAACA ACGGCCAGTT GGAAATAGA CCACCACTTG ACCCTGTCAT	180
	TTGTAGACTC AGCAGTGTTC CTGTGTGTGC GTTCGGGAAT CTCGATGTAC TGTTCCTOCT	240
15	TCATTACTTC CATTGTGAGC ATGGAGAGCT TGCGCACCGC ACCCTCTAGC GTCTCCGAGC	300
	TGGAATCAGC GGCATCGGGG GAGAGAACAC CGTAGGTATT AAACGTGACA TCCTTAGTCA	360
20	GGTAGCCCGA ATTGTGCTTC GCAAAGCAGT ACTGGTATTT GCCATCTGTA GCGGCTTCA	420
	AGGTCAACTC ACGTGGGAC GACGCACGCT GCGCATCCAG CACTGACCGT CCGTCAATCC	480
25	CGTACACCAG CAGGTCTCCA GACAGCTGTT GATGTGATTG TGGGTCTCTG TCGCCGAATT	540
	GATAAGTGAT TGTGAGCAG TCCCCGCCCT TCAACTGCTC AAAGAAACAG CGCCGCCCGT	600
30	AGGGGGGAAG AAGTACATTG	620

(2) INFORMATION FOR SEQ ID NO:715:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 686 base pairs

(B) TYPE: nucleic acid

40

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1469RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

55

EP 0 866 129 A2

	GATCAACTAC ATCTGGGAGC AGCAGCCGAA TTGTAAAGTG GGCATCATAG CATATGACAA	60
5	GTGGCTGGGT TTCTTCAACC TGGCCCGGA GTGAGGCAG GCACAGGAGC TGATTGTGTC	120
	CGAGCTCAGA GAAGTCTTCC TGGCGCTGTA CAGCGGCTC TTGTGAGGC CTGGGAGGC	180
10	AATGCATGTC ATACAGGACA CGTTGGTCAA GCTGAGTGG TTTATCCAGG ACGACAAGCT	240
	CTGGCAGGC GCGAGGGGT GCTTGGGTC GGCGCTGAG GCGCGCTGC TGGCGCTGA	300
15	CACTGCCACC AATGGTAATG GCGCAAGAT CATTGCGACT CTGAACACGC TGGCCACCGT	360
	GGCAACGGC AATCTGAGC TGGCGGCGA CGACGGCTC AAGAAGAGC TGAAGTGGA	420
20	CAACAGCTTC TACACCGGC TGGCGGACAG GATGCTGAAG GGTACGTCG GCGTGGACT	480
	CTTCTGCACA GGCAGCGCT TCATGGACTT TGCCAGCTC GGCCACCCG TGCTGGCCAC	540
25	CTCGGGAGG TTCCGCCACT ACTGGAATT CCAGCTGAC GCGACGAGT CCGCTGGGT	600
	CAACGACATG CTGCAGCCG TCAGCAGCAG CGTGGCTAC CAGGCGCAGC TCAAGGTGG	660
30	CTGCTCCTCG GGGCTGTGT CAGTCG	686

(2) INFORMATION FOR SEQ ID NO:716:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 572 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
40	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1469UP

50	(x) SEQUENCE DESCRIPTION: SEQ ID NO:716:
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	GATCGGGCGA GCAGGACTAG ACATGAGCAG CAATGACAGT GATTATCTCC TGGTTACCTT	60
55		

CAAACTCTTC ACTCTCTCA AGAACTTGTT ACCTGATGAC TCCTTCTTAT TGTCGTGTC 120
 5 ACGCGGCCCC GTGTAGGCGT CTTOGTCTGTC CTCTTCTCTG TCCTCAAGAT AGCCAGAGTG 180
 GGTCCTAGTC AGCTTCAGGT TGGCGTTCTT GGGGTGGGG CCAATGGCG ACGGGACGG 240
 10 AGGGCTTTTC GCCAGCCTGT GGCTCAGAGA CTCTTCTCTG CCCACCGTC TCTGCTTCAT 300
 CGCTCTATA GCGACAGGG CCGCCGGCG GCGTGGAGG AACGTCTGG AGCCAAGCCC 360
 15 CTGTGTACG GGGCATGCA CAAGGTCCG GGTACCTTG GCGTGAAGT GGTCACTC 420
 CGAATGGTTC TTGATAGCGT TCACGTGCA GAGGAGCG TGGCGAGT CGGGGGGGA 480
 20 ATACAGGTAC GAGTGTCTG OCTCTCTGAT GCGAAGACC TGTTCATCG CAGACTTGTG 540
 TGGGTGGCC CCGACAACGT CGAGTTGGC CG 572

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1470RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

GATCTGCTG CTATCCAGAA ATGGGAAGTT CTTAGACRAC GGGGAATTAA GGGCCTTTTC 60
 50 CAATATTTTG AGCGTCGTTT CATAGCTCGG AAGAGCGAGC AGAAGCCCCC CCAGTAGTGT 120
 CTGTTTATGT TCGTCATGA AAGGTGCTC TATCAAATCT AGCTCCATCA TCGCAGAGTA 180
 55 GTTATTATCT TTCTTCCAAG ACAGACGCAC ATGCGCAAC TTCGTCAGGA TTACAGTAAA 240

EP 0 866 129 A2

ATAATGGTAG AACCGCGGAC TCACAGAATC GACGAACGCT CGAAATGAAG TCGGCCCCGTA 300
5 GAAGATCGTG CGGCOCTGCT TCTCTATCAC AAGATGGAAC TCGGAAAGTC TGTTCACGGG 360
GGACACCGTG CCCATAACGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT 420
10 CCGCGCGAGC TCAGTCTCAA GCTCGTGCAT CCGTCGCAGC AGCTCCACAT TGGGCGTTGG 480
AGCTGAACAG CTCCCGTGAG TTCACGTGCT GCGTAAACTC AGACAGGTAC ACACACTGG 540
15 GCAGGCCCTT CCCAATACAT TTAGAGCACT TCGGCGCGC CTTGTTGCAC TTGACGGGCC 600
GCTTGCGGCA GAACACGCAC GACTTCTGTA CCTTCGGCT GGTTCACACA ATCTTGCCAT 660
20 CGGACTCTGC CATCCCGCCA GCTTCAGCAA AATGAGTAG 699

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1470UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

GATCGCGGAC GTGGAACACT GCGCGGAGAT GCGCGCGGCC ATCTGCTGGTGG TTCTTGGCGA 60
45 CCGCAAGGAC ACGCCATCGA CGAGCGGTAT GCAGCAGACG GTGCACACGT CGGACCTCTT 120
CAAGGAGCGC GTCGCGACCG TGGTGGCGCG GCGGTACCGA GAGATGGCGG CCGCGATCOG 180
CGCGCGGAC TTGCGGACGT TTGCGCGCCT GACGATGCAG GACTCGAACT CGTTTCACGC 240
55 CACCTGCCTG GACTCATTTT CCGCGATCTT CTACATGAAC GACACTTCGC GCGGATTGT 300

CAAGCTGTGT CATCTGATCA ACGAGTTCTA CAACGAGACC ATCGTGGCGT ACACGTTTGA 360
 5 CGCGGGTCCG AACGCGGTGC TCTATTACTT GGGGAGAAC GAGGCGGGC TCTGCGGCTT 420
 CCTCTCTGCC GTCTTTGGCG CCAACGACGG CTGGGAGACC ACGTTCTCGA CGGAGCAGCG 480
 10 CGCCACTTCG CCGCGCAGTT CGACGAGTGC GTGCGGGCA AGCTTGGGAC GGACCTGGAC 540
 GACGAGTTGC ACAGAGGAGT TGCCCGCCTC ATCTTCACGA AGGTGGGCA GGGCCCCAAG 600
 15 AACTAAATC CTCGCTCATC GACCCGAGA CGGGCTGCC CCGCTGAGC TATTC 655

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1471RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

GATCAATTAA CTATCTAGAT GAGTCTAATT AATTAATATA CTTAAAAGTC CCGTTAATAT 60
 CATTAGCTAC CCTATCGGAA CAGACCGTCT GCTACTAGGC CGAAAGGGTA AAGCAGTTGT 120
 45 CAGTCAGTAC TTGCTGTTGC TTATGGAATG CCTGTCATAT GCGGCAGCT TGTTTGTCAC 180
 TGGAGTACGG CCGTGCCGC CTTGCAGAGG GTACCCATGA TTCTGAACGC CAAGGTACCA 240
 50 CACCTTCTCG CCACATCTCC TCGAAGCTCTT CCAAAGTCAA ACCCTTTGTC TCGGGGACAA 300
 AGAAGAAGAT GTAGAAGAAC GCAAAGATCA AACAACCCAT GAACAGTAG CCGTAGTAAA 360
 55 ACCTGATCGC ATTGGTAATG TATGGTGTA AGAAGGCGAT CAAAAAGCCC CATATCCAAT 420

TOGOGGCTGT GCGGATAGCC ATGCCCTTGG CTTTGACTCT TAATGGGAAA GTCTCCGAAA 480
 CAATGACATA CGCAATTGGG GCCCAGGTAG TTGCAAAGAA GAAAAATGTA GAGGCAGGTA 540
 AAAACAATCA TAGCATTGCC TGCCGGTCTG GAAGAAGGCT GATCGGGTCC ATTGGGOCAT 600
 AGTCTTGTCA CACCAACGGA GGCAAAAATA ACCATACAAA CGGCCATTGC CGCGGCACCG 660
 TAGAAGCAAA CATTTCTCTC TGCCAAATCT ATGACAGTGT TTACATTG 708

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1471UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

GATCTTGGCC TTCTTCTACA TGTCTTCTT TGTCCAGAG ACAAGGGTT TGACTTTGGA 60
 AGAGGTGAG GAGATGTGC AGGAGGGTGT CGTCCCATGG AAGTCCGAGT CCTGGACTCC 120
 TTCTTACAAG AGAAATGCTT ACGAGACTGA GGAGGTGAAG CCAGAGAAGA CCTGGGCTTA 180
 AAAACTTTAA ACTACAACT TTTTGTCTT GCTAATCATC GGGTTAAAC CTAAACCTAA 240
 TCTATGTCA TTAATATTGT TATGACGTT ACGAGATAGC ATATGTAAAT TACTATTAAA 300
 AATATGGAT TAATCTGTAT TTATTAGTTG TAATTGCAAT GCCATATGAT ACTGCAAAGC 360
 AATACATGCC GAGATAACCA ACGCACTGA GCGGGACTG GGGCCCTTCT CGGGCCCGGC 420
 GAACATGCT GTGTTGGTG GCGCGGTGC CGTCCGCGG CCAGCCGCAT GCGCGTCGTC 480

GGTCATCGCC CCACTTTTCAA ACTTTGTAAAT CGAGCAGGAA ATTAAGATTG GTTATAAATG 540
 5 ATATCAAATT TTTCGTGGTT TCTTTTCAGT GAGTAATATT GTTCCGGCAC CGCAGCGCGA 600
 TGATGCGGCT ACATCGCACA GGGCCAAAGC ACAGGTGCTA AACTATTGCT TAGTTGGGGT 660
 10 CGTTGAGCTC GTTTATGCTT AGTGAATAT CTGCAGCATA TTCAATATCA AGTCTGAA 718

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1472RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

GATCTATCTC CCAGCTTAGA GAGACCGTCC GGATGTAAGT GATACCCAGA CAGCCAATGA 60
 TACTGGTCAA GTTTTGTAGT TTTATAAGAA AACATATATT AAACGGCTAA AGACAGAAGG 120
 40 CGAAAAGCCC GACTTTTATG GGCGTAGAAG TCGTGAAAAA GGCGAAAAAC TATATTTCCA 180
 CTTAGGGCTC CTCCTTCTC ACGTAAACGC GCATCATCAT ACGCCTTCTG TGAGTCAAGA 240
 45 GCACTACGAC ACGCGGTGCA TTCCCTCATA CAACCTTGCC AACACATGAT CATGTCCAAG 300
 GATATTGCTA CGACCCAGA ACTGTCCGAA CCAGACAAGT ACTTCGTTGA GCAGCGCGAT 360
 50 TTGCTGCTAC AAGAAATCAC CTCACGTTA GACTCCATCC TGAACAACCT AAATGGCCTG 420
 AATATTTCCC TGGAGAACTC CATCGCAGTA GGCAAAGAGT TTGAGAGCGT GTCCGAGCTT 480
 55 TGAAGGTCT TTTACGACGG ACTCGCGAAC GGAGCGGCTC CTGAGTTGC CGCAGCCAAC 540

CCGTGCTCTC AGGACCTGCC CACTGAGCCC GTGCGCGGCG ACCAGAATGC TGCAGCGGGC 600
 5 AATAGTGAGC CACCAGCGCC ATCGCAGTAG CGTTTGCACT CTGCCCTGCC TTTACACCCG 660
 TGCACCCACA TTGCGCTCTA CTTTATGTG TCATC 695

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1472UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

GATCTCGATT GAATGCCAAT GAAGGTTTAT GCGCGTCACG GGAGGTATAA CAGACTTGTA 60
 ACGACTTTTG GTAAGACCCA CGGTGAGGAA GATAGCTGGT TTAGCAGCGA CGATGAGAAC 120
 CACGCGAGAC CAGTTAGCGA CGACACAACC AAACTCAGCC TGAGCCAAGA TOGATGCAGC 180
 GAATTACCGG AGGAGACGAT AGGTGCGAAT AGAAAACGTC CCGCGGAGCG AACGCAGACG 240
 GATCCGGTGT GGGAGTTTCT GGAACGCGCG GCATCGGGGC AGAAGCGGAG AAGACGAGCA 300
 ACATGCGATT CTACAGAATA TAGAGAGAGT GCCAGTCAAG AGTTTCTAAA CGCTGTGAAC 360
 GTTGTCAGG GCATAGTGTC TTCTCTCAAG CCTGCAAAAG AGGTAGTTGA GCACTGGGCG 420
 GAGCTTGAGG ATGTGCCAGA GGATCGGGCG AATAACGGGC AGGCGGTCTA TGGCAAAACA 480
 AGAACATGCT TGCAAAAGCG GAAGAGGATT CTGACACCGA AGCTGCTGCA CATGAGTCTG 540
 ACGAACCGCT GCACAGGGCG ACGAAGCACT ATCGCGGCAC TTAAATGAGC TGGGTACGAT 600

GGGCGAGACT CTTAAGTACA GCGAAGATCT GGACTTTATA TTGTCCGACA ACTCCATGAC 660

GACACCGGAA CATAGACGCA CCACATGCTG CGCTTGTGTC TGGATATGAT GAACAACGA 719

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1473RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

GATCGCATCA TCCTGTACAC CAAGCGGAC GTCTGCGGCG CGCCCACCCC CGCCGGGCTC 60

CACCGCTGGC ACGCCGAGAC CGGCGAGAC TACATGCTCC TCGACGCCCC CAGCGCGCGG 120

GACGCGGGG CGCTGCTGGC CGCGGTGGC GCACGCTACG ACGCGCGCGC TGCGCGGGCC 180

GGCGGCTCC CCTCGGCTA CGGCTGCTC GTTGGGGGCA TGCCCAAGGT CGGCAAGTCC 240

ACGCTGGTCA ACCGCTCCG CGGCTCGGC ACCGCGGCGC GCGCCAAGGT CGCGGCCACC 300

GGGCCCCACC CGGCGTCAC GCGGCTACC AGTGAGTGGC TCGCATCGC CGATCACCGC 360

GCGGCGTCT TCATGCACGA CACCCCGGC GTGGCCCTGC CGGCGCGGC CTCTCGGTG 420

CGCGGATGC TCGCCCTGC TCTCGCGGC TCGTGGGC CGGCGTCTG CGACCCCGTC 480

ATCCAGGCGG ACTACTGCTC TACCTCTCA ACCTTCAGGG CCTGGCCCCC TCTACGCGG 540

CCTACAGGCC CCGACCAAC GACATCGCGG CCTGCTGGC CGCGGTGTG ACCCGCCACC 600

GCCTACGCTC CGAGACCGCA GCGGCGTGC ACTGGCTTGC CATCGGGGC CGGCGCTCT 660

GCCTGGAACC GGAAG 675

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAC1473UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

GATCTAGACG GAGTGAATTAT GCGCGGCAC CTCCAGCGAC TGATACTCAA GAATGTGGGC	60
TCCGTGGGGT GGTGGAGGTT CCGAGAGATC CACGAAATTA CGCTAGATCC TAATAGGTTT	120
ACCAAGAAAC AGGGCTTTGT GGGAACTATA CACGGGOCAG ATCAGGATCG GGTGGAAGTG	180
CGGCAGATAA ACAGGGCTGT CATGAGTCAG GACACATACT TOCACTTTGA TAGTCTTTTG	240
AGGGCCAGGT TCCAGAACT CAACTACATC AGTCTGCACA ACGTTTCCGA GGAAATTACT	300
GGCATCATAG TGCTCACC GACTGTATTGC AATGGGCGCA TCAGCATTCG AGGCTGCGTC	360
GTGAAGGGGG TTGTAATGAT CTAAACTTGC CCGGATATCC CTATTGAGAA ATAAACACAT	420
GGGTGAAGTT ATACATAGGC GCGGAAGAAG CCGCTTGAAT ATTGATAGAC CGAATAGTGC	480
GATCAATGTA ATTAAATAGA TAGGTTACAG CCTACCGGG CTGGCATTTC GTCCGAGATT	540
GGTCTGCTC TACCAAGTCA GCCAGTTACC GGAGGGTGAA GTAGTAGGAC ATCATAACTC	600
ATAAAAAACG TTACATTGCT TGTGCTTGTC GGGAAATCAG TAATCATGCA GGTGCGTCGT	660
GAAACCGAAG GAAACGTAAT GCGTGGAAT AAGTAAAGA TGC	703

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1474RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

GATCGTTCAG TTTAATCACC TGGGACGCAC TGCCTTGGGG TTCCAGCACT GCCTGAAACT	60
TGGCCAGGCG TTGCATCAGC GCATTAGCT CCTGTACATC GCGCTCGTGC TGGGCTCCA	120
GCTGCAAGCG CAGTTCAGCG CTGATATGCT TCCGCCCCGG TGTAGACATC TGGGCAAGC	180
TAGGGTAGCT GCGGACCGC CGCAGCGGCG AGCTCGGCGC GCGCTGTCA GCGTCTTCT	240
GTGCCCCCAT TAGTGGCGGT ATCATCTGCT CGATCCCGCC GTTTGCCATC ATCGGTATGG	300
GGTGTGTGTA ATGTCAATT ACCGCACTCC AGTCTCTGTC CAGGTCCGTA AAATACTTGT	360
CTTTTTTGCC GCCAGCGTGG TTAGACCGC CCGTGGTGT TCTCCGAAGC GGGCTCAAGT	420
GCACGCCGCG GTGGCTGCTG CTGTGGCTCG ACAGGGACGC TGCATAGTCT GCGACCTCT	480
GATGGCGCTA ATATTCCCAT CGCTATCTGC AGGCTCCAGC GATGGCGACG CCAGCTGATT	540
CGACTTCGCC GATGACGGCG TCTTCCACGA CTTGATCAGC GAGCCACAA GCGACGAAGA	600
TGATGAATTT GACTTTTGGT ACATTTCTTT GGACCCATTC CCAATTATGGG GAACCGTCT	660
GATAGCCATC ACAATGTATA GCTCGCTACT CTGAACCGCG TGGCAACCAC TGCAAC	716

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

EP 0 866 129 A2

(A) LENGTH: 699 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1474UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

GATCGAATTC TCACAGGCCA GTACCTGGGT ATTACAGGTT TGCCATAGTA TGATTAGAAC	60
CGTAAAGCCC AAGAATGCCA GGGCCAAGAG AGCTCTGGAG AAAAAAGAGC CGAAATTGAC	120
GGAGAACGTG AAGCAAGCGC TTTTAATTCC TGGCCAACT TCGAATAAGC TCTTGACGA	180
TGTTATGGTG GACCTTGGTG GACTCAAGAA GCTTGATGTG AAGCGCTTCA CGCGGAGAA	240
CGAGCTTCGT CCGTTTGAGG ATGGCTGGG TGTCGAATTT CTCAGCGAGA AGAATGACAG	300
CTCGTTGGTG GTGGTCTGCT CCAACTCGAA GAAGCGGCGC AACAACTTGA CATTCATAAG	360
GACGTTTGGG TACAAGGTTT ACGACATGAT GGAGCTGCAG ATTGCAGAGA ACTACAAATT	420
GCTAGCGGAC TTCCGGAAGC AGACGTTTGC AGTGGGGTIG AAACCGATGT TTTCCTTCCA	480
AGGTGCGGCA TTCGACTCTC ACCCAGTATA CAAGCAAGTC AAGTCTTTGT TCCTCGACTT	540
CTTCGGCGGT GAGGTGACCA AGCTGCAAGA CGTTGCAGGG CTTCAGCATG TGATAGCAAT	600
GACGATCCAG GGCGACTTTG AGGATGGCGA GGCATTGCCC AACGTCTTTT TCCGGTCTA	660
CAGGCTTAAG ACGTACAGAA GCAGCCAAGG TGGTAAGAA	699

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 749 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1475RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

GATCCGACCA ACCAGGCGAT CTGCAGCAC ATCGTTGATA ACGTCACCAT GATCGACGAA	60
ACCGAGGAGG ACCAGGCGC AAAGAAGGGC GCCTTTGCTG TTTGAAGCCG GATCCTGOGG	120
CGTTCAACCG TAAATAGTCT TATAGCCAGC AGCCAGGGC CGGCGCGTT CCTATGTAAT	180
CCTGCAATCG CTCGCTTGCT AGCCGACGA TCACAGAATA CAGCTACTTT ATCCTAAATC	240
CACTCCTATC AAAATATCCA GCGCGACAT TTGTTCTCTG TCTGTGGGA TGTGGGGTC	300
GCCATTGTGG AGTAGGCGC CAACTCGGAC AGCGACACA GGTGCGCATC ACAGCTGCGG	360
GTCCCGTGTG CGTCCCTGGA ATCCTGCTCC AAGCCCTTCT GGTCAAAGCC AGCCAAGCTC	420
CCCTGTCTGA TGGGCTCTC GACCGCTGCG TCAGCAAGT CCTGGTATGG ATCTGCGCGG	480
ACGCTTCTGG GGGCGCAGG CGTTGTGTGA AGCCAGTGGC ACAGAGAGGG TGTGCTGTT	540
AGCGCAACAG ACCAGGCGC TGTGCGGCC GCATGGGCG CCGTCCGAA TGGGTGCGG	600
TTTATGTAAT TGCTGCCCTG GTCCGATGTG TATTGTGTCT GCGAAGGGA AATCGGGGAC	660
GCAGGAACGT TCGCTCGCC GCATCGTTC TCGAGCTCT TCGGTGCGG CACCAAAGCC	720
TCCTTCTGCA GCATCCGCC TGAGCCGTT	749

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 740 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1475UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

GATCTTCGGT CCGAGTACG GTCGTCTCTT CGAGATATNA GCACGCAGCG CAACTGTATC	60
AAGCTAACCA ACACAGTKCG CACGCTTTTC GAGCGAGCT CAGGCGGAG GTGAACAGC	120
TCTGAGACAG ACAGACGCC CTTGTTTACA AGTAGCTCAA TAACAGTCC GCTCGCTCG	180
CCGAGGTGGG ACGCGCTAC CTCGTGTGAC AGGAAGSTTT CAGGACTCAA TGTCTCATC	240
TCCAGTGTGG ATACCGGCAC CTCGCAGCA CGCTGTTTT CGACTGTCC ACCTGCAGCA	300
CCCATAGATC CGTTCATTAT GCACTACGAC CTCGCCCTCA CTCAGCCCA GGGCCGCTG	360
GAACGCAATA CTCGCTAGTG CTAGTTCCCA CCTAATATCT ATCTCATGGC CCATCGAGCA	420
GCGGGCCAGC TAAAAAATCA CCACTGCGCG CTCACCACGC ACGGTTCACT AAATACGAAA	480
CAGTTGTTCG TCACGTGTG CTCACGTGAT TTTACCGGC CGGTATAATA TCGGTTCTC	540
AGCGCGCGCA GCAAGGACA CTTCTGTAT CATAACAAAC CAGCACAGGC GGTAGGAGCT	600
ATCGGCAGAG TOCCAATACC CTTGCTACTG TTGACATTAG GTGGTTCAA TGAGTGTCTG	660
TTTAGTGGTT ACCAAGAGTG TGGCGACAG CACATTGGGG ATCTACACCG GGATGGTGGT	720
AACGCGGCAG TTGGTCTTC	740

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 707 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1476RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

GATCGTATCG CTAACGTAA TATCGAAAGA AGCACAGACA TCCCGGAAAA ATGACATCTC	60
AGTGACACTC TTCAACAAAT CATAAGAAGA AAAGTATGIG ACTAATGCTT GCAGAAAAAT	120
AAATTGCTCG CTACCACTAA GCGATGTTAG TAGCGTGCCA TGGCAITCAA TAAATCGTAA	180
GAGTACGTTG GGTGGTATCT CGATGCTTTT GAGGTACGCA AAAATTGGGC CATATAAATC	240
GATCTTGAAT GGTAGCCTTT TGCATATCGA TTCTTCAAGA AGTCTGTTTA TAAGTTCTTT	300
ATCAGAATGC TGCATAGACT GATGCAGGAG AGCACTTAGC ACATGCCCTT TATTCTTAGG	360
ATAGAGCAAA TATTCTTTGA ACGAAGCTGG GTCTTTCCGG AAGTCAGGCT TCATACCATA	420
AAGGTACATG TATACATTCC TTGGGACATC CATATCTTCA ATACTGCTTT CAAGCATGCC	480
AAGGTAAAAAT TCGTAGGAAA ATTCCGGTAC CCAGGAATGC TGTTGAAATT GCGTCCAGAG	540
TTTGATGCT GTCTGGGGT GGTTCCTTGC GACGGCCAAC AGGAAGTTGG GACAGAACCA	600
GCGTCTGACA GGAATCAAG ACCATCTGTT GAGCGAATTT GCGTGAAGAG GCGATCAAGC	660
AGCTTCACAG CAACTTCCAG GGAATCTAAG CTGACAAGCC CAGCTAC	707

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 635 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1476UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

GATCTGAAAC TAACAACAGC AGTGGGTGAA CCAAGAGGCA TTGGAGGGGT ATGACGGGGT	60
GTCGCAAGGC AAGTACACTA TGGGCTTGGG CCAGACCAAC ATGAGCTTTG TGAACGACCG	120
CGAGGACATC TACTCGATGT GTTTGACCGC GTGCTCGAAC TTGATGAAGA ACTACGATAT	180
CAAGCCGGAA AGCATCGGCC GCGTCGAGGT GGGTACGGAG ACGTTGCTTG ACAAGTGGAA	240
GTCCGTGAAG TCTATTTTGA TGCAGTTGTT CCGCGAGAAC ACGACTTGG AGGGTGTGGA	300
TACCGTGAAC GCCTGCTATG GCGGTACTAA CCGTTGTGTT AACTCTTGA ACTGGATTGA	360
GTCCAGTTGG TGGGACGGTC GTGACGCAAT CGTTGTTTGT GGTGACATCG CAATCTACGA	420
CAAGGGTGCC GCGCGGCCA CTGGCGGTGC GGGAACTGTC GCTCTCTGA TGGTCCAGA	480
CGCCCCCAAT GTCTTTGACT CTGTGGGTGG CTGTACATG GAGCAGTCT ACGACTTCTA	540
CAAGCCTGAC TTCCGCAGTG AGTATCCATA CGTGGACGGC CACTTCTCAC TAACATGCTA	600
CGTCAAGGGC CGTCGACCAG GCTTACGGG CCTTA	635

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1477RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

10	GATCTTTGCG AGGGACCACT CTGCAATCCA AGAAGACTAG AGGAGTTGTC TAGGACAACA	60
	AAGTTTATAA GGAGACTTCT GGTGTTTAC CGTCTTTTC GATACCGATT CTOGACAGTA	120
15	TATTCAAAGG CCAATAACGC CAAACAATAC GTTAAAGTTG GCTGCCAGTT TTTCAACACA	180
	CTACTACAAC APTATGAGGG CATAAAGGTG CTCTAGATG ATAGCAAAT CATTCCTCAG	240
20	CTCGCCAGTA CTCTCTATAA GGCTATGGAA GGCATATTT TACCCAGTAA GCTCTTCTCC	300
	TCTTGGGCTC TCCAGAATAC GTTATGTGGC TCTACTTCA AATTCTCGG ATTGCTAATG	360
25	AAATCTAAGG AAGGAATCAA TATATTAGAA AAATGGAACA TGITCACTGT CATCTATAAA	420
	ATGTTTCAGC CATCACCCCT AGCGGAAGAA TATTTGTTAC TCATGCTTCC AGAGTTGGAC	480
30	CTCTCTCACA GCATACATTG TAGGATTATT TTTAGCAAAG CGCTAGTCGA CAGTAGAGAA	540
	GTCATAAGGA TCAATGCTAC CAGGGTTTTA GCGAAATGA TCAGCAGCGT CAAATTATCT	600
35	GATCCCACTC TGAAGAGTT CATGTAAAC CTGTTGGTGG CTCAGTTGTA CGATTTATCG	660
	AGTGAAGTGG TAGCAGTGGC CGACCAGATA CTGTACCATT ACTGTTTAAG TCAAAGTAT	719

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1477UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

5 GATCCGAATG TCCTTAGTCT GTGGGAAGGA ACGATGGTG GTGGTTGGGA ATAGCGGGAG 60
 CTTGAAAATT GGCTGCTGCT CCTTGAGACG CTCCCCGAAT GGTGGGGCTC TGTGGATAG 120
 10 CTTCTGTTT AAACCAGCAA CACGTCCTGG ACAGCAGGAT CGTTGGTGAT CGCAGAGGCG 180
 GCAGGCGCAG CAATCGAGTC TGCATTGCCC TTCAACTCAG AGGAAAAGTC TTGCCAGAA 240
 15 GCGTCTTAG CGAGGACAAC AACCTCATGC AGCTTCTGGG TTGCAAAGA GAACAGTCC 300
 TTGATCTCTG GCTCCAAGGC AGACTCGTTT TCCAAGTCAA CTGGAGTGTG CAACAAGGAA 360
 20 GAGGACGTGG CAACAATAAC GGGTCCCTT CTAGTTTCT CAATTGCCTT AGAAATAGTG 420
 GCAGCGACT TCGCGAAGTC ATTCTTCAG ATGTTCTAC CGTCAACAAC ACCTACAGAC 480
 25 AACGACTGGT TTTCGCCAAC GATCGCTAGA ACGTGTCCA ACTGCTCTGG GTTCTCACC 540
 AAGTCGAAAT GTAGGCCAGC CACTGGAAGA TCACAAGCG CCTTCAAGTT CGGAACGACT 600
 30 GTCCCGAAGT AGGTGGTCAA CACAATGTG AGAGACTTTT CGCACTTAT ATGTTCATAA 660
 GCGTCTTAA ACGCAGACTG TACGTCTCT GCAAGATCTA AGACCAACAC AGGCTCATCC 720
 35 AGCTGA 726

(2) INFORMATION FOR SEQ ID NO:733

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1478RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

5
 GATCATTATG CATTTTATGA TATACACTGC TATCAAAGAC GACCAGTCGG TAGTGAATAC 60
 ACACCGGCTG GCAGACACAA CCAATGCCGA GGATGAGGCT AGTGAGGACG AGTTAGAGGA 120
 10 GCTCGTTAGT AGCAGTCAC ACAGCGGCGA TGCTACTAGC GAGTGAAGAG GTATTTTACC 180
 TGAGCTTTGG AATATATAGG TAGGTGATGA GCTTTACAAT ACGTATTGGC TAACAATGAA 240
 15 ATGCAGGAAC TCTCAAGCT CTTTAAGTTC TGTA AAAACG GTATCAAAA CCGTTTTTCC 300
 AGCGCTGTCT GCGTAAATGA CCTGGATTAT CGCATTGCAA TAGTTGCTGC TCTTCAAGGT 360
 20 CAGATCTATG ACGCCTTTTG CGCGAGGCT GGTACGCAGT TCGCTGGTG GCATGGGAG 420
 GATCTTGICA AATAGGCTA TCTGTTTGT TAGGCTAGCG ATGTTGGCT CACGAGCATG 480
 25 GAGCGTATCG GGCTGGCTTC GTTGTTGAAG CAGCTGATG GACGAACCAG GAACAATGTT 540
 CAAGACGCAC TCGTAACAA CTCTTTTAAC CACCTGTAAG TAGTTTCTAT GCCTTATTCT 600
 30 ACCCAAACA GGTCTTAATA GGAGAAGGTC ACCATCAGCT CTATATTTAT GCTTGAAGT 660
 TGCTGGCTTG AGGCC 675
 35

(2) INFORMATION FOR SEQ ID NO:734:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 706 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: PAG1478UP
 55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

5 GATCTGAGTA TCAAGATACC ATGAGOGATT CTTGCTCACT CTTGTACGGG ACTGCCCCGC 60
 TTATCCAAGT GCAGACAAGA TGCAACATGC ATACTGGCAG ACCAGGCCCT CTGATCATC 120
 10 GAGTTGCTTT AAGCAACATA GTAGGAGGCT TCGAAGGAGG AGTTCTTCGG CTACCTATGT 180
 AAGAGATGCA GCGGATGGTT ACTGCTGGTC ACGTCTAGA ATCATATACC ACGGAAAAGT 240
 15 GGATATGTTG CTTGCCCTTT AGATATGGCA GTTTTGCCAC CCTACTTGAC ACAGCTGTAA 300
 CAACGTTGAC TAAGGATAAA CAAGAGCTAC TGTCAACGGG CTATCCATAC AATGACATCT 360
 20 GATCTAATGG AGGTGGACTC GGGCCATACA CCGGATGTTT ATAGCGCAAG CAAGGACAAC 420
 GTTGACAAGT TTGTGATCTT GCTTCGCCAG GTCTCCAAGA CTACTATAAC ATTGGACTCC 480
 25 CGCTATGTGT GGAAGTCTCT TCGCGAGCTA ATGCTTTTGC GCAAGGAGCT GCAGCAGCAG 540
 ACCCTACCA TCCTTATCAC GTCCTATAT CCGGACGACT CGGCATTCAA GGTGCCATTG 600
 30 CTTGTTGTGG TGAACCAGAA CTCAAAGCA GGTGAGGA TGCGGAGGCA TTCCAGGGCA 660
 AGTACCCCGC AGACTTTATC AGCTGACTGC TGACGGCAAG ATTGAC 706

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1479RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

GATCGCTTA CAGTAGCATT GTCCTCGCAG GTTGCTGCC TCAATTTTAT CCGGGCCCTC 60
5 GAAGAACTCC AACTCGAAGA GGAAGTTCGT GCGGCACTGG CATAAATTGT CTATGCCCAG 120
CCCTGTTGG CAGAAGCAT GCTTGCACTC TGCAAACTGC TGCACTCGA ATTGGGGAT 180
10 CAAGAGCTGT AGCTCCACGA GCGCATCCTT GGTAAAGCTG CTGCTCGGG AGGGTGGGC 240
GCACCGTTTG TCGATGCATT CGTTGATCTC CTCTGTTAGG TTGCGTCTG TGTGGGCGA 300
15 ATTCTCGAAA AGGTCGGGC GCACTATCTC CCTGCTGAA GGCACCTTGT TCTCCTTGT 360
COGCTGTCG TTTTCGTAGG GCGAGGTGAC TGATGATGAA TCATTCATAA AGCTGTTTTT 420
20 ATTCCGGAGG CTGGGCTTGC GCTGCAAGT CACGTCAAAT TGTTCAACG CCTCTTATA 480
AGGTCCTTTC TCATTATTA TAGCACTATG CCAAGATCCA GATGIGGCAA TCTGGGATTA 540
25 CTAGACCTGT TGGCCAGCA TGAGTCTC TTATATACAC TGCCAGTTTG TGTCTGACAC 600
AAAGACGTAA AATTGGGACT ACCAAAAGG AGTGGCCAAA CAAGTGGCAA ACGTGTAA 660
30 AGGATAGTGT ATATTATAC TATTAGTAAT TATGT 695

(2) INFORMATION FOR SEQ ID NO:736:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 716 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1479UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

GATCGGGCA TTACGGTGC CATCTACGAG GAGGACATTG TCGGGGACCA GGGCGGACG 60

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GACGTAGACG GGCAGCCGCA GAAGCTGGGT TCGTACCGG CGGGGCGCG GCGCTTCTCG 120
AACACGCTGT CCAACCTGCT TCCAGTATC AGCGGGAAGC TGCACACAA CCGGAAGGGC 180
GGGACGGGA AAGTCGCGC GTCTGCTGCG GACGCGGACG CGGGAGCGG GTCTACCGTG 240
GTTGCGGGAG AGATGGCGGG CAGCATCAG CCTCCGAGG ACCTACATAA CGTGGTCAGC 300
TTCCCGGAGC CACACGGGCT TGCACAGCCA CGCACTTGA GCGAATCGTA TACGTATGGT 360
TCTGGATACA GTGGCCACCT GCAGCCACA GTCTCCAACC CTGCTACGCG GACTCGGAAT 420
AATACTGTAT CTTCGCAGAT TACTTCGCTT TCAAGCATGG GCGAGCTGGG AAGCCCCAGC 480
ACGAGCAACA TCTGGACCAA CAATGGCTCA AGCCCCGCG ATCCAATCAG CAACATGCTC 540
ACGACGCGT TCAACCCGAT CCCCCTCCCC GACTTTGGCC AGTCGAAC TAACGACGTA 600
ATCAGCAGC AGCAGCCTCC GCAGTGCAG AACTCACTGA ATGTGCCCTC CGGGGGTAAT 660
ATTTCTGGGA AAAACGTACT CGTTCTCAAT CTAATGCTTC TAGCATATAC GCAGAT 716

(2) INFORMATION FOR SEQ ID NO:737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1480RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

GATCCTCTGA GCGAGCCCT ATCCCAAGTT TATTCCAAC TCTTGCCGAA AGGTAACAA 60
CGTTTATTT ACATGAGTTT ACACATAACA CCGGAGAATG TTGATGTTAA TGTGCATCCT 120

ACAAAGCGTG AAGTACGATT TTGTATGAA GAAGAGCTAA TAGAGCGCAT TGGTAATTTG 180
CTCCATGAGC GGTATCTCA GCTGGATACT TCGGAACCTT TTAAACCGGG CTCCTTGACA 240
CCTGGGAAAC ATAGTTC AAC TGTCCTCC GCATTCGGC AATCAGCGAC CCCCACAAGT 300
ACACAACCAA AGGCAAAACG TGCAGAAAC ATGCTTGTC GACTGATGG TAGCCAAGCT 360
AAAATTACTA ATTATGTCAG AGCAAGTCAA AGCTCTACCA GCTCATCCTT TTCACTTCT 420
TTAAGAAAGA AATCACATGC GGCAGCAAGT GATGAACCTG GCAGCATTGG CGAGGACTCC 480
CAAGATACAG CAACATCGAT GACAACCTCT ACACAAGAGC CTAATCATAC CAAGTCTAGA 540
GCCATTTTAA CCTTATTGAA TAATGAGTAT GAAGTCGTAC AGCGGAAAG AACGGAAGTA 600
AATCTCACCA GCATCAAAC TCTAAAGCAG GAAGTAGACG AAGATATGCA TAAGGGAATT 660
AACAAGTGT TTTGCAGATA TGACCTATGT TGGTGTGTT GATGCAACAA GCGGACTTGC 720
ATCTATACAG CATGGTTTAA AGTTATTT 748

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1480UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

GATCGGTCA TGGGATACAT AAACCACGGA ATCAATGAAA AGCTCGCTTA CGAACAGTTT 60
GGATCTGTAC CGGAGAAGGG CTAATATATT CCTCCACAA TATTTCTGGA CGTTCTCAG 120

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AGCTCGAGAC TCTGCGTGA AGAGATATTC GGCCCTGTGG CCGTAGTTGC GAAATTCAAG 180
 5 GACTACGATG AAGCTATTTC TTACGCTAAT GACACTAACT ATGGGCTGGC ATCCTGCGTT 240
 TTCACTGAAA ACATACGGGT TGCGCACGGC TTGTCCGTG ATGTCCAATC TGCACTGTG 300
 10 TGGGTAAATT CCTCTAATGA TGAGGAGGTG GGAGTGCTT TTGGGGGGTT CAAGATGAGC 360
 GGTATCGGAA GGGAGCTGGG GAAGGCAGGC CTGCAAACCTT AACTCCAGAC TAAAGCAGTA 420
 15 CACCTGAACT TTGCTTAGAT AGAGCAACTC ATATATTAGA ATCACTTCAT ACATCAACTA 480
 TATATCATT TGTATATGAC TATGCCAGAG GTGTAGTGA ACCACTATTT ATCAGTGAT 540
 20 AGGCGTTGCG CGGTATCCC GCCAGTACCT GCGTTGCAGA ACGGGGGGA CACATTCAGC 600
 AGGTCTATA TACAGTTGTC GAGGACAGTA TGCAACGAG TACCAATTATA GCAAGTAAGC 660
 25 CGTGTCTGT TTGCATAAAG CGTAAGGTCA AGTGGGACCG GCTGGTTCCC TGCAAGAACT 720
 GTGTCAA 727

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1481RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

GATCGATAGG CCACACTTTC ATGGTTTGTA TTCACACTGA AAATCAAAAT CAAGGGGACT 60
 55 TTTACCCCTT TGTCTACTG GAGATTTCGT TTCTCCATGA GTCCCCCTTA GGACATCTGC 120

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GTTATCGTTT AACAGATGTG CCGCCCCAGC CAAACTCCCC ACCTGACAAT GTCTTCAACC 180
 5 CGGATCAGCC CGTATAGGAC TTAAATGCT AGAAGGTGGA AAATGAATTC CAGCTCOGCT 240
 TAATTGAATA AGTAAAGAAA CTATAAGGT AGTGGTATTT CACTGGGGCC GAAGCTCCCA 300
 10 CTTATTCTAC ACCCTCTATG TCTCTTCACA ATGTCAACT AGAGTCAAGC TCAACAGGGT 360
 CTCTTTTCCC CGCTGATTCT GCCAAGCCCG TTCCCTTGGC TGTGGTTTCG CTAGATAGTA 420
 15 GATAGGGACA GTGGGAATCT CGTTAATCCA TTCATGCGCG TCACTAATTA GATGACGAGG 480
 CATTGGGCTA CCTTAAGAGA GTCATAGTGA CTCGCGCGGT TTACCGGGC TTGGTTGAAT 540
 20 TTCTTCACTT TGACATTCAG AGCACTGGGC AGAAATCACA TTGGGTCAAC ATCACTTTCT 600
 GACCATGCCA ATGCTATGTT TTAATTAGAC AGTCAGATTC CCCTTGTCOG TACCAGTTCT 660
 25 AAGTTGATCG TTAATTGTAG CAA 683

(2) INFORMATION FOR SEQ ID NO:740:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1481UP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

50 GATCGGGTGG TGTTTTCTTA TGACCCACTC GGCACCTTAC GAGAAATCAA AGTCTTTGGG 60
 TTCTGGGGGG AGTATGGTCG CAAGGCTGAA ACTTAAAGGA ATTGAAGGAA GGGCAACCACC 120
 55 AGGAGTGGAG CCGCGGGCTT AATTTGACTC AACACGGGGA AACTCACCAG GTCCAGACAC 180

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AATAAGGATT GACAGATTGA GAGCTCTTTC TTGATTTTGT GGGTGGTGGT GCATGGCCGT 240
 5 TCTTAGTTGG TGGAGTGATT TGCTGCTTA ATTGCGATAA CGAACGAGAC CTTAACCTAC 300
 TAAATAGTGC TGCTAGCATT TGCTGGTTGC GCACTTCTTA GAGGGACTAT CGGTTTCAAG 360
 10 CCGATGGAAG TTTGAGGCAA TAACAGGTCT GTGATGCCCT TAGACGTTCT GGGCCGCAAG 420
 CCGCTACAC TGACGGAGCC AGCGAGTATA ACCTTGGCCG AGAGGTCTGG GTAATCTTGT 480
 15 GAAACTCCGT CGTGCTGGGG ATAGAGCATT GCAATTATTG CTCTTCAACG AGGAATTCTT 540
 AGTAAGCGCA AGTCATCAGC TTGCGTTGAT TACGTCCCTG CCTTTGTAC ACACCGCCCG 600
 20 TCGCTAGTAC CGATTGAATG GCTTAGTGAG GCCTCAGGAT CTGCTTAGAG GAGGGGG 657

(2) INFORMATION FOR SEQ ID NO:741:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 694 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1482RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

45 GATCCATTGG TTAATATGGA TTGCTACAG TGAGAGCAAA GAGGGGGGGG GATTTAAAGC 60
 ATGGTGGGGC GACGCTATT TTAAATGGGG GTTGTTTGCA ACGTTTGTG CCGGCTTCT 120
 50 TGCTCTGCAT AGTGAAAAGT TCATTGCCCA AAGAACGTAC GAATCTTTC TGATACTGCA 180
 CAAGCTCTTC AACATTGTCT TTATTGTATG CATGTATATG CACATCAAAA CGCTGGGATG 240
 55 GCACGGCTGG GTCTGGTGA TGGTTGCCAT CTA CTGCTTC GAGCGTGTGG CCCGATAGC 300

TCGCATTGTA CTTGCTGGAG GCATCAAGAA GGCCACATTA ACAGATGTTG GGGATCGCGT 360
 5 GCTCAAGATG ACAGTGGAGA AGCCAAAGCA TTTCAAATAT TACCCGGGGG CTTATGTTTT 420
 CGTTTATTTT ATTAGTGGGA AGGATGCTTG GTTCTATCCA TTCCAGTCGC ACCCGTTCAC 480
 10 CGTCCTTAAT ACACCCAAGA TOGATGGCGA CAACTGGTG ATTTATTTCA AAGTGCACAA 540
 GGGCGTGAAG CAGCAGCTGC TAAACAGGAT CTTTCTATCC GGGAAAGAGT CCATCGAATA 600
 15 CAAGGTGCTT CTAGAAGGGC OCTATGGAAA CACCATTCGG GGGCTTGCTG CTCTGACCG 660
 GCGCTAAGTG GCGGCCAGCG CAGGTCTTGG CGTA 694

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1482UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

GATCGCGCGG TTCGGCGCGG TGGCGCCAAA GCTGAACCGG TCCGCGCCGA AGGATGCGAT 60
 GTGGCGGCTG CGGAATTACT CGATGAAGTG CAATGAGGC AACGATGTGT ATCTGCTGCT 120
 45 GAACGGGTCC AGCCACGTAG CCTGCGAGCT GAGCGACACA CTTCTGATT GGTGGCCAG 180
 CACCGAGGAT GAGCCGGTGA TGGAGCTGGT GCTGCGAGAG TGGCTGACG TGAACCGGC 240
 GCTGGAGTTC CGCGTGTTTG TACGAGGTGG GGAGTCTG GCGCGTGCC AGCGGGACCT 300
 55 GAACTACTAT GACTACCTGA AGCCGCTGGA GGAGAAGCTG AGGACGCCA TTGAAGACTT 360

CGTGCAAGAC GTGATGCTGC AGCGGCTCCC GGACGACACC TTGTGTGGG ACGGTACAT 420
 5 CCGCGGGCCG TTCACAAAGG TCTGGCTGAT CGACGTGAAC CCGTTTGGC GCGAGACGA 480
 CCGCTGCTG TTTTCATGGA ACGAGCTGTG CACCTGAAGC CCAACGCGA AGGGCACCGG 540
 10 AGCTGGGCTT GGTTCGGGAA AACTACATCG GTGCTTGGC GGAAACAAC ATGGTGGCT 600
 TCGCAGCGAA AGGAGCACTC GGAACACCAG GTACCTCTGG ACGTGGTGA GGCAGGGCTC 660
 15 AATCCGCAAA GCATGCAGAA GCTGGTTGAG A 691

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1483RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

GATCCAAAAA ACCTCTWAAG GTACAGTCTC TAATTGCTTC CATSTCTTTT TGAACATACA 60
 40 TGGACCATGC ATCTCTGTTT TTGTACCGA CAGAATCTTG YAATGCAGCA ATGGCACTTG 120
 GCTGTTGAC GTGCTTATAA CCACCATCCC TCCAATGGTA TTGCGCGCT TCAGGCAAGT 180
 45 TGACAGATCT CTTAATCKTA AACCTGATG GATAMCCGG CTCGTGCAAT GAAAAGGGT 240
 CTGSGCAAT GTATTCAAAG GTAACACCTT TAATTCTAGA AGCGGTTCCG GCAAAACACA 300
 50 AATCAATCAC TGAGTTATCA ATACCTAAAG CTTCAAATAT CTGCGCTCCC TTGTAAGATG 360
 CCAGAGTAGA GATACCCATC TTCGACATGA CTTTGTAGTAT ACCGCGGTCA ATTGCTTCCT 420
 55

TGTAATTATG CAACAGTTGC TCATCTGTAA TATCAGAGTA GTCATOGTTA ACATTCCGAA 480
 5 CTAAACCTTC GTTATTCATT CTGACCAGG TTTCATOGC TAAGTAAGGG AAAATACCGT 540
 CACACCCATA GCCAAGAAGA ACACAGAACT GGTGAAC TTC G 581

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1483UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

GATCATCAGC CCGCTGCTC CGCCGAGTA ACGGCTCCAC GTGGTAGTCT GCGTCCCTG 60
 CTAGTCGGTG GTCATOGAG AGGTCTCTT CTCAGGCTC GGAGTTGGCC ACGGAGGCAC 120
 TTGAAAGACT CTGTCTTGA TTCAATCCC CCGCCCCGTA TTCTCGCCC TGTGGGGTG 180
 GCTTGGTGAG GCCCTCCCGC TGCAGATCTT CAACGTCATC CTTGAGCTCC TGAAGTTGG 240
 CAAGAATTCC GGTTCCTGA GAGACATAGA ATTGTCAAT TGGCTCAGC TCCTTATCCA 300
 GCGCCGCAAT GAATCTTTG ATGTAGCTCT GTGCAAGCG CACCGCTCG GGTCTCTGTG 360
 CAAACGTCTC ATGCTGGTAC AGCTTGTCTT TCTGAGTGT GTACAGGAGC TTCTTCAACT 420
 GCGAGTACGC GATATACTTC GACGAACACT CAGGGACCGC GTTGAATTGC AGCGAATGTG 480
 AGAACTTCAT CTTGGCTTCT ATCGCCTAAC GGCCTGGTC CGTCGCGATA CAGGTCTGTC 540
 TCATTGAAAG TACGCAGGC AGGCATAGGT TTAATTCCAG GCTCCAGGA GATTTTGGTG 600

CAAGAGGACG TTTTAATTCT CATTATATCA CGTGCCCTGG CTATATTIAT AAAGTTGCOCT 660

CTAACGGG 668

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 707 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1484RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

GATCCTCTTC TATAACTCAA TTAACAATGT TTCTCTCTGT GGAGTCGTTC CTGCATCTTC 60

CGTAACCCCTT TCATTCTGAG GGTAGCCAT TTTTATCTTC TGCGCTGGAA CACTCGGGAA 120

TTCAAATTGA GTTATTGGCA CCTGTGCTC CTCTCTCTTG TCGGTATAC TTTCTTCAGG 180

AGGATAAAGA GGCTCCGATG GTGATGATAG CAGTGTCTTC TTAATATCCG GTTCTGAGAC 240

CTGCGGCTCA AAGCCAGTTA CTGATTGCGA CTGGCGATTC TCCATCGGG AACTTTGTGT 300

GGTATGTAGG ATTGCTGGAG TGAGTCTGC AGGTTTGAA GAGCTCCTGG CATAGCTACG 360

ATATGTTGGC TCAGGTTGGC TCTTCTCGTA CGGAACAGTG TTGGCTGGAG AGGACTCTGG 420

TTGTGGTGC ATTTGATAAG TGTATGGATC AGAAGGTAAG TGTGGCATGG AATATTGTTG 480

CGAAAGATTA ATATTCTCA ATTGTCTCTC TAACATGGTG TCATAAATGC TCATTATATC 540

CGAAATTTTG GCATTTCATGT CTACCAAGGT ATTATATTG TGAAACGTAT CGTTAAGGGA 600

ATGGTTTAAC CGAGGCCGAG TTCCAAGGAC CTCTGGTAT AGCATCTGCA GCTGTGTATC 660

CTCTAACACG GCATTCATTG GCTGACCCCTT CCTCTTCCTC CACTAGG

707

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1484UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

GATCTGGAG AACGTGCTAC AACACTCGTG CCGGGTCAAG CCGGACCGA AGCTGATCGA	60
CCAGCAGCCG GAGATGAACC CCCAGCACAC GCGGACTGCG ATCGTGAACT TTGCGTTGCA	120
GCTGGGCGCAG AAGACGCGGG TGACGAACGG GATCTTTTTC CACGCGGTGC GGTGTACGA	180
CGTTACTGC TCGAAGCGCG TGGTGCTACG GGACCAGGCG AAGCTGGTGA TTGOGACCTG	240
CCTGTGGCTG GCGGCGAAAA CGTGGGGGGG GTGCAACCAC ATCATCAACA ACGTGAAGGT	300
GCTACGGGT GGGCGCTTCT ACGGGCCCAA CCGCGGGCG CGCATCCGC GTCTGTCCGA	360
GCTGGTGAC TACTGCGGGG GGTGAAAGT GTTTGACGAG TCGATGTTCA CGCAGATGGA	420
GCGCCACATC CTGGACACGC TGAGCTGGGA CGTGTACGAG CCGATGGTGA ACGACTACGT	480
GCTCAACGTG GACGAGAACT GTTTGATACA GTACGAGCTA TACAAAAGGC AGCTGGAGCA	540
CAATCGGCAG TACGCCAACA AGCGCAACTC GCAGGACAGC AACCGGACCG AGGAGGACGT	600
GTCCGAGGAG GACGAGGACC TGGATAACAA GATCCAGTTA ATCAACATCA AGAAGTTTCT	660
GATAGACCTG GCGTCTGGC AGTACGACCT CTTGAAGTAT GAGGTATTCC GAGCTA	716

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1485RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

25	GATCCCCGCG TTATTAGCAC GGTGCCCTTAA CCAACTGGGC CAAGGAACCA ATTACACTTA	60
	AGATGCTATT TGCAGATAIT TGTAGTCCAC TCAAGTCAAC ACGGGCATAT TTTACTTTCT	120
30	AATTCTTAAA TTCTTAACTC TAAGCCAATC TAAGTAGTTT ATCTATCAT CACTTGATCC	180
	TTGCGTTTGT TTGGTCTATA ACCTTTAATT GGGTAGTGCT TATGGAAATA TATATAATGA	240
35	GATATTACAT GGTGCCATA TAACTTCOGT ATGAGAGTTT GCGCGAGTGG TTTAAGGCGT	300
	CAGATTTAGG TTATCTCTCT AAAATCTCTG ATATCTACGG ATTGCGGGT TCGAATCCCG	360
40	TAGCTCTCAT TATTTTTTGT ATATTGTCCT TCTCAGGCAT GTGACATTTT GCATCATAAT	420
	CATACCGAAG ATATGGCTCC CACCGTGACC TGATACATTC TCGCATCTGA AGGCATGCAA	480
45	TTTAATGCAA CTGTGGCTGC AGATGCTCTA GGTAGGAACT AGCACAACAT CTAACAACCTA	540
	GCTGCCATA TACAGCGCAA TGACAGCGTC TGAGTCGTTG TGGCACCGAT CATAAGCCAA	600
50	TTCTGATTGT CTGAAGACAG GCTATGAGTC TOCCACAGTC CTCCTTGCTG TOCCATACGC	660
	ATATAAATAC CCTTAAACT CAATTAGCCG GTATTTTATT TGAGCTGCAG AAGGTATCTT	720
55	AACTCAGGTA TAATATACTG TAATGGGG	748

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 755 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1485UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

GATCGGAGGT AGTGTTTTTC GTGGGCACGG AGCTGTAGCA CGGGGGGTCC AAGAGCGGCA	60
TTGTGCTGTG TATGTGTGGT ATGACCTCGA TGAGCTGCTT GCGAGGTGC TCACGTAAT	120
CTTCGGTGGG GAGCCACAT TCCTTCGGT CGGGAAAAT GGTGCAAG TACTCGAGCT	180
GCTGCGAGAC CTTCTGTAT TCTAGCTGC GGTCAAGCA GACGATGGG TTGGCTGAA	240
GGATCGTGAG CTGTCGAGC ACGTCAACGA GGTGTCGAA TTGTGGCACC GCGCTCAGG	300
CGCCGTGAT CGCTTAACA AAGGCGGCG GGGCTTCAG GGCTGTCCA CTAAAGAGAT	360
CACTGGGCTC GAAATGCTG ATTGCCCTGC GCATGTACGG CACAAGCTGG CGGACACGA	420
ACAGATAGCT CATGTGCGG GAGTTCGAG TCACGCTAAC TGCCGAGTC TTGGTTGAGT	480
GGCTGAAGGG CCTACTGCCC CGGTAGGCG ACCCGAGAAA TGCGTCATCA CCTCGTCTTC	540
ATCTGGCTTG AGATACAAAT CCGAAGCGG CAGTTGCCT GTCATGCAG AGTTGTTTGA	600
CAAGAGCAGC TCGTCTAGT GCTGCTGGAG CTGGCCCACT TTGCTTTTGA GTAGTTCCAC	660
TTCACTGCCC TTTCGGATA GCATGAGCTG CAAGTGCAG TTCTGTTTT GCAACGCCAG	720
CACCTCATCG GCGCGGTAC CGCTGCTCTT GCAGA	755

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1486RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

GATCCTTCTT GTACATTTCT GATTTTAACA ATGTCCTCAT AGCGTATATT TTACCGGTAT	60
CTTTCTTCTG CACCAGACGG ACCTCACOGA ATGCACCCCTT TCCTATGACT TTAACAGTGT	120
GGAAATCTTC CAGGGATAGC CGTGTCTTAC GCAAGGCGAG AAATGCGAC TCCTTTTTCAC	180
CCAGTGAAGA AAGCTGTCTG TTCTTTCTCT CTTCAGACCA GCCATGAGAT AATAGCTGGG	240
ATTCAAGTTC CACGGTCTTT TGGTTGCGCT CAATGGCATG ATTGACAGAT GATTGGTAGA	300
AATTCTCGAC TTTCAGCTTC ACTGCAGCGG CTTTTTCTTG TGTGGATTTG CTCAGTAGCT	360
CTGGAAGTCT CTGGAAGTAC ATATAGTTCC CCACTCCCGA GGTTTGCCGT TGGCCCCCAT	420
TGGGCGATTG TGGAACTGAA GAGCACTGCA GGGACTGACG GGATAGCATA GGGCCCTGGG	480
AGCTCTGGTT TCCCACTAGC GTCTGATGCG CAAGGCTTCC GTCTAGTAGT CCAGGTAGAG	540
CTGCAGGCTG TAAAGGGGAC TCCGACCCCG CAACTGTATT ATACGCAGAG GAAGCAGGCT	600
GCTGCCCACT GTAGTCCGAG CTGTTGGAGT AGTGTCTTGG TGAAGAATGG CCGGGGGCAA	660
GAGTAGTGTC GTTCACGTTT CGTAAAAGAG TTGTTGTTCT GGCTGTAAAT GCTGGTGGCC	720
GTAGGCGGG	729

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1486UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

GATCAAAACA GCATGTCTAA GTCTGTTGCG CGCTGCCCCG AGTGCCACAC GGAAGTGGT 60
 AAGTGCCCTCA TACAGCAGAA CTACAGCATC GTGATTTGCC CGAAGCAGCA GTGCATGTAT 120
 CGGTTCAATG AGGCGGAGGT GATCCAGCAC CTGGTGCAGA CAAGTGACAA GGAAATCCTG 180
 GAGGCTGCAA AGGTGCGGCT GAAAAACGAT AATATCACAG GCAGCGGAGG CGCGCTCATG 240
 GAATAAGGAA CCAACCGTGT GCTATATACG TGTACTGTCT ATGTTAAGTA GGTCTCGTGC 300
 GCGCGAGGCC CTGCGTGGCT AAAGCTTTAG ATTGGAGTTG TACATGATGT CGCCATCGAC 360
 GCTGATGCTG ACACTGAACT CAAGGTCTTC GTGGTGGAT ATGTCCACG TTTTATATAT 420
 CATCATCAAC GCGAACACAT TGCAAATGCT GCGATGAAC AACCCTGCGA GGTAGTGCTT 480
 GACGCCCCTG CAGATCTGTT ACGAGATGGT ATACATCAAC ACCTGCCCAG TAGTTATAAA 540
 AATGACACCC AAAATGGTGG ACCCTGTCAT CCAGAAGTTG GAGAGCAGA AGATGGAGAC 600
 CACGAGCTGG CACACCGAGT ACATTAGGAA CGCGAGGCCA TTGAGGCGGT ACATTACAAC 660
 GAAAAGGCGG TCGTGTTTGT TTTTCATGTC GGGTGGTGCT GAATCCAATT TGGTGAAGG 719

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1487RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

GATCGAGCGC GAGCCCATCA ACAACGAGGA GTTTCGCTAC CAGCAGGAGC TGATACGAAA	60
GCGGGACGAG GAGATAGCCA ACATCGAGCG TGGTATCGTT GAACTCAACG AGGTCTTCCA	120
AGACTTGGGG TCATCGTGC AGCAGCAGAG CGAGCTGGTA GACCACATAG AAAACAACAT	180
ATACACTGCG GTAACGAGCA CGAACCATGC ATCTAACGAA CTGTGCGCG CACTGAGATA	240
CCAGCGGGGT TCCAACAGGT GGTGCTATA TCTGCTTCTC GCTCTGCTGG CATGCTCTT	300
CCTGATCGGG GTGACAGTGC TTTAGAACAT CTCAACTAGT CTACTATGTA ACGCTTTAAT	360
ATACTACTGG CTGACCTACT CCTCCGCGAG TTOCCACAGG TTCAAGCAGC CGTCATCGCC	420
GCCGGTCACC AAAAGAACGC GCGCGTCTAA CGCCAGCCAT TTCACCACAT TGATCTCGTA	480
GACCGTGTGC GCGCAATCTA CGCGGGCTAC CACTTCCAC CGGCCAGCCT GTACCTCTTT	540
GTATACCGCC AACACACCAT CCGAGCCAAC GCTCGCGATA AGCCCGTCCG CCCTCCAAC	600
TACGCTGTAC ACAGCCCGCG TATGCAAGGC CGGCAGGACC GTCTCTTGGA TCACTCTTT	660
GTCGAAGACG TGGCGTGGT CAGTGAGGCA CGCCAGATG CGC	703

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1487UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

GATCCCAATA CTGGGACTTT ACTAATACCA GCCATGCGGG CAGCTCTGCA GCAGCTGGTA	60
ATGACAAGGA GGACAAGAAG AACAAATACT GGAACGCAGA CGOOGAGTAT CTGATCGAAG	120
AGGTGAAGAA AAACAAAAG AGTGTAGTAA ACTACCTTGA ATCGAAGACG AACGACGAAA	180
TGACCCGCAA GGGTCTGATC CGGAACCTGC AACGATTTCG AAAGACAATT CTAATGAAGG	240
AAGGGTTCGA AAACCTGGAG GATATGCTCA CGCTTTCTCA TTTGGAAAAT AGACTGCTGG	300
TAGCCCTAAA ACTTAACGAG ACAATGAAT TTACCAAATT ATTGAAAGTC TATTGCATCA	360
GCCTAGCAGA AATGGGCTTC AAAAATAGAT TGGATGATGT GCTGAGCTGG CTGTATAACG	420
ATGGAGAATA CAAGGTGGC ACAATAGCTA ACGAGAAGCG GGAGGAACTG CTGAAGCAGA	480
TATTGGTTGC ATGTGCTGAT ATCCGGCAGG TCCAAAGAGT GACAACCAAT TACGCATCTG	540
CTCTTGGTCT TCTTGATGTA TCTTTATAAT TATTGCTAGT CTATAGACAA AGTTGGGAAT	600
CTGAATATAA CT	612

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1488RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

GATCAACAAA TGATTTTCTT ATTTTCCGCG CACCGATCAA CGAGATATCA TAGGAATCAA	60
TGTTGCAGGC AAATCCCTCA CCGAGTATGA AGCTCTGGTA TGCTGTGGC GTTGTTCCTT	120
TCATTAAC TG CCGTCCCTG GGCAGTCC TTAAGTTTG ATGATCGAGA TATCCACAAT	180
TGGCTCATT CATCGTCTCC AATCCAATGA TGCAGTTTTC TTGGAACAAC TCAGGCGCGT	240
TGTCCTGAAT GTACTTGTAG AACGTCATTA CGCTTTTCAA GAAGTGCCCC TGGAGGTAGT	300
CTTGAATATT TCTACCAATTA ATTACACATT TAGGGGCAAA TAACTTGCCG CTAAAAAAGA	360
GAGTGAACAT AGTCTGGCAG GCTAGGCGGT AATAGTTTGT GGACCAAATC ATTTCTGGAT	420
ACTGTGCTTT TTCCGCCTGC GTCTCTGAAT CGATATAGTA GTTGTGCAAT ATGGCAGCCT	480
CAGTAGCTAG GAACCTCTTC GGCTGAAAGC CTGCGCAATG CAACTGCCAT AATGGCGCTC	540
CTGATCCCC AGAAAAGCGA GACCACAGT CCTGGTGGG GTCTAGGTAT ACGTACATGC	600
CGCCCGCTC CTGATCTTT TTAAGCACCA TCACCGTGTA CTTGATGTAT TCCTCATGCT	660
ATATCCCTGG GCGCCATGC TCCAAGGCTT CCAGGTGAA CAAATAACGG ATACA	715

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 684 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

EP 0 866 129 A2

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1488UP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

10	GATCTCGTTT AAGCTGCTGG TGAAGTTTGC GAAGGGTAT GAGCTTTCAC GACGCGAAAC	60
	AAACCAGCTG AAGCGGTCTA TGGGCGATGT CTTCCGGTTG GTGCCCTTTT CTGCCTTCT	120
15	GATTATTCOG TTTGCAGAGT TGTGCTGCC CTTCCGCTT AAGCTTTTCC CCAACATGCT	180
	GCCATCCACA TATGTTTCTG GGACGGAGAG ACAACAGAAG AGAGTTAAGC TAGAGGAGGT	240
20	GCGGCGCAAG ACGTCCAAC TTTTGCAGGA GACACTAGAG GAGTCTCAT TGATCAATTA	300
	TAACTCGGTA GAAGGTTTCA AGAAGCGCAA AAAGTTTCTG AGCTTCTTCC AGAAGGTGAA	360
25	CTCCCCAAG GATGGCAAGA CCACTGTTT TACCATGAA GAGATTTTGT CCATCTCCAA	420
	AATGTTCAAG AACGACACTG TGCTAGACAA TCTCTCCAGG CCGCAATTGG TTGCCATGGC	480
30	GAAGTATATG TCCTTGCGGC CTTTGGGCAC TGACAACATG CTTAGGTACC AAATCCGTTA	540
	TAAATTGAAG AGCATCGTGG AAGACGATAA GAAGATAGAC TACGAAGGTG TTGAGTCACT	600
35	GAGTACAGAG GAGCTCTATA GTCCGCGGC TTCCGCGGG ATCAAAGCCT TCGGTGTTTC	660
	TAGGGAAGAT TTGGTGAAA AAAT	684

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(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PAG1489RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

5	GATCACGCGG GAGCACGTGC AATCATTTGAA CGAAAGCCCG GGGTTGCTTG CTTTGGCGAT	60
	GGAGAGTCAC AGGGACCCAA TTACCGGTGA GAGTACATTG GTTGGTTTTT CCTACGTTGT	120
10	TCCGGGCGGT CGTTTAAATG AACTTTACGG CTGGGACTCA TACCTAATGG CTTTGGGTCT	180
	TCTAGACTGT AACAAAGTGG ACATAGCACG TGGGATGGTT GAGCATTTCA TCTTTGAGAT	240
15	AGAGCATTAC GGTAAAATAT TGAACGCCAA TAGGAGCTAC TACCTCTGTC GGTACACAAC	300
	CCCGTTCTTA ACCGACATGG CTTTGAAGGT CTTGAAAAG TTGGGTGGTG ACCAAAATCC	360
20	TACCGCTGTG GATTCTTGA AAAGAGCATT CATGCGAGCC ATTAAGGAAT ACAAGAGTGT	420
	ATGGATGGCA GAACCGCGT ACGACAAAAC CACGGGTCTT TCATGTTATC ATCCAGATGG	480
25	TATCGGTTTC CCACCAGAAA CCGAGCCTGA CCACTTTGAC GCAATTTGCC GGAAATTTGC	540
	GGAAAAGCAC AATGTAAAGA TTCCGGAGTT CAGGTGCATG TACGATGCGG GCGAAGTACA	600
30	CGAGCCCGAA CTAGATGAGT TCTTTTTCGA TGATGCTGCT GTACGTGAGA GTGGACATGA	660
	CACCTCTTAC CGTCTAGAGA ACGTCTGTGC TTACTTAGCG ACGATTGATT TGAATCGTTA	720
35	CTATACAA	728

(2) INFORMATION FOR SEQ ID NO:756:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 698 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

	(ii) MOLECULE TYPE: DNA (genomic)
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50	(vi) ORIGINAL SOURCE:
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	(A) ORGANISM: PAG1489UP
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

5	GATCGTAACA TTGCCCAATA GCTTGTTTAG CTGTCATCG TTCTGATGG CTAGCTGTAG	60
	ATGTCTTGGG ATGATTCTGG TCTTCTTGTG GTCTCTGGCG GCGTTACCGG CCAACTCTAG	120
10	GATTTCGGCG GCCAAGTATT CTAGCACAGC GGTAGGTAC ACAGGCGCGC CCGACCCGAT	180
	TCTCTGTGGG TAGTTGCCCT TTCTGAGCAA TCTGTGGACT CTACCGACAG GGAAAGTCAA	240
15	ACCGGCTTGA GCGGATCTCG ACTGCGAAGC CTTGGCGGCA GAACCAGCTT TACCTCCTTT	300
	ACCAGACATT ATTGTGTGTG TGTTGTGTGTG TGTGTGTTTA GTGTGAACTG CGTGTGCTAT	360
20	GAGAAAACAC TACGCTGAAA CTGCTAAATA ATCCAGACAG GTCCCCCACC CGCAAAGGAT	420
	CCACGCTATA CTTCTCTCTA CATATTTATA CTTGTCTTTT TGCTTTCTAA TCCTCGATCG	480
25	TACCGGTCTG ACGCTTCAAC AGACCTTCAC TAGAGCTCG ACCTGTGCGG GCTGGTTTTT	540
	TGCGATGACA TGTCGGTGCT GGTTTTTTTCG CGCTGAAAAG GAAAGCGCGT GGCTCCACG	600
30	ACCAGAGCGG TACTAGCTCT TTGCGTTCG TGCTCTATGT GCACGCGAAA TTTCATACTG	660
	TAGAGTGTGC CATCAGCTTC ACAGGTACA ACGGTAGG	698

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1490RP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

5	GATGACCTTC CGATACTATG CGAGCCTTC ACGACATCCA AACTGAAGTC GTTCGAGGAC	60
	CTGAGCCGCA TCCAAACGTA CCGGTTCGCG GGAGAGGCAC TTGCCAGCAT TTCTCACATT	120
10	GCGCGACTAC ATGTGGTGAC GAAAACGAAA GAGAATCACT GTGCATGGAA GGCTGTCTAC	180
	GAGAATGGGG TAATGGTGGG GGAGCCGAAG CCGACGCCAG GCAAGGATGG GACGACAATC	240
15	CTCGTACAGG ACCTCTTCTA CAATGTGCGG TCCAGGCTGC GGGGCTGGG ATCTCCAAGC	300
	GAAGAGTTTG CGAAAATAGT GGATGTGGTC GGCAAGTACG CAATCCATTC GGATGGTGTG	360
20	GGATTTTCGT GTAAGAAGTT TGGCGAAACA CAGTACCGT TAAATGTACG TGGGACTTCT	420
	TCAAATCAG ACAAGATACG GGCTGTATTT GGTGCTCCAG TCGTGGCAA TTTAGTTGAG	480
25	GTAGATATTT CTGCAGACCC TGAGCACGGT CTTACATCCA GTTGGGGCCA GATTACAAC	540
	CCAGACTTTA ACAACAAGAA GTCTATACCT GCTGTGTTT TCATTAAATA CCGCCTTGTT	600
30	TCCTGTGATC CTCTGAGGCG AGCCTATCC CAAGTTTATC CACTTCTTG CCGAAAGGTA	660
	ACAAACCGTT TATTTACATG AGTTTACACA TAACACCGGA GAATGTTGAT GTTAATGTGC	720
35	ATCCTAC	727

(2) INFORMATION FOR SEQ ID NO:758:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 728 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1490UP

55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

5	GATCTCAAAG ACCCAGTACG ATCGCGTCAT GGGATACATA AACCACGGAA TCAATGAAAA	60
	GCTCGCTTAC GAACAGTTTG GATCTGTACC GGAGAAGGGC TACTATATTC CTCCCACAAT	120
10	ATTTCTGGAC GTTCTCAGA GCTCGAGACT CTGCGTGAA GAGATATTTC GCCTGTGGC	180
	CGTAGTTGGC AAATTCAGG ACTACGATGA AGCTATTCTG TAGCTAATG AACTAATA	240
15	TGGGCTGGCA TCTGCGTTT TCACTGAAAA CATACCGGTT GGCACCGCT TTGTCCGTGA	300
	TGTCCAATCT GGCAGTGTGT GGGTTAATTC CTCTAATGAT GAGGAGGTGG GAGTGCCTTT	360
20	TGGCGGGTTC AAGATGAGCG GTATCGAAG GGAGCTGGGG AAGGCAGGCC TGCAAACTTA	420
	CCTCCAGACT AAAGCAGTAC ACCTGAACCT TGCTTAGATA GAGCAACTCA TATATTAGAA	480
25	TCACTTCATA CATCAACTAT ATATCATTAT GTATATGACT ATGCCAGAGG TGTAGTGGAA	540
	CCACTATTTA TCACGTGATA GCGGTGGGC GGTATCCCG CCAGTACCTG CGTTGCAGAA	600
30	CGCGGGGAC ACATTCAGCA GGTGCTATAT ACAGTTGTTC AGGACAGTAT GGCACGAGT	660
	ACCATTATAG CAAGTAAGCC GTGTGCTGTT TGCATAAAGC GTAAGGTCAA GTGCGACCGG	720
35	CTGGTTCC	728

(2) INFORMATION FOR SEQ ID NO:759:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 716 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1491RP

55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

5	GATCATCTCC GAATAGGTCT CGGCACGAC GGACACAAAG CGCGGTCGG AGTCACTGCC	60
	GTCCTGCTGG GCGGGTGGG AGAAGGAGAA GATGAACGAC CCGACTTCG ACTGTGCTC	120
10	CGACGCCAGC TCCTGGACGA CCGTGTCCAC CTTGACCTGC ACCAGGTCG CAGGACACGA	180
	CAGAAAGTGG TCCTTATTCT CAGACAGCTT GTTCACAGCT GTAGGCTGGT AGTCCACCAG	240
15	CGCGTCGGCC GCGGGGTGG CCGGTCTGG TCCACCACGG ATGTGCTCTG TGTACACGAC	300
	CGTCGCTCC ATGTGCAGGA TCGAGCCGAC CGGCACTGGC GCGCGAAGG TGGTGGAGTC	360
20	CAGCGATACG AACCGCGCA GAGAGTGGG GATCGATGAC GCGGCGAGT ACGCCAGCTC	420
	AAATGTCTGC CGCATCAGGT AACCGCCGA GATCATGTAC GAGTGTGGT TCCGTATTG	480
25	CGGCTGCATG AACATCGTCG ACTTCAGGTT CGTGTCTGTC ATGACACCA CGCGCGCGG	540
	ACGCAGCTCG CGCGCGTCG CGCGGACGC GCGCACAAAC CCGTGATCA TCCGCGACTC	600
30	CTCCGCGGTA GCGGGTTCG TCTCTAGACT CTCGCTCTGC GCGTGTAGCT TCTTCGCGCT	660
	GTGTGGCTC TCCGCGCGC GGAATCCAC CCACTCTGTC TGGTCTGCG GTAGCA	716

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 729 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: single |
| 45 | (D) TOPOLOGY: linear |

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- | | |
|----|-------------------------|
| 50 | (A) ORGANISM: PAG1491UP |
|----|-------------------------|

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

GATCTTGAAC AAAAAGTAGT TTGTTATTCT CCAGCTGCGC AGTCTCTTCC AGGGTTTTAC 60
 5 TTCCGATGCT TATTAATACT GGTTCTTTAG ATGGTTCTTG ACTTTGGCTA TAGGCCATTG 120
 GTTCCGGCGA CTTGIGAAGG TATGCATTGA GAGTCTCTTG GGTAGAAGCT GTGGTCTCTC 180
 10 CTGTAGTTTT AGCAGCGGGC TTGGCCGGGA CTGGTACATC AGGCTGAGGT AAAATCTCGG 240
 CTGGCGTTGC AGGTTCCTATT TCTGTGGGTG GCTCTACACT AGGATCCAAT ACTTGGGGCG 300
 15 TACTAGTATC GCATTGGTCA ATATCATCTA TGGCCACGAT GACAGAACTT TCTTCTTCCA 360
 TAGGCTGGGA GCATGCAGTA ATCTCGGAAC ATGTGGTAGT ATTATGTAGG TGATCGTCTT 420
 20 CGAATGTCCC AATCAGCTCC TGGCTGGGAA CGAGTTTGGC CCTTTTGACC TTCAACTCGG 480
 AGTCTTGATG TGGGACTGGC AGTGACGGTA AAGATTTAGG CAGCATGAGC TCCTGTTCTG 540
 25 TAAATGCCC GTCCAGTTTC TCTGCTAAAC TTGGGAGGAC ATACTCTTCA TTGTGAAGCA 600
 ATACAGTCTT CTTATCCGGA GTCACATTCA CGTCTACAAA CTGGGGGGAG AGCTCAAAT 660
 30 TTAGAATAAT GACGGGATAC TGGACGTTGT TGAAGCTTCG ATATATGTCA TTGCAACACT 720
 TCAGGACTT 729

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1492RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

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GATCTACTTC TOCAACAACG ACCTCCTGTG GTCCAATGGC TACCCCGTGA ACOGCTTTGG 60
 5 CCAGGGGCGG TTCCGCATGC TTATCGAGCG CCTGTACGGC GAGCTCAACG CCGCTACAG 120
 CCTGGCCCAT ACCACCTACG GCAAGCCCAA CCGCATTGCC TAOGACTATG CTGCCCCGGT 180
 10 CCTGGGCGCC TGGTCGGGCC TCAGACCGC ACAGCCGGCC GGCACGGTAT ACATGGTTGG 240
 CGACAACCCC CACAGCGACA TAATAGGCGC ATACAACTAC GGCTGGGCGA GCTGCTTGGT 300
 15 GCGTAGCGGC GTCTATCGCG ATGGAGACAC GTTACCATGC CAACCGAACC TCGTGTGGA 360
 CTCGGTCTTG GAGCCGTAA CCGCGCTCT CCAGCACTCT TCACATTAC TTCTATACTT 420
 20 TTACGTCTTC TATATACCGG GCTCGTCGGT CCGCAGATGC CTAGATCTGA ATCTTGGCA 480
 CCACAGTTTG CTCTGAGCC AACTTGTCTG CGTTGGCGCG GGCATATGC TCCTTGACG 540
 25 TCGGAGGCC GGGCAAGTA TGGTTTCCA TCAGCCGGTG GCGGAACAG AACTGGCCGT 600
 CACAGAACTG 610

30 (2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 553 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: PAG1492UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

50 GATCATGTTG GTGGCCTCCT GCGTCGGCTG CCGGTGAAG TTGGGGTTTG ATTCCGGAC 60
 GAGCGCTGC GTGAGCCGGT TGATCTGCC CAGTTGGCC TCGAGCGCG AGGCCTTGTA 120
 55

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CTCGTCGGCC GACACGTGCT CGTCTAGGGA GAGCTGCTTC GAATTGGAGT TATACTGGAG 180
5 CATTTGGTGAT CTGCCTGTCC GCAAGAGTGG TGAAGACGT GTTCTTTGGC CTGTTGCGTG 240
AACAAAGCAC TCCGTGTTTT TCATGGACGG CGTGGTCCCA GGAGGCGAGA CCGGAGAAGC 300
10 GAGCGTCAGG GCCGCGCGGC AGGACGTTAG GCGGCTGCTC CCCACTATGT AATGCTGGAT 360
ATGAAGAACA GAAATACTAG ATAATATATT TGTATTAGAC AGTCGTGCGG ACOGGCAGAG 420
15 GGCGGCGTTC ACAAGTCGC ATCGTCTCA TCCGCAACG GCAATGCCGT AGCGCGCTCC 480
AGCTCTGCT GGTACTGCTG CATCAACTGC TGTCCCCCT GCACCTCTGG AGGCGCCTAG 540
20 GCAGGCGAGC CAC 553

(2) INFORMATION FOR SEQ ID NO:763:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 719 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1493RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

45 GATCGAATAA AGTAGGTTTG GCGCTGACCG GCATCACCCG CGGACGTAGC GGGACAAAGT 60
TCCCCGIGTA AATGTTTGGC TAGTCGATGA AGGTATTAGT ATTCATCTTC TCCAGCAAAG 120
50 ACAATTCATA CTGTTGGGCG GGCCGCGAAG AGTTACCACT GTATTCTGCC AACGCTGCGA 180
CGCTTCGGCA ACTAGATTTC AGTGCCTTCT GGAGCTCTGA AACATTATCT AGGATGTTGA 240
55 ACGGATCGAA AGCGGTGTG CGGGGCATAG CGGACATGGC AGTTCTCAGA TTCTGCATAG 300

AACCGGCATA TAGAGCCAGT GCCTCCTGAT GCTTGCCCTC CTCTTGGTAA AGGGGAGCGA 360
 5 GCGCGCGGCC TACAAGCTGC GCACGGTAAA ACACCTTGAC AAGCTTCAGA TATGCAGTGA 420
 GCTCATOGTC TGAGTAGACA CCGGTAGAC CCATAGCCTC CTCTGCATGG GTGATTATGT 480
 10 TGTGATGAC GTGGTTCAGC TGCTTGTAAT TCGTGAAGCG AGCGGTCTCT CGGCCTTCTT 540
 GCCATTGAC CCACAGAGGT TGCAACAGCG CAACATGCGG GCCCATGTC GCGCACAAGT 600
 15 AGTGAATTG GAGGTATGTG AGCAATATCT GGTGCTCTC TCCCTCATAG TGCAACCTT 660
 CCTCCTGTCT GCGCTCCATT GACTGCTCTT GGCATCAAT TGCCGGTTC CACTTCAGT 719

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1493UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

GATCATACTT ATCCACCGGT CAAGCCAGGT CTCATCTTG ACGATGAGCC AGCCGGGGGG 60
 45 CGTGGCCATC TGGAGCCAGC GCTCCCGGAA GCAATTAGG TACCCTAGAC CAAGCCCGAT 120
 TAGGTGGCCG ACAAAGCTGG AGCCGGGCAT TAGCAGCGTG ACAAGTACCA GGAACACCAG 180
 50 CCGGATATAT AGGGTCGGCA TCTTCAGACT TGGAGCTCG TAGTGGGGGC GGAAGCCCCC 240
 CTCTGCACT GCGAAGTAGC CACACAGCGT AAAGCACCAC CCGCTGCCC CGCTACGTA 300
 55 AACGTTTGGG TACAACAACA TGCCAACTAA GCAGTACAG ACGCCCGTCA CAATGGCCAG 360

GAGGTTGAGC GTGATTCCCG TAAACACCGT CCGTGTGAC GCTTGAACA TCGACAGGG 420
 5 CACAAACAGC GACATCAGAT TCAACAGCAA ATGGAAGATT GACAGGTGGG CCAGTGGATA 480
 GAGGGAGAGC CGGTCAGCT GCAGCTTCTT AAGCGCCCCC GGATCCAACA GGATCTTCTC 540
 10 GTTGATTGGG AACACCCAAT TCAGCACATA CACAAGCGTA AGGGAACACC GACAAGCCTG 600
 CAGTAAGAGC GCGCGGCTTA TGGACCCCGG TCGTAACAT CGACTTCCAA TCCATCTTGC 660
 15 TCAATCAAAG TGGCAGTTTG CTTGGGCGTG GCAGTGGACT ATGCTCGCC AGTTGCCCAT 720
 CAAAAC 726

20 (2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: PAG1494RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

40 GATCTTCGTT CGTGAAAAC TTGCAAGTCT TCATGAGCTC AAGAATTGCC TCTGCATCTA 60
 TTCTGTCCGG TTGGATTCTG CTTTCCTTAT AGTCTGAAT CATGCGCGCA AAAGCGCGCG 120
 45 GCGTCAGTC ATGACGGGAT CGGCCCTTAT AGGACTTCCC TGCAAGCGGC ATGAGGCTCC 180
 GCCAGCCATT TTCTTCAATA ATATTGACAA GTCTTTCGTT TTCCAACAG ACCTTGTTCG 240
 50 CGAGACTGTG GAACGTGTTT ACGTCTATCT GCTCAAGTAT TTCTACCTT TCCTCAGCAG 300
 ACCATGCAA GTTCAATCT GCCTCTTGA ATGCTCCAT AAGCTTTTCA TTGATGTTAT 360
 55

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CCACTGCTTT ATTTGTCAAG GAGAGGATTA GTATTCATT AGGAGCTACA ATCCCTTCGT 420
 5 AAACCAGGTT GTAGACTTTA TGCAGTAGTG TCAOGGTCTT GCCAGACCCA GGTCOCGCTA 480
 CCACATTGAC AGTTGTACAA GGCTCATATG GATGTGTAC TACTCGTGAT TGGGACGTG 540
 10 TCAGTCTTTT CATTGATGTA TGATACATGC TCGAGCGTCG GCGAAGGAAA TAAATTCGTG 600
 AATTTCCGTT TTAAGATACT CAAAAGAGAT GAGATAACCG CCGCAAGGC GGAGTAGAAT 660
 15 TACAGCAGCT ATTGAATATA TTTAGTTTAT TTATCTGGCT AGCTTAACCA CTAGTGT 717

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1494UP

(x) SEQUENCE DESCRIPTION: SEQ ID NO:766:

GATCCTTTAG GCCATCCTCT CCAAATTACC CGTGCTTGGC TTCAGTAGCT CAGTCGGAAG 60
 40 AGCGTCAGTC TCATAATCTG AAGGTCGAGA GTTCGAACCT CCCTGGAGC AAGTTTTTTG 120
 CTCGGGAAA TAAGTATTTG GAGCTGGACT GAAGCGCAA CCTATGCAGC TTTGCTGGTG 180
 45 CGAAGTGTTT ATTCATGTCT GCGGACTATG TCTATATATC TTGCGGTCT TGTCTCTCTG 240
 CTGGGAAGA GGAATTGGAT TCTTGGCGT GGTCTGCAAG CTCTGCTAGC TTCCTGGCGG 300
 50 GCAGAACTT TTCAAACGCC TCTTTCAGT CATGGTTGTC AAAGTATCTG AGCATGATCT 360
 55 GGATAACGTG GGTGGTGGTC AGCACCTTCC TGCCGCATAG CTGATGTAC TCTCCTATTG 420

GTAGGCGACG AGTAGGAATG CCCAGTTCCTT TGGCCTTATT GTAACAGAGA GCTTTGTGGC 480
 5 GGTTCTTGTC CACAATGCGG CCCACTATAT ACGTCGTACC GGGTTCAGC GTCTCCAGCG 540
 TCTCATCAGT ATCTGCAGTA AGGTAAACTG CGTTCGTAGT TGGAGGGGGG GATTGCTCTG 600
 10 TGAAAT 606

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1495RP

(x) SEQUENCE DESCRIPTION: SEQ ID NO:767:

35 GATCGAATTA GCGGGTTTTA ATGAACATA AGGAACGAGG TCTAAATGCG CAACATCCTT 60
 GAATGCAGTG CCAAGATGTA TGCCGTTCCTT GGTAAAGAAA ATTGTACCAT CGACATAGTT 120
 40 AATGCCACAT CCGATCACGT CGTCTCGACC ATAGGGCTTC GAGTACGACT TGAACAAAGA 180
 GCCGTCATTT ATGTAAACGT CCGACCCGTT GTAAATGTAG ACATCCTTAC CAGTCTACT 240
 45 CTGTTGOGAA GTTGGCCTGG AACCTCAAA AGGCCCTCTT AATATGTTGG AAGTTTGGCG 300
 GTTCAAGGCA GAAAATTCAC CCGGTCCCT CGAAGGTGGA TCGCTAGTGT TTGCTTGGCC 360
 50 AGCATTTGAC GCGACTTTTG ACCAGTCCTT AAATCCAATA TTGATATTGC AGGTTTGGCC 420
 TGACTGCGCG CTGGTCACCG ATAGTACCTT AATTCATAG TAAAAGATAG CCACTTTCCTT 480
 55 ATGATTAAATA CAAGCATTCG CCCAGGTGGA AGCCCACTGC TGCTTCTGGT TATTAACTGA 540

AGTCGGTAGC CTATTATTTA CAATAGGGCT GTGTGCATAG CCAGAGTAGA GCTGCCAGTT 600
 5 GGGGTTAGGC CGCAAGTTTG TGAAACCGTC TGTGAGACC AAAACTGAGT TGTTCGACTG 660
 TGTGGTCCAG AGGTGGGGCA AAAGGATACC TATCGAGGAG TATACGCTCG AGAAA 715

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1495UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

GATCAGCCAA CAGCTGAGTT CTGATTGGAT GAGAGCTATT AGTAACTTT TTGTGTTTAC 60
 GGTGCTGGTC CTGGATCGT TACAGTACTA CTGTGGAGCG TACGGGCGGT GCGCCGCGCA 120
 GATTGCAGTG ATAAGCCATT ATACGTGGCC TTGCACTGAC GCGCCGCGAG TACGGGATAA 180
 ATTAGGGAAG GCCAGCGAGT GGTACGGGGC CAATGCGGCT CCGCATGTGT CCGTGGGAG 240
 CCGGTGGATG CAAGCGAAG TGATGCCCA CCTGACGAAA GTATCCAGT GGACGGAGAA 300
 GCATGTACAA CCGGGATGC GGCAGGCTGG CCGGGACGCG ATAGTAACAG CCGCGTGGC 360
 ATGGAATGTC GTACAGCAGT ACCAGCGGCG GCATGIGGTG CCTCTGACAG GGCGACTGCT 420
 GGCGAAGTGT CCGTGTCTCG AGAGGTGGGC CGAACAGCT GCGCGCGGCT GGCAGTGGCT 480
 CTGCAAGCAT GCTGGGCGC TACCACAGCA GTACAGCAGC AGTATCCTGC GTTTGTGGCG 540
 CATATGGGGG GCATATGGGA GCGTTTGCAC GCGCGCTACA ACCGGATCTA TCTGGACTTG 600

GGCGGCCAG TGCAGGAGAA GACGTCCGAG GACSCAGTGC GGCGCCCGGG GGGACTCAKT 660

5 ACATCACATC CACTATCACA ATGACCATGA CTGGCTCGAT GAACTC 706

(2) INFORMATION FOR SEQ ID NO:769:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 749 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1496RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

30 GATCGTTTTC TGTCAAACCG CAGTCGGGTT CAAGGAGTAC GTTGAATTTA GCTCTTGCAT 60

TCAACAAGTC TTCCCAAGTT TCACAATGT TGTGATAAT GAAGGGTTTA AAGTCTAGAA 120

35 GCTCTTCTTG CGTGAAGCCG TTCTGGTGAA GAATCTTCAG TTGTTCAGT ACGTGCATT 180

TCCCGCTCTC GCCAGAACC AACACAAAA CCTTGAGCCG GCGATTGCTG GCACTGGTT 240

40 GCGCCATTGA CCTGGTCCA GCACTGCCG TTGTCTGCTG ACTGTCGCC GATACCAAG 300

AGCGTTTCCT GCGGCCGCT GTAGCGCCG ACGTCTATG ACTGGGTGAC GTCTCAGTT 360

45 TGACTTCTGC ACCGTAATCT ACCCTCTTTG CTCTGTTC TACCTTCTGA GAAGCACCAT 420

GTCGTCTTG ACGCGCTTT TCCGGGTG TGCTGATCC CTGTCTTC GACGGCACA 480

50 ACCCATTTAT GTGGGCTCT ATATCCACCA GTACTTGAG CACTCTAGG CCTGGCTTTC 540

TTTGAAATAT TACCGTCCG GCAAAAGCCA CTATAGCC CTGATCAATG GATTCCACTG 600

55 CTAGAGGCTA ATTAGGCTGC CGCTGTAC TCGGGGCC ATCACATTAT ATTCATAGCA 660

AAGTAGGTGC CAACAGAAAA AATCAGCCCG CCTCCTTTAT TGATCAGTG AAGAAATCCA 720

CATGAACAAT CACGTGAACA CACATTGG 749

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 754 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1496UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

GATCGAAGTC AATGCCAGAC TATCTCGTTC TTCTGCATTG GGTCCAAGG CAACAGGATA 60

CCCCCTGCC TATACTGCCG CTAAGATTGC TCTTGGGTAT ACATTACCAG AGTTGCCTAA 120

TCCTGTTACC AAGTCGACGG TCGCAACTT TGAACCTCA CTGGACTACA TTGTGGOCOA 180

GGTCCAAGA TGGGATCTCT CCAAATTTC AAGCTGGAT AAGACTATTG GGTCTGCCAT 240

GAAGTCGTA GGTGAAGTGA TGGGATCGG CCGAATTTT GAGGAAGCTT TCCAAAAGGC 300

TTTCGTCAG GTTGATCCAT CTCTACTAGG TTTCAGGGC TCTGACGAAT TCGCAGACCT 360

AGATGAAGCC TTGCAATTTT CTACAGATAG AAGTGGTTG GCTGTGGGAG AAGCGCTAAT 420

GAACAGAGGT TACTCTGTGG AACGTGTACA CGAGCTTACG AAAATTGATA GATTTTTCCT 480

GCACAAGTGT ATGAATATTG TCCGAATGCA GAAGCAATTA GAGACCTAG GATCAATAAA 540

TCGGCTAGAC GAGGTCTGT TCGGAAGGC TAAAAGCTC GGCTTCTGTG ACAAGCAGAT 600

TGCACGGGCT ATTTTCAGATG ACCTCTCTGA ATTGGATATT AGAGGCTCA GAAAAGCTT 660

TGGCATTITG CCATTITGTA AACGTATCGA CACCATGGCG GCAGAAGTTC CTGCGGTAAAC 720

5 CAACTACTTG TATGTTACCT ATAATGCGGT CAAA 754

(2) INFORMATION FOR SEQ ID NO:771:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 740 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1497RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

30 GATCATTITG TCTTCTTGGC CTCTACAAAC TGTGAATATC ATACTAGACC TGAAGTCAGG 60
 TAGGGAGCAA CCCAACCCCTT CGGTGGCAGT AGAGGCTGSC AAATCCATTA AAAAGACCGA 120
 35 TTGAATGGG AACTCTAAAA TTGAACTAA GCAATTTCAT GAACTCTCGA CAGTTCTCTG 180
 TCTTTCCAGT ATTGACTATT ATAACCTTAA GAGAAGGTAT CGAACTTACA AATCTCTGAA 240
 40 AAGGGCGACT ATTGAAGATA TATTACATGT TGTGTGCGAC AGAGATCTGG CGGAGCGCAT 300
 TGTTACTCAT ATCCAAAGAG AATCTGAGCT GCAACAATAT GAGGAGGATG GGAGGAATGA 360
 45 GGTATGAAAT GTTCCCCATT TGGATTAAAG TATCAGGTGG TCACGATATC CACTATATGG 420
 TGCTATTAAAC GGCATGCAAA GTGTAGAATT AACCTAAAGA ATATGTTATA TATATATATT 480
 50 ATAACTACA AACTAACGGA CGCAATGAAA TCTAAGTGTG GCAAGGTTAG CCTTAATACC 540
 GGTACTTGGG TAAAATCTCC TTTTTCAAAT GATACAAGCG TCCCATTTCA AACGCCATGC 600
 55 CAGAATCACT GGCTGGATTG ATCATGATTG TGATTGCGGT TGCCCTCAGTC GGAAATAAAT 660

TAGCAATACT CATTATACCC TTGCGGACCT CCAGCCGCTT CTCTTGGGTA GGTTCAAATG 720

AGGCAATTG CATACTCTTT 740

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1497UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

GATCCTGTCA CAGCGGGCGA CGCCGAGGC CGGTACGGC GACCTGCAGG ACGAGGTGAA 60

GGTAGGAGGG TCGAGGGGG CCTTTGGCGA TCGGGCGTTG TTGGGGCGA TGGGGGGGG 120

CGCGCCGAG GATGGCGAG AGGGCCACA ACTTGGTGCC GGGGTGGGC CCATGGTGAC 180

GCCGCACTT CGATGGAAC CCTGCGAGC GCACGGCTG CCACAGCAGG CCCCCACTCC 240

GCACCAGCA CAGCAGCCG CCAGAAGCG AATGCACATG CTCACACAGC TCACGAAGA 300

GCAGAAGAAC TATTCTTACG TGGACCGCA ACCGTCAATT ATGCAACAGC AGCCACACAT 360

GATGCAGCAA CTGCGCAAC AACGGCTCG GATGCAGCAA CTGCGTTGC AGGGCCAGTC 420

CGAGACGGC AAGCCCGCAG GCAGTCTCC AATGGTGGTG CCGTCAAC ATAGGCAGCT 480

GTTCAGAAC CTCGACCCA GCATCCAGAA AAGAGTATCA CAGGATCTGA ACAGCAAGCA 540

GTATGAACTA TTTGTGAAGT CTTTCATGGA ACATTGTAAG CCGTGAATA TTCCGTTTAA 600

CCCAACCTG AGATAGGCGG GACGCGGGTG AACTTATTCA TTTTATACAT GTTGGTACAA 660

AGAATGGGCG GGGCAGATAA TATCAGGAGG CTGCAGCAAT GGCGGGGCTT GGCAGAAAAA 720

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1498RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

GATCACTACG TGACATTGG TACGGAATGG CACTOCAATG CCGACAAACC TCTTCTTACC 60
COGTGACTTA CCCCAGTGTG CCAACTACCA CACATCTGGG CCATAGCCCC AGCCATCTGG 120
CACCAATGT ACTCGATATC GTTATTACAT GTCTACGGCC TCAAGTGCAT CCACCATCTG 180
ATATCATGTC TGCTCTAGGC TATATATTTT GGTTGGGGCC ATATCTACCA GAAAGCACCG 240
TTTCCCGTCC GATCAACTGT AGTTAAGCTG GTAAGAGCCT GACCGAGTAG TGTAGTGGGT 300
GACCATACGC GAAACTCAGG TGCTGCAATC TTTTTTTTTT CCTCTCTCTG CAAGCTGGCC 360
GCCAACACAG GTCACCTAG TATGGCTCAC ATGCAATICA GATATCTACT TCTGACTGGT 420
CTGGTGGGCG ATGGCCATCA TTGCAAACAG TGTGCTGGCA TGGGACTTTA ACGACCTCGC 480
GATAATAATC AGAGATCGTC TACTTATAAA ACATCAGGCA CAAAAAGAAA GGTGCAGCGA 540
AATGGTATAT ATAGGTCTC CAGATCCACC CACCGGTACC TCCTACTTGG CGTATCTGC 600
GCTCCGTGG CGCTTGGCCG TGAGATGCTG TGGGCCCCGAA ATGTACTCTC AAATGGGCTT 660

GTTTCAGTGGC CCATACAGCT CATTAAAGCTC AGTGGCCCCG ATGCTTAGTA GTA

713

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1498UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

GATCTCTTGG TTCTGGCATC GATGAAGAAC GCAGCGAATT GCGATAAGTA TTGTGAATTG	60
CAGATTTTTCG TGAATCATCG AATCTTTGAA CGCACATTGC GTCTCTGGT ATTCCAGGGG	120
GCATGCCCTGT TTGAGCGTCA TTTCCTTCTC AAACCCCTGG GTTTGGTAAT GAGTGATACT	180
CGTGTGTAAG ACAAGGTTAA CTGAAAATG CTGGCCATGG GCGGAACCTG CCGCGACTGC	240
GGTCTGAGCT AGTTTCTACA CTGCGTATTA GGTTTGACC AGATGTGGA GTGGAGCTGG	300
CGCTTGAAGA ACGTACGACA AACAAAGGCT TCCAGGCGAA TAGTATTCCC AAAGTTTGAC	360
CTCAAATCAG GTAGGATTAC CCGCTGAAC TAAACATATC AATAAGCGGA GGAAAAGAAA	420
CCAACCGGGA TTGCCTTAGT AACGGCGAGT GAAGCGGCAA AAGCTCAAAT TTGAAATCTG	480
GCGCCTTGG CGTCCGAGTT GTAATTTGAA GAAAGTACCT TGGTTGCTAG TCCCTGTCTA	540
TGTTCTTGG AACAGGAGCT CATAGAGGT GAGAATCCG TCTGGCGGG GTCTAGTGC	600
CATCTAAGGT TCTTTGACG AGTCGAGTTG TTTGGGAATG CAGCTCTAAG TGGGTGGTAA	660
ATTCCATCTA AAGCTAAATA TTGGCGAGAG ACGGATAGC	699

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1499RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

GATCAGCTTC ATGGAATTACC CAGAATTCCG CTTCAACAGC AACGAGGCCA CCGAGATGCC 60
 CTTCCGCTAC GTA CTGGAGC CTGCTGGCAG GCCATTCTG CCATCAGGCA TGCTAGAGCT 120
 CATCAAAAAG GACTCCGAAC AGAGTCTGGA TGAOCTACTT TAGGCTCGTT GAACAACAGC 180
 TTATAGATGA TGTATATATG CCGTCTGTCC GCCAGAGACT GGCATCGGAA GCCACGCAAC 240
 CTAAAGTCGA TAGAACTCTG TCAACAGAAT CAGTCTTTTT CCTCCTTCAG CATCTGCCA 300
 AGCAGCTGCT CGAAATCGAT ATCATCAGAA GTGGTTTTTG CAGGAGCAGC TACGGCGGGC 360
 TGCTGGGACG CACGTCTCTT AGCCTTGTAC AATGACACAC CCCCAGACAG CGTGAATAGC 420
 GTGCCAAGCA CCAAAACATG AGGCTGAACC GCTTTTCCAA AGATGTTGTA AGCTTGACCC 480
 ATGCTAATC ACCGAATCCG CTGCAGATAT GGGTCTGAT GGTCTGGTGT GTAGCGGTGT 540
 GCATTGTGA GCTCCTATTG GCGGAGGAGG CAAGTCGATC TAGAGGGCTA CAATGAGGTG 600
 TTGGGGTGT TTGTCAGGTA CCGAGGAGGT AGCAGTGAT CGTTCAAATA TCTGTACCGC 660
 CCCATGAACA TCTATTGGT GCATTGGGTT TGGAGCACGG GCGATCATG GAGACTAACA 720
 CTCACGAATT TTGCTGGCG GA 742

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1499UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

GATCGCAATG GAGAAGGTAA CGCTGCTACC GAAGGTTATC AGTGTTTTGA ATAAGGOGAA 60
CCTTGCGAGC ACAATTTTGG ACAATAATTT GCTACAGAGT GTGCGGATCT GCCTTGAGCC 120
ACTGCGGGAT GGATCCCTAC CATCCTTGA GATACAGAAG TCTCTCTTTG CCGCGATTGA 180
GAACCTCCCC ATAAAAACAG AGCAOCTCAA GGAGAGCGGA CTGGGGAAGG TGGTCATATT 240
TTACACCAAG TCTAAGCGTG TAGAACACAA GCTGGCCCCG CTAGCTGACC GCCTGGTTGC 300
AGAATGGACG CGCCCTATTG TOGGGCTTC CGATAACTAC CGGGACAAGC GTGTCTGAA 360
GATGGACTTC GACGTGGAGA AGCACCGTAA GAAAGCGGCA CTTGATTCTG CCAAATCTAA 420
GAAACGGAGA AAGGCTGCAG TGGACGAGGA GAAACACAAG TCACTCTACG AGCTTGCCGC 480
TGCGAAGCGG AACAGAGCCG CAGCGCCTGC GCAGACAACC ACCGATTACA AATACGCACC 540
AGTCAGCAAT ATCTCGAAGC TACAGACCGG GATCGGCACG GCAGGCGTGG GCTCCAGCT 600
CAACAACAAC GATCTGTACA AGAGACTCAA CTGAGACTT GCCAAGTCTA AACGGTCCAA 660
GTAAACCGCTG TGTACTTCAG CTAATAGTAT TATAATAACG TTTAATGATA CTGAAA 716

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1500RP

(>i) SEQUENCE DESCRIPTION: SEQ ID NO:777:

GATCAGCTAA TGGCTGCTTG TCAAAGACCA AATCCTTCAC CCTAGAACT TTTCCTAGAG 60
 CATCCATTC GATAACCTAG GTGCTTTGT GTCTTAAAG AATATTGGTT TAATTGCTT 120
 TCGCGACGG AGTAAAGGT TATGTAGCAT TTTCAAAG AGGCTTAATG GACACATCCC 180
 AGGATAGTAT GAATGAGAA GTCCAATTG TGGACCAAT GTCTAGTTC TTATATTTAC 240
 TGTATACAT CTA CTG CAGA GTCAAGCATA TATACCAAT AATTCACCA ATACTAGCTC 300
 TTCTAAGTCT TCAGCTGATG GATTGCGCC AAGGCGCGC AGAGCTGCAG GTAGGTACCC 360
 ACACCTTCCA AAATCCTCAT GTGCGTGAAT CCTATTCTT TAATCATCTC CAGCGCAGG 420
 GGTCTTTAA TCTCTGTCAA GTTCTTCATG ACACGGAAAC ATGTAGTAT TATGTCCACC 480
 GCGAGTACC TTGCCCCAC AATCGCGTA AGTAATTGAG CGACTCATCA AGAGTAGCAG 540
 ATAGCAGCAT TTCTTGATG ACCAGGGGAT GCGGCGAGTC CACTATCTTA AAAACGTTGT 600
 CGCGTTCAC TAACGTGAAG CCGGCCACG TGCTCTGCAG ATTGTTGATG GCTGCGCA 660
 TGTACCTTC CGCAGTGAAT ATCAGGGCT CCAGACCATC ATTGGTGTTC TGTACGTTT 719

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1500UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

GATCGCGACC CCGCGGTCA CGGCAAGGCC CGCCAACCGC GAGGAGGAGA TCAATGGCTT	60
TGACCTCGAG GCGCGCCCC AAAAGAAGAC CAAATACTA TAGTAGTACG TACATTGTAA	120
TACATGCGCA AGACTTGCGG CCAGTTAGCC GCGCGCTCC CAGGTCTTCA CCAGCGCGGT	180
GCGTCCGCA GAAGTGCTCA GCAGTGGCG GCTACCTCC TTGTAGACGG TGTCATGAC	240
TGCGCCGCA TGCAGAGAG CCAGCTGTC GGACACCACT ACCTGCTGG TCACTCCAC	300
TACGTAGCGG TAGCGCGCA CATAGCGTTT GTCTCTACG AAAGCGACC GTGCCAGGAG	360
GCGTCCGTG TTCCGCGCAG GGAGGGCAA TCCCGCCTT AGACGCTGC CGGCTGCTG	420
GCGTAAAAG CTCACACTGT CATCGAAGCC CAGCGCACAC ACCTCTCTC CATGCGCGGA	480
AGTGACACAG GAGGTACAC CACTCCGGT GCGGTCTGC GTCTTCACA CTGGTCTCTC	540
GCTGCGCGC TGCTGTAGG CTGTACCAC TGGCTCAATC CCGACGTGT ATACCGGCC	600
GGCGAGACC GGCAGACGG CGGTGATAG CAGCGGAAAG TCGGTGGCCA CAAAAGCGC	660
CGGG	664

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1501RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

GATCTATTTA AATATAACAT ATTATTTTATT TCTTTTTTTTA AACATTTTAA ATTAAATTAA	60
TTATTTATTT ATTAAATTAA TTATTTTATAT TAGTTAAGAT AATTTTATAA CTTTAATTAG	120
AGAGCTAAGG TACACACCCC TAATGCTTTC AGCATTTCTTG TGGTACCACT CTAATTAAAG	180
AGTTATTATA TTAATGATAT AATATGTAGA TATTCAGTTT TGAAGTGAAG ATATATGTCC	240
CTAAACATA TGTTTACCA ATTAACTAT ATCCACTAAC TTTTATTATA TAATTTAATA	300
ATTAAGAATA TTTTAAGATT GAATTAGAGG AGTATTAAAT GAATGAATAA GAGGTGGTGA	360
ATTTAATATA AACTCAATAG ATGATGATTT AGTAGTATTC ATTAAGAAAA TATTATTTGA	420
TTCAATAAAA TCAGGTAGTT TTATATAATT AATAGATTTA TTATTAACTT TATTAGTTAA	480
ACCATTTATT AATTGATCAT AAATAATATA AAGGAATAAC ATTAATGATA TAATAGTTAT	540
TATAGAACCA AATGAAGATA CTAAATTTCA ACCTAGGAAT AGATCAGGAT AATCAGGAAT	600
TCTTCTTGGT ATACCATTAA TACCTAAGAA ATGCATAGGG AAGAAAATAA TATTAAGACC	660
TAAGAAAATT AATCAGAATT GAATGTGAT AATTTT	696

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1501UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

GATCAAATAA AAATAGAAAT TAGCTTAATG GTAGAGCATT CGTTTTACAC ACGAATAATT	60
TGAGTTCGAT TCTCAAATTT CTAAATAATA ATTAACAATA ATTTAAATTT GGGTAAAAAT	120
TAATAAATAT TAACGTATAT AATAATTATA TACTTTATAA AATTACTCAA TGTTATTAAAT	180
AAATTTATTT CTATCAATTA ATAATGATGT ACCTACTCCA TATAATATAT ATTTTCAAGA	240
TTCACTACTA CCTCATCAAG AAGGTATTTT AGAATTACAT GATAATATTA TATTCTATAT	300
GTTACTTGTT TTAGGTTTAG TTTCTTGAAT AATAATTATT ATTATTAAAG ATTATAAAAA	360
TAATCCATAT CTTTATAAAT ATATTAAACA TGGTCAAATA ATTGAAATTA TTTGAACTAT	420
TTTACCAGCT ATTATTTTAT TAATAATTGC ATTTCCATCA TTTATTTTAT TATATTTATG	480
TGATGAAGTT ATTTACCAG CTATAACTAT TAAAGTTATT GGTTTACAAT GATATTGAAA	540
ATATGAATAC TCAGATTTTA TTAATGATAA TGGTGAACT ATTGAATATG AATCTTATAT	600
AATTCCTGAA GAATTATTAG AAGAAGGTCA ATTAAGAATG TTAGATACTG ATACTAGTAT	660
TGTTATTCCG GTTGATACIC ATGTAAGATT TATTGTTACA GCTCTAGATG TTATTCATGA	720
TT	722

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 710 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1502RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

GATCGCTCC AACCCCTGCT TGATCTCCAT ACTCATCTGG TTTTTCAGGT AGCGCGGGTG	60
GTTGAATACG GACTTGTGCA AAACGAACAC ATAAGAGAAT GACGCCACGA TCAGGTACAG	120
CAGCCAGCCA AACACTGTGG TCACCAAAAA CAGAGACAAG CTCTGCCGCA ACAGGCTGTA	180
TGCGGCGAGC ACGGACCGCA AAGCATGCGG GCTAACCTCG AACATAAAG GTGCATACCC	240
ATATACCTCC AGCGGCTCT CAAGCGACCT CCGAACACG CGGTGCGCAT TTACCATCTG	300
CTCCTTAATC ATGCGCTGCT GCCAAGTCCC GCCCATCTTC GCGACAGCG ATGCTGGCAG	360
CAGTGTGGCA TACACATAGT CGAAGAAGTA CGAGTGCAG AACTCGAGCA CTAAATCCAT	420
GGTCGGAGAA CGCTATAGAC TAGGAGAAAC AATTITAGCT CTAGGTGCC TGCTTCTAG	480
CGTGATAACA GATCTGCTA CAGCTACTAA AGCCCATCTG CCGCTCTCCT CTGGCTTTTT	540
GCACTTTTAT ATGGTCCATC CCGGCACTGA CCTAACGTAC GCGCTCTAT ACGACGCTAA	600
AAAATCAAGT TACGAATGCA CTATACGAAT GCGTTGAGCA AGGAACGAAT CCTTTTGG	660
ACGACGATAT CAGTGAACG AAGCCGCAAC GTTGGGGTGC CCGGGGCTTA	710

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 692 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1502UP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

10

GATCAAAAAT ATTGACGCA TTGCGGCTC TTTAGTGTAC TTCGGTCAT TATGGAGATG 60

GCCAATTTAC ATCGGTATTT TOGCTTACT CATAAGAGTA TACAGTGCCA ATTTCCGTGA 120

15

ATTGAGGCT ATAAACATCT GGTATGTCTT ATCTTCAGTT CTCTCTGGGG ATTGCCCCAT 180

CACTGGGATT CCATTCAGTT TCAGGCTGCC AGGAGTTGGA ACTAAAACGT GGTTTTTGA 240

20

TCCTCTGAGA TCTCTGTTC CATCAAGGC AAGATAGGCA GCGGTGCTTT TGTATGAATA 300

TGCGGTGAG GATGTCTCAC TCCAGGTGG AAACCTATAT TATGGTGCAA TATATATTAA 360

25

TGATAAGAC TTCTCTGAC TAACAGCAGT AACTCTTAAT TGAAGTATTT GTTATTTCCA 420

ATCTTCATAC AGTATGTAC CCTGTGTAT TATAGATTTC GTTACGAAT TCGATGTGC 480

30

TTTCGTGGCT GCGAGGTCAG AAGATGATA TAATAATATA TATATTATTA AATTATGGTA 540

GGTAGGGAAT TGCTATTGT GTCTAGTACT CGATGCTTA TCTACAACCT CTAGTTGCAA 600

35

CACATGATAT GCTGTGGACC AAAACGCTAC GCGTTATTG ATTTTATCA AGGTCAAGAT 660

CATATATTAG CGTAATATCT GTGGAGGTTT CT 692

40

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 716 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1503RP

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

5 GATCTTCGTA TACATGTGCG AAAGCTCTC CAAAATCTTT TCGTCTCCAT CATGAGAGGC 60
 10 TGCTACAGCT TTTGAGCOGA TAGAATTGGA AATACCATIG GAGATTGCTA TTAGTAGGAA 120
 GACAATATAA GTACCATCTG TCGATGGGGC AGAGGCTTTA TCAAGAAGGT CCATCAGCTT 180
 15 GTTCTTGGAT ACAGCAGTCT CATTTAATAA TAATGCCTGC TCACCACTGG GCAAAAATTC 240
 AGAAACATTG AGCAGTTCAG AGAGTGAGTT CGACTCAAAG TTTTGGGTCA TTGTCTCTAA 300
 20 CAAGACAAAA ACAACGTCTT TCTGTCTCTC ATGAACATCA TAAGCCTTGA AAACCTGAG 360
 CAAAATAGTA TTGTCTCTGA TCAGTTCAA AAATACCTCT AGAATTAATG CCTTCTCTCA 420
 25 CAATAAAGTG TCAGATTTAG GAGACAGAGT GTGGATTAAAT AATGATAAAA TAACTTCCAA 480
 TTCCAATTCC AGCAATGTCA AATACTGAAC CTTTATGAGA AGTGTAAATAC ATCTGGCGCT 540
 30 ACGAACCACA ATTGCAAAAT TTTTGATGA GGAAATGTAC CTCAATAGCA GGGCACCGC 600
 CTTTGTTCGC AACAGAAATA ACAGATCTCG GTGTGTCAA AATAATAATT CATAGTTCAA 660
 35 TAAAACCACT TCTAGGAGCT CTAATCCATA CTCTCATTT ATGCAATTGC TATCCA 716

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1503UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

5	GATCTGCGCG CTTCGAAGGG AAAGGCGGGC CCCAATCCCC AGTCTATGTT CAAGAGGGCG	60
	AACAGCAGGC CGTCATGGCA TTCAATAAGC GAATGGGCAC TCGAGCGTGG GCACATCATG	120
10	TGCTGGATAG CATCATATAC TACACAGACA AGGTGGTGGT GAAGGGGCTT GGAAATTTGT	180
	CCGGAGCTT ACCTTCCAAG ACCTCTCGG CGACAAGCGT CAGGGGTGGT GTAAGGAAAC	240
15	GCATTGGTCT CGAAGGCGCA AATGATGTCT TTGTATACCG CACAAAAGAC CTGGTATTGG	300
	ATAGTGATGA AGATATAACC AGAACCTAAC TACTTGTCGTC GATATTTCTC ACACCGGCTG	360
20	GTGCGGAACC GGGGGCATAC ATTGGTTTTA CACAAGAGGG GTTGATGCAT AAAACGGGCT	420
	TTCAAAAGTG GCAAGCGAGA GCTGCGGACT GTGGTGGCTT TTGGTGGCGC GACTGTAGGC	480
25	AATGTGOCAT CCGTGCGCC TTCTTTTACG CGAGATCCAG TCTGGCAAGC CTGGCTGTAA	540
	CCAGAACACT CGGCTGAAGC CCGGACAGG TCCCTGGTGG ACCAGGCAGG CAGCCTTGCA	600
30	TCTGATAGGC CGGATACTGG GTATCTGCCA AGAGAGG	637

(2) INFORMATION FOR SEQ ID NO:785:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 708 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1504RP

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

55	GATCAATTAA TAAATGGTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA	60
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CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT 120

5 ATTGAGTTTA TATTAAATTC ACCACCTCTT ATTCAATCAT TTAATACTCC TCTAATTCAA 180

TCCTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAATTG 240

10 GTAAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATWAT 300

ATCATTAAATA TAATAACTCT TTAATTAGAG TGGTACCACA AGAATGCTGA AAGCATTAGG 360

15 GGTGTGTACC TTAGCTCTCT AATTAAAGTT ATAAAATTAT CTTAACTAAT AAAAATAATT 420

AATTAAATAA ATAAATAATT AATTAAATTT AAAATGTTTA AAAAAAGAAA TAAATAATAT 480

20 GTGATATTTA AATAGATCAA AATTTCACAA ATTTCCATTT CATTTAGTAC TACCATCACC 540

ATGACCAATT GTTACATCAT TTAGTTTATT AGGTTTACTA TTAACTTTAG CTTTACTAT 600

25 ACATGGTATT ATTGGTAATA TTTATCCCTT ATTATTATCT TTATTAGTAG TTTTATTACK 660

AATAACTTTA TGATTTAGAG ATATTGTAGC TGAACCTACT TATTTAGG 708

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1504UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

GATCTTAATT TAAAATTTTA ATTAACCTATT TATAATTTAG AAATATATAA TCTAGAGATA 60

55 TATAATCTTA AAATCATAGG TAAAATACA TAAGATAGTA AGAATGAAAA TTAGTAAAAT 120

	AAATAGAAAA CCATAAGTTA ATTGATTCAT AAAGAAAAAT GGAATTATTT GTGGCATCTT	180
5	AATTTTAAAT ATTTAATTGA TTATTATCTA TTAAACATAA AACATTTTAA AATGTTATAA	240
	AATAAATAAG AAATTACTTA TAGAATATTT ATTAAATAGT ATTTAATTTA ATTTTAATAT	300
10	TAAATATACC ATTTTATATTA ATAAATAGAT TATTAGTTT ATTAATATTA AGTGATATAT	360
	AATTTAATTT ATATAAATTA TTTAATTTAC TTCATTGATA TATATAATTA TTAAATGTAC	420
15	CTTTCATAAT ATTTATTTT ATTAGTCTAG TAATATTTCT ATTTAATAGT CTACCTTTTA	480
	ATTGGATATT ACTACCTACT AAATATTTAC CTAATAATAT ATTATTAAGA ATACTTAAAT	540
20	CTAATAATTT ATTATCTAAA GTATATAAAT TAATTAAATC TTTTATATTA TTATTTAAAT	600
	TATTATTAAAT TAGTAAATTA TATTTATTTA TTTTAATTTA CATAATTTT GATAATAATA	660
25	TACATTATTA AATGGTAATT TATTAATAAT TATCTTTAAT GATTTAATGA T	711

(2) INFORMATION FOR SEQ ID NO:787:

30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 710 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1505RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:	
50	GATCATCTTT ATACCATTGG CTCCTGTTCC GTGTGCACCA ACGTAATCAA AAGCGTGTGC	60
	CCCTCGCTA CGCAGGAAGC ACTAGAACTA GCTGAGTAAA GCAACGGTGA AAGTOGATCC	120
55	CTGATATATA TACGAAACCA GAGATACCTT CATCACAAGG ATCTTGTTCC TCGTGGCCCA	180

ATGGTCACGG CGTCTGGCTA CGATAGTAGT TACTTCTGAA ACCAGAAGAT TOCAGGTTG 240
 5 AGTCCTGGCG GGGAGTCCT TATTTTTTTT GTCCCTCTT GTTCAGCTT TTGICTTAA 300
 AAGGAGCAGA AAGATTATTT TGCAGCTCTC TTTTGGCGCC AGCTGGCAA AGCGAACTGT 360
 10 TGATTGACAA GCTTTTAACC TGTTATTAAC CACCAGCAAC CTCTOGAATT TATCATGTCT 420
 CCATCAAATA AGGATATTGC TGCCCTAATT GTTGACTTCC TAACTACGTC CGCCAAAAC 480
 15 GTAGGAGAGG ATTACGAAGA TTCCCTCAAA GTGGCAATTG ATTGTATCAC TGAAGCTTTC 540
 GAACTTGGAC CAGGCGAAGC TGACACATTA GTTCCGAAA AGTGTGGCGG AAGAAGCCTC 600
 20 TCTCAGTTGC TCACCACTGG CATGGCTCAC AACTCAGATG CAGGCGAACC GAAGGTAGCC 660
 GCGAAGAGT TGAAGAAGGA AGCTGAGGCC TTGAAACTGG AAGGTAACAG 710

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 715 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1505UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

45 GATCAAGCTG GACAAAACT TCCGTAAC TA TCTGAACCTA CTGGAAATGG TTCAGGGGTA 60
 CGTGGAGCTT AACATGTATG AAGATGTCTG GCGAAAGCTC GTTCAATTAA ATGGGAAAAA 120
 50 TGAGCCTGAT AGAGTTCCAG GATATTATAT TACGAGGTCT ATCTCACTGA ACCAGCTTTC 180
 CACCAATATA TATCCTGAGG AGTTGGATAA GTTTAATCTA TCTCCTGTCA CCGAGATAGA 240

AAAGAGGGTC GTGCAAGCCA CTGAGTGTTC CTOGAACTA ACATTAACAA ATAGCCATCA 300

5 TGAAAAGGCG CGCATACTGA TATCAACCTT TCAAAAATTG ACAACGAAAA CTTCTCAAGC 360

TACTTTGGAT CCAATGATTG ACGCAGATAC CTTACTGGGT TTGATGGTTG TTGTAGTTTG 420

10 TCGCGCACAA GTTAAAAACT TGAAGAGTCA TCTAGATTAT CTTAGAGAAT TTGCGCAGAA 480

TTCGGATGAC GTAAAGTTTG GGCTCCTTGG GTATTGCTA TCGAGCTCG AAGCGGTGGT 540

15 CGGATATTTT GATATTGGCG GCAGCTCAAT TAACTTGAA AGATTGATCA CACCATGTCC 600

AAGGAATAAG ATCTTCTGGA ACTTGATAGA GCAAGGAATT CCAATAAATT TAAAGGAACA 660

20 TGAAGAAGTC CTCATATGCG GCACTCCGTC CTGTGAATCA TTTTGTCITT ATGTT 715

(2) INFORMATION FOR SEQ ID NO:789:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1506RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

45 GATCTACCGG TTCGGTATCC CCCTTTGAAA ATAAATTCTT TGTCITTTGC ATGCAACTAA 60

AATGGGATGA AGATGCAAGG GATGTTATTT TTAAGTATCT CCATCTTTTG GAGCTTTCTT 120

50 CACAGGCTGT AACATTAACA AGGTCAAAAA CTCTACAGGT TATAGAAAGG CTTTGTCA 180

GAAAATTAGC GTATACGAAG TCGGATGAGT CTATTTTCAG CAGCATTAGT GATATTCCGA 240

55 TTGATGGACA TGACTTGTCA ACCGCTGAAA CATCTTCCGA AGAGCAGCCG AAATCTCAAT 300

CTTTGTTCGA GCTATTTGAG GAGAAAATAT ACAGCCTAAA CACCGACGCT CCTTATATGA 360
 5 CTCACGATGA CCACTTCATC CAATTTGTGG CTCTCAAAT TCAATTGAGC ACTAAGGAAT 420
 CGCCCGGAAC GTGTGTGCTT GTTACTGCCC CTTCGATGAA ACTGAAAATT ATAGACTTCG 480
 10 ATTCAAATAC TTGGGACAAT GAGTATWATG AAAATGTCTT TATGACGAGG TACTACTGCAG 540
 CATTGATTCA AGCAAATGTA TTTATCTTCC AAGAAAGTGA CTATAAAGTC TTTGAGAACT 600
 15 CATTGTTTAA TCCCAAAGGC TACGGTGCTA AAAGTACAGA AAATTGGCAA CCTTGGCTAG 660
 GACTGGAACT ATGTTTTGAA CCGGAGCCCT TGCAAACTAA TACGGTTATT AAAGAATTTC 720
 20

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1506UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

GATCTCCCCA TAAGCTCAAC ATTTTTCGATA TAAGATATTT GCGTCCCCGC CCAAAACACG 60
 45 ACGGTCCGTC CCAAACTCAA TGCCCCATTT GCAACAAACG GCAAATCATG ATTCCATCTG 120
 TCCCTCTCGT CAATCACCGA ACTTAACAGT AGTTGACGCT TTGTCACTTG GACTAGATAG 180
 50 TTGTTGGTAA CGAAGTAGTA TATCGTGGCG CCAGCCAAGT CGCTAAGGAT GCCATCAACT 240
 TCGTCGCATT CCATGTCTTC TTCGGAAGAA AAATAAAGTA CAAACGCCCT GGTATATGGTC 300
 55

GCCCCATCAG AACCAATAAC CAAATAACCT TTATAGGCTC TATCATCGCC ACAAAGTCTT 360
 5 GTATACACTT CTTCGGCAAC GGCATCCAGT CCTATGGTCC ATATGCTGTT AAAACGCAGG 420
 AATTCTCGCA GSTACAATAT GTTTTAAAA TGGGCTACAT GACCAITAGT TGATATGTTA 480
 10 GACAGCACGG ATGATGAGCA AGAACATAAC TCTTCTGTA TTGTACCTGA AATGGCAGGA 540
 GTTTTATGCG GGAAAGAGAT CAGCTCTTCC GCGTATGCAA AGCTGGTATC CTGGTGTGT 600
 15 CTCTAAGAA TATTGACAT AGACTCCACA TAGGCTCTGT CATOGAGGAT TGCAATGCCA 660
 AGAGAGATCT AGCGTTATCT CAAATACCTT CCAAACTTA TAATCTGTAA TTT 713

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1507RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

GATGGGCTGC GCTCCAACGA TGGCAGCATT GCTCCTAACG GGGCTGAAAT ATATGTGGGA 60
 45 CTCATGGCTG ACTTTAGCGT CGGCGGGCCA GACACGTCCA ATGCGCCCGA GGGCTGTGTG 120
 CTGCGGATCC ACCTCGAAGG ATGGGGTGC CAGATGGTTC TAGACGGGAT CCATATCCCG 180
 50 AACGCTATCA ATTGGAGTGC AGATGGCTCG CAATTCATC TGACTGACTC GCTAGCATTT 240
 ACCATATGGG CGTGCCCGGT AGTGGACGGT AGCCACAAC TCCTCAAGAG AACCCCATTC 300
 55 TACTGTACCA AAAATACTGG CAATGACTCA CACACTTCG CCGAACCGGA TGGTGGATTT 360

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GTGGACTGCT TTA CTGGGCA CACTTTGTG GCGGTGTGGT CCACTGGCAA AGTCOGAGAA 420
 5 CTGACAACG CAGGCAGACT ATTGCTGCA TATACACTAC CGACGCCAG AGTCAGCAGC 480
 TGTTGTGGG GCGCCGAGG CGAACTGCTC CTGTCCACGG CGCAGCAGG CGATTTCAG 540
 10 ACTGGGCAC ACTCTGACG CGTCGGAGGC AGCATTTTCA GAGTGGTAAT CCGGGGCGC 600
 CGGTTATCC CAAGCCGCAT CCGCGGTCT TCGGAAGCA TCCTTTAAAT AATATTTACT 660
 15 TCTACACCT CTGTCCCT CTACGCCCA GTCATTGAT GGGCGT 707

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1507UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

GATCGTACCA GTATAATACT GGAATTGAC GCGGCAGCC AAGGGTGGT AATCATCGTG 60
 40 CTGATAATTA TGCCATAGC CATCATWAT GGAATTAGCA TCAGCTATTT GCTTACGGTG 120
 TTGACGAGCG ACTGTTAATC TCCATAGAGA ATTCTCTCA ATAATTTCTG AGACWGTCT 180
 45 CTTTTTTAAA ATCGGCTTTG GCGCGGAGG TTGAGGGGG CCAGTGCTAC CACCAGACTT 240
 CTCTCTGGAA ACCCGCTTGG AATTTTGGTC ATCGGAACCA TAGACAAGCT CTTCATATC 300
 50 CGCTACGGCA TTGGGTGTC ATGTCTGAGC GTGACGGCTA TCAGTAATA TAGGCCATA 360
 CAGCCATGTG ACGTCGAGT CCTTGGACCA GTGACAACC TCTGGGCTCA CGTGCGTAG 420
 55

ATTATTCGG GCTTTGGCCC ACCTCTCCA GGATGCGTTC TCGAGCCGG CCGCGTTCAC 480
 5 GAGGTCTGTC TCTCCCTTCT GTCTCTTCTT CAGGATGATG TACTTCCAGG ACTGAGAGAT 540
 GTCTCACTCA GCCCAGTCGT GCGAAAGGTA 570

10 (2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1508RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

30 GATCCACAGG CAAAATTTAT GCATATAGCT TGCTTATATT TATGCGGTGG ATTCTATATG 60
 TCGCACGCTA AATACTAATA GCGGCGGTA AAAAGTAGTC CTCGGCAAAC TCGGTACCG 120
 35 CAAGGTGCGA ATTATAGAAA CGGGACTCAG AAAAATAAT CCAGAGTAAT TAAGGGACTC 180
 GGAAAGCGGA GCGGTTCTT ACCGAAAACC TCAACGGAAG TATATGAAAA AATTATCCT 240
 40 GCAGATTATA CCCATGCCIG TTTTATCCAA GGTAGCCCAA ATATATACTA CAGGAAATGA 300
 GTGACTTTTC ACTTCGAGAG CCCAAATAAC AATAATTTTA GTAAAATTTT AGCATTGCTG 360
 45 CTACTCCAAC TTCCAATGA ACACTTCTGA AAGCGTAAAT ATATAGCTAT GCGGTTTGCC 420
 TCCCAGGCTC TAACTACAAA TTCCACCTTA TGTGTGTAT TACGAAATG CAGGGGAATA 480
 50 GTTGAATCAA CGAAATAGCG TTAATTTGCA ACCGCTTGT ACGTGTATAA AACCCACCCC 540
 CCTCCGAAAA AGATGACTAT CGTTATAAAC TAAAAACAT CATCAAAAAA GAACTAAGTT 600

ACTGAAAAGA AAATGGTTTA CCGTCTAGCA GTGAATTTC A GCAACCAGCC CACATGGGTA 660

5 ACCAATTTC GAATCTATCG TTGCAGAATA CT 692

(2) INFORMATION FOR SEQ ID NO:794:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 716 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1508UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

30 GATCTGGTAA CGACTAAATA AGAATCCTTA CCGAGCAACG CCGGCCGGGT CTCGGCAGTG 60
 TAGTGTCTCT CAAGTGCGCG TCTGGCACTA GTTAGGTCTT GCAGGTGCG TTTGAACCAG 120
 TGGGCTCGG TAAGCAACGA GATGGCGGAA ACTCCCGCT CCGCATATGC AAGCGCTGT 180
 TCTCTGCAA GCGCTCGCT AATATTGCCA CCGACGGAG ACGCAAGTTT TATCTCGGCT 240
 ACCACAGCCA GCGCGGGGC GTCCCGGCC AGCGCTCAT GGAAGTCAC CAGCGCCGC 300
 40 AGAACCCCA ATCGAAAGCT CGCTCCAGG TCGGCATAC CAGTTCCGG CATAGCCATC 360
 TCGCTGCA CGTCTCTG TCGTTGAGCG TATATCTGC TCAGCACAGA GCGCGCGCT 420
 GCGCGCAGT GGAGCTTGT GTTCTCAGC CAGTACGC CTTCAGGC TAGCATGTTG 480
 CGCACATTA GCTGCCCGTG GTCCGTCAGA ATGACTCG GGTGGAAGT CACACCTCC 540
 50 ACGGTGTACT TCGGTGCG CACGCCATA ACCAGCGT TCTCCGTGG CCGCGTCAC 600
 TCCAGCTCG CCGGGAAGT TGACCCAGT CCAGCCAGG AGTGGTACG TGTCAGTGC 660
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ACGGCTGGGG TACCCCTGGA AGAACCGGCG CCGTCGTGAC GCAGCTCCGA CGTTCT

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(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1509RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

GATCCAGTTT CTCTGCAATT TTCTGAACGA TGAGATATGA GTCTAAGTTG GCTAGATTAC 60

TATATAGCCA GTTGTTGCTT CGACGGGCCA AAACCGAGAC CGGTTCTTTC CTTTGACAAG 120

AAGAATAATC GCCATCTACT TTGTTTGAAT TCTTTAAACC GTCTAACTCT TGCACTACCG 180

TTTTTGGTAC TACTATGCGA TAGCTGTATT TTGGGGCAAG CACTGGTAGT TCTTCAAGGA 240

TATCCAGATG TGATAACACA TAATTAGTAT CAACGACCAG TGCAATATTA TGCAAGTCTT 300

GCGCACTTC AACCTGGGGC TGAATTACTT TTGCGAAAGT CTCTTGGCCC GGAATATCGA 360

CTCTCTTGTC AGGAATAGTC TTAATGTGTG TAATTTCATG GCTGTGATAT TGTCTATAT 420

CCATCATGCG TTCAGCTTCG TGTTCCCTTA TAATTTCATG TTCAACCAAT GCATCCAATT 480

CTGCAATGCT ATATTTCTTA TTAGAGTCTT TAGGGTTCCA AGTATGCGGC GAGCTTATGG 540

TATGGGTCTT ATTCTGATGC CTACGCTTGC TCTTCTCTCC ATGGTCCCTA GACATCTCCT 600

GTGTAGCTTG GTGCATAGAC TGTATATGAT TGGACTCCAT CGGAAGTAGT GGCACGTTTA 660

AAAGACATTA ATTAGGTATC AACTCCATTA ACGTACCTTT GATATTTATT ATATGA 716

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1509UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

GATCTCGAGT TTCATGACGA GTGCATGGAA GATGIGITTC TAAATGCAAC TAAGGTCCGT	60
AAGGTCAGTG AGGTGCAGTC CTTTATCACT CTAAATTCCT CCTCTTCCCT TGATGATGAG	120
ATACTCGAGT CATCGATGCC AACTACAAGT CACCATCAAG ACTTAACAAC TCAAGACGTA	180
CTTGGTGGAT TGGTCGATGC TATGGATGAT AGGCGCGACC AAGAAGACGA TATCGATTGG	240
CAACAACCCC TGGATGTACT TCCTTTGATC GGCTGGGACA GTCCAGTTTC CAACTTGCCG	300
CGGATTACGG GGGTTGCTCG TTGGGAGGAT GCAGACGAAT GGGATCTTGG ACAGAGCAGT	360
ATTACTCCTA ACAAACTAGA AATCCATTGG GTCCAGACGC CTACCACACA CCGTGTGCGT	420
GTCCTAGAAG AAGAACAATC GCCTTTGATC ATGCTGCAGA AGCGCAGACT AGCCAGGAAT	480
GGGTCAAGAA CATTAGCCAC AGCTACAATC AACCATGACC AGGAACTGCA ACTAGAAGTG	540
CCAGATAGAG AAGCCGCTTC GCCTGCCATT GAACACGAGC AAGCCACCTC	590

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1510UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

GATCAGAATT GGAAGGGATG TTTGCGCGAA GAAGTTGTG ATATCGAGGA GGGCACTATA	60
CCCGTCATTG GCGGAAGTT TTTCAAGTAC GAATCTCTA TAAAGCACTT GCTACCCCC	120
AACGCCACTA TAAACGACCC CATTCCTCAG CCAACTGAGG GAGGGTCAA TGCTCCACA	180
TTGGTTGGCG CCGTTTATCT ACGCCCAAAA ATTAAAAAGG ACGACTTAGG TGAATATTC	240
ACCTCGATG ATTGTCCAG GTACATTATC AGGCTGTG ACCCGCTGA GGTGTGTAGA	300
ATCGACCCAG AAACGGGAAC CATCATTAAC AATTCCAGA CCGCAGTGT ACTACCGAAA	360
ATGAATATGT CTACACCAG TCTGTGTCT TTGAACGCA ACGGTAGCTA CTGAATTG	420
ATAGGCGGTT CCGGTAGCCC AATTACATG ACCAGGTCCA CCAATACTT CGCACCAGTT	480
CCTAACGGCG ATCTGAGAAA TCTGCCAATC GTGCAACAAA TACCGAATAG CACTATCCA	540
TCTGGCAGT CGTCTGAAA AGGCGGCATA CAGGGGACC ATGGGGGTT CAATTACGG	600
TACTACCCCT GCATACCAAC CCGCTTCAT TATTAATAAC CTAGCCGCC AGGCTAAGAC	660
AAACAATACC GTTCTTGAA ATATCTTGGT CGATACGCC GGTCCTACG TTCTCTATA	720
TCT	723

(2) INFORMATION FOR SEQ ID NO:798:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 693 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1510UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

GATGCGCGCT ACTGTTCTAC GACCACGGGC GGGGGCTGAA CCTGGCGATG GGGTTCAAGC	60
TGGAGGACCC GCACGCGCGG GGGAAAGAGC GGCGTACTG CCTGGTGCTT ACGGTGGACC	120
TGGGAGAACG GGGCGCGGCA ATGGAGATCG TGTCGCAGCA CTGGAAGTTC ATCTGGGGCG	180
CGTTCGAAAA CATGATCGAG TACATCAAGC AGCAGCGGCG CGGGAGCTG CTGCGGGTGA	240
TGCAGCAGGG GCAGGTGCAG GGCACATCGA ACTTTTGTGTC CATGGTCAGC GGCACCTATC	300
TGGCGGGGAA CAACCTGAAG ATACCGAAGA ACATCAAGGA GCTGACCAAC GATAGACTGC	360
TGTTCTGTCAG GATACACAAG TGAATGCAT TTATACTGGA TAGACTGGGA GGGCAGCTGG	420
ACTGAACCTT TGGGGCGGTG GCTGCGCGGC AACAGTTGGA AGATAGAAGA CAGAAACGCC	480
CGGGAAGCCG AGGCGGAGG TCGGAGGCGT TACATAACTT ACATTCTTAA CTAGATAGTG	540
TTCGCCTGTA CATCAAGTTC AGACGTTAAG GTTGAACGCG GCATCGGTGA TGTGTTGCT	600
GAAGGGGGCC AATGCAGATT TGACGTCTT GTTGATGAAC TTCTCCACCT GCTGTGGGGC	660
CCTGCCACAA AACGTGGAGG GGTCCAGCAG GGA	693

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 676 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1511RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

GATCGACCAG CTGGTGATGG ATAGGCGGCT GGTGCCGCTG GGGCGCTTCG TGCGGGGGCC	60
CGATTTTGGG CTGTTGTGCT GGGTGAGGTG GACGCTGCAC AAGGTGGTGG ACCTGTCTGT	120
GAGGAGCCGG GTGCGGGAGA ACGGACGGTA CCTGCGGAAC TGCGCATACG TGAACATGGA	180
CGTGCTGGCG GCGCGGCACG GCGCGGTGGA GGGGCGCTG GAAGAAAAGG TGGTGGCGCG	240
GCGACGCGA TATACGGACC TTGTGTTCTC GCGGAGGAG TTCTACGCGG TGGTGGCGGA	300
GAGCCTACGG GGACGCGGG AGTACGATGT GGTGCTGGCG GACCTGGACA AGCACCGCAA	360
GGCGATTCTA GTGACGGAG ACGTTGTGAA GGTGGTGATG CCGCGGTGC GCGCGCTGGT	420
GCAGCCGTTT GGGCCTGACC GCGTGACCGC AAACGACCGC CACATGCGAG AGTTCAAGGG	480
CTCGCTGCGA TTGGTGGAGC GGCAGGTCCA AGCGATCCAC GGGCAGCTCG AAGAGACAAC	540
CCGGGCGCTG CGTTGGCGCC GTCCCGGCGG GCGCGCACCC CGATGTGCAG CCGCGGTACC	600
TGCGGATGAA CAACTCGCGC AGGCCAGCCT GTCTGCGCG CTCAACCACT TTACGAACCT	660
AATGGAGATC AAGGAC	676

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1511UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

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GATCTTGCCC CACGGCCCGT CGCTCAAGTT CCCCCCGTCC GCCACAAAG CCCGGAACAT 60
 GCGTCATCC ACGCTGGGCT CGCTCCACGG CGTCTCCCCA GTCAGCAGCA CAAACACAAG 120
 CACTCCCGCA GACCAGATGT CCGCGGTGTC CCGGTGGTAC GCGCGCTCGC CCACCACTTC 180
 CCGCGCCAGG TACGGCAGCG TCCCCCGCGG GTGCGCGGCG AGCGCGCGCG TCCCGTCGCG 240
 CCGCGGAAC CCGCTCGCA GCGCGAAGTC CGCCACCTTC AGGTTCCCGG CCGGTCCAG 300
 CAGCATGTTT TCCGGCTTGA TGTCCCGGTG CGCCACGCGG CACGCTCGT GCAGGTGTGT 360
 CAGCGCCCGC ACCAGCTGCT GGTAGTAGAA CGGCGACCT CCGAGTCCAC CCCCAGTCC 420
 GGCTCGATCT TGTGGAAGAG GTGCCCCCGG TCCGCCAGCT CCATCGCGAT CCATAGGTAC 480
 TCACGTGACA CATTCGAGTC CAGCACCTTC ACCACATGTC GGTGCCCCGG CACCGGTCT 540
 GCAGCACACC TCGCGGTCA GATCCTCGTC CGTCATCCCT CGCGCTTTGC AGCGCTCGAA 600
 GTGCACGAAC TTCACAGCCA CTATCGTCTG CCGGTCTGCG CGCAACGAAG CGTTTTTGAA 660
 GAACGCAACG TGCCCTGCCC AATGCTCTCC CGAAGCTCTA ATTCTTAAT CTCGGGAAG 720
 CA 722

(2) INFORMATION FOR SEQ ID NO:801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1512RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

GATCTTGACT GGAAGGATGA GGAGCAAACC CCOGACAGCG GAGAACTGC TATTGCGTG	60
TCTACACGCG GCTCTACTCG CATCCAAGTT TAGCTATACC TGCATTATTA CTAGATATCT	120
AATGCTACC ATATGTTGTG ATGACACTGA CATTACGCT TTAACCACTT CAGCTTATTA	180
AAAGATTCCA GACATACAGA AAAAATCCGG TGTTAAAAGT TATACATATA CACCATTTTA	240
OCTATATACG TGTAGACGAG TAGAGCTACT AAGCAGCCCA AGAAACACTA CCATATTCAT	300
AATGGCGAGC CTAAGGACTT TOGATGCGTT CCGTATGTGC CGAGGGTTAT AGTCACACA	360
CGATGCAGTA CTAACAGTCG TAGCAAAAAC CGACCAGCAG CAGTCCGTC GGTCACTCTG	420
CGGGGCGATT ATGTCCATAA TGATGTACCT GTTCTGCTG TTTATCGCGT GGGGGGAATT	480
TGGCAGCTAC TTTGGGGGCT ATTGGACGA ACAGTACATC ATCGACCCCG AACTGCGGCA	540
GACAACGCAG ATTAACATGG ACGTGATGGT GCAAATGCCG TGCAAATACC TCGACGTCAA	600
GGCAACTGAT ATTACCAGG ACATTAACTA CGTGTGAAA AGACTGGTGT TCAAGAATAT	660
CCCTTCTTTC GTACCGTACG GCACCACATT TGACTCTGTT AATGAGGGTC CGCACCOCGG	720
AC	722

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1512UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

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GATCGAATGG CATCCCATTC ATCCGATGAG GACGCTATGT TAAATAAATA TTATCTATAT 60
ACTCTAAATA CTATATGGTT TCATCOGIGT TACCGGATT TAGAGATGCG CGTCTCGTC 120
TCCAAGCTTT AACTCGTGTG GCTGACGATT CTACATAACG TGTATGACC AGGCTGAGCA 180
GTAACGTTAG CAACTTGGAC ACCAGTTATG AGTACCGATT TCGACAGAAT TTATTATAAC 240
CAGTCAAAGG TGAGCGGTG CTTCGGTTTG GCGAAGGTG GCGTGGGATG GAAGGCTTC 300
GCCACTGGCG GGTCGGCTGC CATGCAAAC AACGAACCA TTCTCTTGAC TCGGACGAA 360
CTGGCTTCG TGCAATGGAG TAGAGGGTGC CGTGGCTACG AACTAAAGAT TAACACGAAG 420
AACAAGGCG TGGTGCAGTT GGACGGTTTC TCGCAGGAAG ATTTACATT GTTAAAGAAC 480
GATCTCCAGC GCAGATTCAA CGTGCAGTTG GAACACAAG ACCACTCGCT TCGGGGATGG 540
AATTGGGGTA CTACCGATCT GACAAGAAAC GAGCTGATCT TCTCCTAAA CCGGAAACCA 600
ACTTTGAAA TACCATATTC GCATATCAGT AACACGAATT TAACATCAA GAACGAAGTT 660
GCGCTGGAAT TCGACTTGC 679

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 721 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1513RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

5	GATCAACTGT TGCTCCAGTT GCTCCTTGA CTGGTCTC AATTCAAAG CTTTACACC	60
	GGCTGAGAT GAGATGTTAG TACTCCGCGC ACCTATCAAG CTGGGAATGA CATTGCTGGC	120
10	AACCTGGGG GCGCATCTA CCCCTGGCT ACCGCTGCT GGCTAACCG GTATGCGCTG	180
	CTGTGCGCA CTCTGTCCC ACGATTAA GCTCTAAG GTACCTGA TACCAACA	240
15	AAAGCTGCAT GCCATCATC CAGCTATAC ACCGCTGAC ACATACCATT ATGATTGATT	300
	TTGCTGTATT TTGACTAAG AGCCACTCCA AATGAACTGC CTCTCTGT GAAGATGTTG	360
20	GCTGCTGTG GAAACCGACT GTGCTCGCT CGGTGTGCGC GAGGAGTCT GTCGAAGAC	420
	GCAGAATCTT CAGCTATACA ACCACACAC CTCGAATGT ACGATGCA CAGTCAAACA	480
25	CAATTCACAA TCACGTGACC TACAGGTGAA ATTAACGATT TGGCAGATC GCAAAGTGAG	540
	CGCCAAAGC GCGACGGAAC ACCGAGCG GTACAGATG GGTGCGACTT CTTACACTAT	600
30	ATATCGATGG TAACAGTGCA CGCACAAAA AAAGTAGTAT ACTAGGGTCT ACGAGACTTC	660
	GCTAGTTCAT TTACAGCCTA ACCTAAAGAT TAATTATGCC AAGACAGTGA TTGGAAGGAG	720
35	A	721

(2) INFORMATION FOR SEQ ID NO:804:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 726 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1513UP

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EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

5	GATCTTTTAAA ATTTGGCAAG AACAGCCAAC ACTCCCGTCA AAATAAGAG CAAAGCGCCT	60
	CCACACCTCT ACGAATCAGG TCCGAAAGGC GATCTTGCAA TGACGAGCAA GGTTACAAAG	120
10	AAAGTTAGAG AGTCGCACAG TGCATGTGAC GACCAGCAGC ATAGTTCTCG GGCTCGGGC	180
	ACTGCAGCAG AGGGAGCGCC TAGTAACGTG GTTCAACCGT CCCTGGTGA TTTGAAGAA	240
15	CTGCGAGAAT ACACACTCTC CACCCCTACG TCGAACGAGT GCATTAAATA ACGGCTGGG	300
	TCCACGAACG TGCAGGAGGT GAAGCTGGGG GGACTGCAGT TTCTGTTTTA CAAGACGCTA	360
20	CTACTGTGTC TTACATGGC ATATGGGTTT TACCGATACT TCCAATACCA GTACAACAGG	420
	CTGGGTATCA AACTACTGAA TCTGGCCTAC TCGCCGTCCA ATACCCCGCA GCTGATCAGA	480
25	CAGGACGTGC TAAAGTTGCA GAAGGTCCCT AAGCGGCTGG CAGCGATTTT GGCATACAAG	540
	TCTGAAGGGG AGGTGGGGG TGGCGTCCAC GGCTTGATAA ACGACGGAAG CAACGTANTA	600
30	TGCTGGACTG TGTTCTGGGG CATCAAGCAC CTGTGCTTTT ATGATCATGA CCGGGTGCTC	660
	AAGGCCAACG TGCACCAATT CCGCCAGGGC GTGTACGATA CCTGGCGCGC TACTACGGCC	720
35	CAACAA	726

(2) INFORMATION FOR SEQ ID NO:805:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 736 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1514RP

55

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:805:

5	GATCTGGGTG TATATTTGGA TGTATATGGA CTTACACTTT TCGGAAGCAA TCGAACTCGA	60
	AAGCTGGTTG ACCACTCTGC TGTATICTCG TAGTCTTTCT GAAACGACGG TAAGAAAATT	120
10	AACCTTCAGC GCGATAGGG AAGATGCAAC TTTAAATTTC TCTACTTGGT TACTCAAATA	180
	CTGATATAAT AATGCAGCCT CAAATATGCT GTGGAAAACA CCACTTTGCG CGTTGGGAAC	240
15	ATTGGGTGGG ATTTCGATAA CCTGATTGGA GATCGGGAAC AAACCTGACG TAGTAGCCAG	300
	TAACGTTAG GAAATATACT TTAAAACGTC GGCTCGGGC ACCATGTTGC TGTAGTATGG	360
20	GTTAGACAGA TATGCCAATG GAGTATCGTG CTGCTGGGC CGCTTGGGA CGGGCCGCGC	420
	GTATGCAGAG GTTACCGCGG ACGGCGCTC TGAAAGCGC TOCACATTCT CGAACGACTC	480
25	TGCATAGACA CTAACCGCCC TCGACGGCGT CATCAGCGAG TTGTGCGGTT GCAGCGTGGC	540
	GTTCGTAAGA TATCCAGACG CGGTGCGCCT GTGTGGAAG GCGGTGCTCT CCTGCGGCAC	600
30	GCTGTTTCAGC ACGTTCAGGT ACTTCAGCAC CTGCTCCTTG CTACCGAAAC TCTCCAGCAC	660
	TTTCACGAAC ATCTCGAACT TCCCCACTG CTGCGTCTGC TCGGCGTCC GCACCATCTC	720
35	CGCCCGGTAC ATGCTC	736

(2) INFORMATION FOR SEQ ID NO:806:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

45

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1514UP

55

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

5	GATCTCCACC GCGTCCAGCA CCACGATCCG GTCACCGTCC CACCGCGTCA TCGCCACTGT	60
	CCGCGCGAGC CTTTGGAAAA CCGCCCGTCC CTCGCGCGTC GCAGCCCCTC CCCCCTGTTC	120
10	GTGCGTCCGG TGCTCGGCCT CCCGCGACCG CAGCGTGGC ACCACCCGCT CTATATTAC	180
	GCCCCGGGC TTCAGCGTGT CGCGCTTGAT GCCAGGGCTG GTGGGTTTCT CTCCCACCAC	240
15	CTCCAGGCTC TTGATAAACG TCGTCTTAAT CACCTTAAAG CTCGCAGTAT GGCCCTTGCG	300
	CCCACATAGT AGCGTCAGCG TATGGTTTCC CGAATCGTAC GCGTATATCT TGCCCTGTGT	360
20	TACACCGTGG AGGACGTTGG TCACCCGCAC CTGAATCCA AGGATATGTT CCAAGTTGAT	420
	GCTCATCTCG CTCACTTCCA AGCCACACA GCTATCCTGG CCACCTTAGA ATGCCACGCC	480
25	TGCTCCCCGT CCACTGGCTG ACTCCCAATC GTTCAGTTTG CGGTGTGGT ATTTTTTTGA	540
	AGTGGCGCTC TAGCGATGAA GTAAGATTTT CTATGTATTA CTATGTGCA CAAAGGTTAG	600
30	TTCCAATAGT GCTTGCAACT ATCAGGTGCT GTGGAGTTCC CAAGCAGACG AGTTGCTGAT	660
	AGTGGAGCCG ATAGAGAATC CGATAAAGAT TATTCOCGAA AATCTAAGGA CAGGTGG	717

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1515RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

5	GATCCTTCGC CGCGTGGTCA AAGCCCGGAT AGGATATCAC AGGGCACTGT GCAAAGGTAT	60
	CGCATATTGT TTCCATGAGC GTTTCGCCCT TCGGTCTCTT CGCCGGCTTC CACTTGCAAG	120
10	TGGCCGCCAG GAGCTTACAG AGCTGCAGAT AGTTATTACT GTCAAAGTC CAGGGTGCC	180
	CGCGCCGTTT GTGCGCCGA GCAGCATCCG CGAAGTGGTC CAGGTGCGCC CGGACAGAT	240
15	GGAACCCGTC CATGGGCACC ACCTCAGCTA TATTGACCGA TGAAGCTGGA TCCAGGGCTT	300
	CGCTCGGAT GCGCAACGAA TTGGGGAGCC CGCCCGGCC GAAGATAACT GGGTCCCAT	360
20	CCCCATCGTA GAACTTGTTT GCCTTGAACC CCGGTCTCT CACGTGCGG AAGAACCC	420
	GTGCGGCTC CTCGACCAGG GCGCTGAGC CAACCGGCAC AGTCTGTCC AGGCTTTCC	480
25	CAGCAATGCC CGCGGAAATC CTCAATCCAC CCGTCTGTGC CTTCAAGTGA CTCTGGAATT	540
	CCTGGTTCAG GTCCCGCTTA AGCCTCTGCG CCATCGTAGA CTTGCGGAC CCAGGATGCC	600
30	CCACCACCAC TACAGCCACC CGATAGTTGC TCTCGATATT CTGAGCAAGG AGATCCACA	660
	CTCGCTTCTT TAAGTCTTCG TAGTCCATGC CGCTGCTGT GTATGCTGC TGGT	714

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1515UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

EP 0 866 129 A2

	GATCTAACGC CGGCTGTCTC CTCCAAGCGT GTTCCTGCCT CTCTTATATC TGTATCTGGT	60
5	AGCTTCAGCA TTAAAAAACC GTCCAGAGAA TTGGCTTTTCG GCCATGCTCG AAAGCTCACT	120
	AGTCGGAGCG CAGCATCTAG GACACCAGTA GGATGCAGAC AGTGTTTTAGG CCATTGAGAA	180
10	GTGTGATTCT GACGCCCGCT CGAGGCCTCG CGCGGTCCAG CAGGCTGCAG TCGGGACACA	240
	ACAAGTGGTC GACGATCAAG CACGATAAAG CGAAGAACGA TGCTGAGCGG AACAGGCTTTT	300
15	TCACGGGAT GCCCAACCAG ATATCGGTGG CAGTCAAGCA GGGCGGGTCT GCCGACCCGA	360
	CGCTGAACCT GCGACTGGCG GCGGCGATAG AAGCGGCGTC CAAGGCCAAT GTGACCAAGA	420
20	AAGTGATCGA AAACGCAATC CGCAAGGGCG TCGGCGAGGG TGGGGCGCGC GACAACGCCG	480
	AGGCATGCAT GTACGAGGCG ATACGGCCCG GTGGCGTGGC GTTTGTCTCG GAGGCTCAC	540
25	CGACAACAAG AATCGGACCG TGACCTGGTA CGCGCCGCGT TCAACAAGCA TGGCGGCAAC	600
	ATGTGCGCCG CTCAGTACTT CTTCGAGCGC CGCGGTACG TGGCAATCCA GCCACCGGCC	660
30	TCGTGCGAGA GTTACAACGC GGIGTTTGAG GTTGTGTCCG AGGTGAGGG CGTAGAAGAA	720
	CTGGA	725

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1516RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

EP 0 866 129 A2

	GATCGACCT TTGGTGGCTT GGCTCGAGTC TTCTTCAAT TTAAACCCCT GTTCAACAGC	60
5	AGATGAAATT GTTAGTCTAT CGAGTCCAG TAAAAGACAA TTTTGCAGC TTGAGATGAA	120
	GGGTACGGCC TCTCCCGACA AGCGGCATCG CCTGCACCGA AAAGTATCG GTCACTCCTT	180
10	CATCATAAGG TACCTTCACT ATCTCTTTC GCGGAAACT AAATACAGAA ACATACCTTT	240
	AACATCCTTA TTCTGTTTAT CCTTTCTGA TTTGACTGG AATGTAGCG CGAAAGGGAT	300
15	CTGTTTCAA AATTGGAAAC GCTTACCACC TCACCAACAC ACCAGGACTT TATTTCGTAG	360
	AAACAGGCGA TCGGCTGAA CAACAGTCAC TAGAAACGGT GCACCAAGC AGCTTGGCAA	420
20	CGAGGAGGCA CCTAGGGCT CAATGGGTG ATAGTAAAGC ATGTACAGA GCTTTGTCTC	480
	CGAGAGAAG AACGACGTCT TGCCTCGA CACGTACGAA TCTGAGATAC ACCACCAAGG	540
25	GTGGGTAGTG GTGCGACGTA AAGCCTTCAG TTTGGGGGA CGGCTGGGG ACGGGGAGT	600
	ACTTGTGGC AGCCGAAGAT ACGCGATGA GCTGCAGAG CTGGCTCGG AGCTGTCTG	660
30	CTCGCTGAC GGTCCGGCT TGGAGAC	687

(2) INFORMATION FOR SEQ ID NO:810:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 724 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1516UP

50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:	
55	GATCATTAC GAAATCTTG TGGTTGATTA CGATGTTGTA TGGGAAGATA TAGCTGGTCT	60

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	TACAATAGCA AAGAAGTGT TGAAGGAAAC AGTTGTTTAC CCATTTTTCG GGCCAGACCT	120
5	TTTTCGGGGT CTCGGGAAC CTATCTCCGG GATGTGTTA TTTGGACCTC CAGGAACAGG	180
	TAAAACGATG ATTGCCAGGG CCGTTCCGAC TGAATCGAAT TCAACTTTCT TTTGCATCAG	240
10	TGCTTCTCT TTTTATCGA AATACTTGGG TGAGTCGGAA AAACCTTGTC AGGCCTTATT	300
	TTACCTAGCC AAACGGCTTT CCCCCTCAAT TATATTCAAT GACGAAATCG ACTCTCTACT	360
15	AACTAGCCGT TCAGATAATG AGAACGAATC ATCCAGAAGG ATTAAGACGG AGCTCTTGGT	420
	CCAATGGTCC TCCCTAACGA GCGCCACGGC TAAGGAAACA AGAGAAGGCG AAGAGGCCAG	480
20	ACCGGTTCTT GTCTTGGCCG CAACCAACTT ACCGTGGGCG ATAGATGATG CTGCTATTAG	540
	ACGTTTTTCA CGGCGTCTAT ACATTCATT GCGGAATAC GAAACAAGAC TGTATCATTT	600
25	GAAGAAGCTT ATGGCCCTTC AAAAGAATGA ACTTTCIGAA TCTGACTTTC AACTCATTGC	660
	TCCATGACT GAGGGCTACT CCGGATCTGA CATAACTGCT CTTGCCAAAA GAAGCAGCTA	720
30	TGGA	724

(2) INFORMATION FOR SEQ ID NO:811:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 710 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1517RP

50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:
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55	GATCAATGAA AAACATGCAT ACGATTTTCAAT GAAGCAAAAT TTGGCTTGGA ATATTGCCAA	60
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EP 0 866 129 A2

CTCTATTTCAC AAAACAGAAA TACTAAAGGA AGAGAACTTC ACGTTATTAT CCAAAGCCCA 120

5 AAGAGATGAC GTGAAAGGAA GAGAAGCGGA GTTATTACTT CCAAGCGAAT TAAATCAATT 180

AAAGATGGTC AATGAGCGTG AGCTGAACGG CCATGCAAGA AAAATAAGAC TACTATOCAT 240

10 GTGGGAAGTC TTCAAAATGC TTTAGGTTCT GCATTATTAT ATACACATTG TAGATACAAC 300

TGAAACTAA TGCAATTCAC GTCAGCAGTC TAAAAGTGGT CATGCAGTAA CTTCAACCT 360

15 TCTTTATTCC AAGGACAAAG GTATATTCCC AGCTGTGTCT TAGACAGTGT CCCAGCTTG 420

AAACATGTGT TACTCAAATG GTTGGCAGTA ACCTTACATT GCCCAGAATG GGTGATGCGG 480

20 TTAGAAGTGG TATAATCCAA CTGCTTCCAA ACATCAGCGT TATTAGGTGT AAAGAAAGCG 540

GATCTCTGCC ACAGAATTTT AGATGGAGCG CGCAAATTCA GTGCTCTGGA AATCTCATCC 600

25 ATGACAAGTG GAACATCTTT GTATTGTGCC GACAGGATGC CTTTAAATGG TAGGTTAGCT 660

AAATCTTTCA TCAAAATIGA AAGTGGTCCA CCTGTCTTC CATGAGACAA 710

30 (2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 662 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: PAG1517UP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

GATCCTCAAA ACTACAGAGC GAAGTTGAAA AAGATCATAT TTTGATAGAG CGTAAGCAGT 60

55 GGGATGAAGC ATACGCTCTT CTCAAAGGTG TTGTGGATAG ACATCCACAT CTATATGATG 120

CACATTCAGC ATTGGTTGG TGTCAGCTGC AGTTGGGCGA CACTGAAAGC GCTTTAGAAA 180
 5 CATTCCAGCT TATTATTAAT AATGTGAAGA GCAGCGACGG CACGTGCTCT CAGTTCATTA 240
 GCTCAGTACA CTGGCGAACC GCACAAGCAC TTATTACTAA GCAGCAGCAT GAAGATCCTT 300
 10 CAGGTAATGA GTTTATAAAG ATTGCTTTCC AGCATCTGGT ACAATCCCTG AAGATAACCG 360
 ATCTTTTTCG TOCAGGTAT TCCCTTCTTG GACACATTTA CGAAGTGTAT TTTCAAGACC 420
 15 TGACTCGGCG ATTTAGGTGT TACGTAAAG CCTTTGAGCT AGATGCCGCG GACCTGCTCG 480
 CTGCTAAATA CATGGTGGAA TACTATAGTG ACCTGTGCAA TTGGCAGGCG GCGGGCAACA 540
 20 TCTGTGACCG TGTAATCAAG AATGATATGC ATCTCAATTC CGTCAACTGG CCGTACAGAG 600
 TTCTGGGTGT TTATTATTTG GAGCTTCAAC AGGAGGCTGA ATCGATCGAA TGGTTCCAAT 660
 25 CC 662

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1518RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

50 GATCAAATGC CCTTCCCTTT CAACAATTC ACGTACTTTT TCACTCTCTT TTCAAAGTTC 60
 TTTTCATCTT TCCATCACTG TACTTGTTCG CTATGGTCTT CTGCGCAATA TTAGCTTTA 120
 55 GATGGAATTT ACCAACCCTT TAGAGCTGCA TTCCCAAACA ACTCGACTCG TCGAAAGAAC 180

CTTAGATGGC ACTAGCACCC CCGCCAGACG GGATTCTCAC CCTCTATGAC GTCTGTTC 240
5 AAGGAACATA GACAGGGACT AGCAACCAAG GTACTTTCTT CAAATTACAA CTCGGACGCC 300
GAAGGCGCCA GATTTCAAAT TTGAGCTTTT GCCGCTTCAC TCGCGTTAC TAAGGCAATC 360
10 CCGGTGGTT TCTTTTCTC CGCTTATTGA TATGCTTAAG TTCAGGGGT AATCTACCT 420
GATTGAGGT CAACTTTGG GAATACTATT CGCTTGAAG GCCTTGTTC TGTACGTC 480
15 TTCAAGGCC AGCTCCACTC CAGATCTGG TCGAAACCTA ATAAGCAGTG TAGAACTAG 540
CTCAGAACGC AGTCCGCGCA AGTCCGCCC ATGGGCAGCA TTTTCAAGTT AACCTGTCT 600
20 TAAGACCGAG TATCACTCAT TACCAACCC GAGGGTTTGA GAAGGAAATG ACGCTCAAC 660
AGGCATGCC CTGGAATACC AGAGGACGCA ATGTGCGTTC 700

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1518UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

GATCGTCAGA TACCTTAGTC TCTATACAGC GCAAGACATG GGTGATGGCG GGTTCGTCT 60
50 ATGCAAAGTC ATTGGGTTTC CCTCTGGCGG CGCATACAAC ACCTGCTAA CCTGAACAGT 120
CTCATCTGG GCATCTAGCG ATCCATGGG TGAGCAGCGG AGGATTGGT GGATTACTAG 180
55 CCAATGGCAA TCCAAACCA AGAAACGAC TTGGGGGAAT GCTCATTGA ATAGCCGGTG 240

TTTCGACACT GTGATTCTCT GAGTGTAAAC TCTCTTTGG TTGCGATAT TAAACCTGTT 300

5 CTGTGAAACA TCGGAGCGGT GTTTAGTGA AAGCAACTAG AGGAACTCAA AGAGTGCTAT 360

GGCATGGGG CAGCTGTTGC GAAGGTGTAA AAACCCGAGC TCOGGTTCG TTGACACAGA 420

10 AGTTACTTTC TGTATCTCTA TCAGTCTATC ACCGAAGGAC CCGTGGTGTG CTTTGCGCAT 480

TTTCGGGTG TTCTTTAAGA TAGTTATCTG GTTGATCCTG CCAGTAGTCA TATGCTTGTC 540

15 TCAAAGATTA AGCCATGCAT GTCTAAGTAT AAGCAATTTA TACAGTGAAA CTGCGAATGG 600

CTCATTAAAT CAGTTATCGT TTATTGATA GTTCTTTTAC TACATGGATA TCTGTGGTAA 660

20 TTCTAGAGCT AATACATGCT TAAAATCTCG ACCTTTGTGA AGAGAT 706

(2) INFORMATION FOR SEQ ID NO:815:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 699 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1519RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

45 GATCAGACTG AACCATATA TCAGCGAGGT ATGGTACGAT TTGGGCACTT TGTATGAGAC 60

ATGCAACAAT CAGCTCAGCG ATGCCCTGGA TGCATATAAA CAAGCTGTTT GCTTAGATCC 120

50 GAATAACGTC CACATAAGGG AGAGACTAGA GGCTTTGACT GCCAGCTAG CCAACCCAGG 180

GGCCCAGCAG CCTCAGCAGC AGCCTCAACA GCAACAGATG CAACAGCCTA GAGGGCCAGC 240

55 ACCCATTTATG TTGCAGCCAA CATTGCAGCA GCAAGACCAA ACAAATCCGT TGAATAACAA 300

ACCTGCGTTC TACCGGTCTT CTCCCCACGG AGTTGCGGTT GCGGGAACAG AGTCCGCAGG 360
 5 CCACACACCA ATGTCAGGAC GGCTCAGCC GTTGCAGCAG TTGAACAATA ACGGAAGTAT 420
 CCTGGAACCG TCATTGTGTG CGCAAAGAG GCCTATGGAG GGTGGAATGG ATACATTGGT 480
 10 AAATGCCATT TCGCAGCAGG AGTTGCAGCA ACATCAGAAG AACATATGC CTTCTCAGAA 540
 CCATCCTAGT TTGGCCCTGG CTACAGGACA GCGCAGCAG TTACCACCCG ATGCGGCTCC 600
 15 CATAATACCG CCGGAAAAGA AAGGTGCGGC TCTCCCCCAG TTTCAGAAAA CTGAACCAGA 660
 GCATGCGGCA AAAAGACTGA AGCCCGAGCA GAATAACGT 699

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1519UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GATCAGGTAT CGGCCAACAT ATCGGCTCTG TCGATAGCGT CGAAGATTAT CGTGATAGAT 60
 45 ATAGACTATG AAGTGACGGA CGGCAAGGTG ATCGATGTTA AGCTGGTGCT GGCAAGCAAC 120
 TTCGACAAGT TTGACTACTT CAATGGCGAG GCGAACATCC TGCAOCCGTC ACTTACCAAG 180
 50 TATAGCGACC TGCACGAGTT CCACCACAAC CTGAAGTTCT TAACCTACT CGACGGGTGC 240
 TCAAGCATCG ATATCGAGTC CAATGTGTG CAATTGATT TGTTCAGTA TTAATCGATG 300
 55 CTGCCGCGAT ACATGCAGAG CTACCTGGAC GACAATGGCG CGCAGCTCAC GGTGCAGACG 360

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AACCTGAACG ACCGTTTTGG GATCTACTTG CTGACCATT CCGAAAAGAA GGTCGCCAAG 420
 CTGACATTTG CCGCTACGCA GGACCCGAAC CAGCGGTATT ACGAATACAA ATACTOGAGC 480
 GAAACGAAGG AGTGGATCAA CCAGTCGGCC GAGTCCTATA CGACCGGCAT CACGCTGGTG 540
 TTCGAACTTC TCGGTGACCC TCCGACGTAC CTGCTAAGG ATAGTTTGCC GCCAGAACAC 600
 CCTGATGAGG GCTTCACGAG TGCTTCGGG TCCGAGCTGC AGCGCCGCTT TGCATTCAAG 660
 TGTCAAATC CACGAGTCAC CCTCGTAAAT GACTTC 696

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1520RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

GATCTTCTGG ACGCTTTCTT TGAGTTGGTT CATCTTGCCA AGCAGTGA CGTTGGGGTT 60
 GCGCGCAAAA GAGTTGAGCA TCGGCCAAG GCGGCTGCA ATGGCGCAA ACTTGTCTAG 120
 CACCTTCGTG ACGGTAGTTG GGAGCTGCAA AAAGCGCAAC GTATGGCCCG TGGGCGCGGT 180
 GTCAAAGATC ACCGTGTGGA AGTGCTCGCC GTGCGGCTGC TCTGCTTCT TGATGTGTTT 240
 CATCACCTCC ATGAACGAAA GCGCTCGTC GATGCGCGA ATCGACCCCG TGAGATCTGC 300
 GAGTGGCGCG CCTGTAGCA AGCCGAGAG CCGTCATCA TCGCGCGGT TCGGATGCG 360
 CATGTGTTT ACGTCTTCA ACGCGCGGA AGGTGCGATT TCCATACAG ACAAGTTGTC 420

CATGCCCCGTC ACCTTGCGCG CGTCCTTCCC AACCTTCTCG TTGAACGCAT CGCTAAGGTT 480
 5 ATGCGCAGGA TCCGTGAGAG TCAAAAGAAA CTGCTTAGTG GGCTGGGCAA GCGCCATCTG 540
 GATGGCAATG GAGCACGAAG ACGTGGTCTT GCGCACACCG CCTTCCCGC CGACGAAAAT 600
 10 CCACTTGIGT GTTGTAAGT TGATCAACGA GCGCAAAGAG GCCTCTGGTG TAATATCAST 660
 CATGGTTGGT GTACCGCGTG AATCTGAGAG TGCAGGCGAT CTGAGATCTT 710

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1520UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

GATCAAACAG TAATGACTTT GTTAACGGTT TTGAAGTACT GCACGAGCTG CGACTCCTCA 60
 40 CTGCCCCTGTG GCGCCACAAG CGCCGAAATC ACAGCAACTT CGCTTTCAA CTGAATGGCC 120
 TCCTGCATGT TCCGTGGGAA CCCAAGTAGC ACGACGCTGT CCCCAGCCTG GCACACCTCC 180
 45 TTCAGATAGC GCGCCATCAA CGCAACCAGC GCACCCCTGG GCAGGTGCGC CGAGTAGTCA 240
 TCGCCATGCA CAGCATGCAA CTCCTCTAAT AGCGGTGGT ATTTGTCTGT CTGTGGGTG 300
 50 CGGAACCGCT CCAGCGCCTG CTGCACGGT ACGGCGCGGG CCCCCGCTG CCGCCGGATC 360
 TTCTCTACGG GCACATCGGC AAGCACCGCC AGCACCTCCA GTCATCTGG CTTGAACACC 420
 55 GTCACCCGCC GCTCAGGCC GGAGCGGACC TTCTCGAACT CCGCTTCGCT GAACTCTGTC 480

TGCGGCTTGC TCGGTCAAT CGACTTCGCC GCCTGCACGA AGATGAGCGT GCTGACCACC 540
 5 GCAACGCCAA CCATCTTCCA CGCGCTAGGT AGATCTTCGG AACCAGGGGC CTTGCTGGCG 600
 TATGGCCGCA AAAGTCCTTG CTGACGCCGC AGAAGGAACA ATCTAGGCTT ACAAGTCTGC 660
 10 GAAACATTTG TCCTGCGAGT TAGCC 685

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1521RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

GATCGAATCT KGCTGAGGG TCTTCCACGA WITGCAATGC AATCTCCGGA TATCCGGCCT 60
 35 TCTGTAGATA CGAGATGATG TTCTGGCCCC CAAGGTGGA CGTACGAATG AGACGCAAGA 120
 CTTCAGGGAA GTTCTTGTTT ACCAAAGCTT TCTTAAAGCG GFACTCGGTT GGGTCAATGG 180
 40 TCAATATCTC AATATCGCCG TCTCTGTTCA AAGCATATAT ATGCTTGCCA TGAGCTTTGG 240
 TAAATGTATAG GGTCTTGCTC AAAGTTTTTA TGATCCCGCT GTCACCAATC AATAGGCAGT 300
 45 ACTWAATATG GTTCAAAGTA GACAAGAGCA GAACACCAGT TTCATCCAC GCGCTGACT 360
 TGATCCTGAT CGTCTCATGG TTAGACGTAG TAATCTCCAA CTTCCTAGTA GCAATGGTCA 420
 GCGTGTGTTT ACTCATTAAG GCAACGTATT GCCCATCTGG GGACCAGACT GCATATTTAA 480
 55 CCATCTTCAG AGCTACCTCC GCCAATTTTT TCCCTGCTG CACGTGGAAC AAGACTACCG 540

CCTTTGGTTT CAAGATGAGT ACCGCACCAG GGCTCCATA GACAATGTCT TTAACAGTTC 600
 5 CTCTATCTT GATCGATTG GTTACCTTGT TGTCCAACC ACGTACTTCA AGAGATTCCG 660
 ACGCAGAGTT GTAGACAGCG TTACCTATGC CGAGCGACAA AAGTCGCAA GCTTCCCTTA 720
 10 TC 722

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1521UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

GATCCACTTC CCAGATTACA TGATAACATC GAAGCGAAG GTGCAAGGG AAATGTTGGA 60
 35 GCAGTATGAC TTTATWCATA GCGGCTTCAT CAGCGTAGAC GGCAAATCAG AAAGCCTCAT 120
 CTGGGCATG CCGAAGAAGA CCACCGGCAG TTTGATCAGC TCATCGAAAG TTTTCCTATA 180
 40 TGGCAGAGCA GCGTCACCA TGAAGACAAG CAGAGGCCCA GCGTCATCA CCGCAATTGT 240
 ATTCAATGTC TCTACCCAGG ACGAGATAGA CTACGAGTTC GTGGGGAGCG AGCTCCATAC 300
 45 TGTCAGACG AACTACTACT ACCAGGGCGA GCTCAACCAC TCGAGAATGC GCGCCATTTC 360
 GCTACCCCTC AACAGCCACG AGGAGTACCA CATATAAGAG GTTGAATGGG ATGCCGAACG 420
 50 CATCCACTGG ATGGTCGACG GCGAGATAGT GCGCACTTG TTCAAGCGCG ACACCTGGGA 480
 CCGGTCCAC AAAATATACA AGTATCCACA AACGCCCATG ATGCTCCAGA TTTCCCTCTG 540
 55

GCCCCGGGGC ACCCCCGATG CGCGGCAGGG CACCATC

577

5 (2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 705 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: PAG1522RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

GATCAAAAGC GAACAGGCA CTTATGTCCT GOCOAACCGA CGGTGCTCC TGAATACCCA	60
ACGAGCACTC CCTGGCCTGC TATCTGCGCG TATTCTGTCA GAACGATCGC CGCTAGAAAG	120
TTACCAAGCG CGTCACACCT GTATTCCCTG GCTTCTCTCT CGGCTTCTGA TGTGCTGGCA	180
AGTAGTTCTC CACGTTCTGC AGCTGCCACT GGAAACGTGC AAACCAAAAC AAACCTGACA	240
CCACTTCTGT CTCTCGATCG CGTCCAGCCT CCAGAACTCC CAGCGCACAG ATTTTGACTA	300
TAGCAACCCC CGCGACTAGC ACTCAAGAAC TTTCAATTTT CGCTTGAGCC CGACCTTGTT	360
TTTGAAGAT TCTGACCTAT CCTCCTATCG ACGTCAGGGA CACAAATCAC ACTATAGTAC	420
CTCGAACAAC AGTACAGAAA AGAAAACCAG CTGCTCCAGC CAAAATTCAC AAGTCCCGTT	480
AGCTGCTAAG GCCAATTGGT GATACTCAGT CTTTAATCTT TACCCAATTG GGAAACTTCA	540
CCAAGGAGAG TCTTGGCTCT TAAGGTTTGG CAGTTTGGTT TAAAAATTTT CTTGCACGAA	600
ATGTCAGAAT GTCTGGGTTC CCTTGTCTGG TCACGTGGGT GTGGTCAAG TGGGTGCTAA	660
TCACGTGACA CGTGGATGAC GACTGAGGCG GAAAATTTGC AGGTT	705

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1522UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

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GATCGACAAT ATTCCCCAC CAGGCGCAAG AATCGAGTGC ACACAGGCCA CGCGCGCATC      60
CGGGCTCGGA TGGGCGGGCC TGGGCTGCAG TGGGCGGCTG GGGGGCGAAG CACACTACCA      120
CAGTGTGCTG TGGTGGGGCG GGGACGCCAC GCCGCGCAGC TGCGGGCTGC ATTCCAGCCA      180
CGCATGCACG AAGAGCGGGG TGACACTGCC ACCGCTGGCG TGGCTGCTGC AGTCCAGCGG      240
CTACATGGGG TTCAACAACG AGCCGCGGGC CGTCACGGCG TCGTGTCTAG GGGCGACACA      300
TCCGAAGGC CATTACGGCA GGGACATGCT GAGCAGCGCG GTGGGGCAGC CCGCGTGTTA      360
CGTGGGGGCG CAGAGCCCGT TGCTACCGCT GGGCGACGCG ATTGGCGCGG CGCTCCCAAC      420
CAAGCCATCG CATCGCTGG TGGGGGGGAA CGCGCAGCTG CGCGGGCAG TGCTGCCCAT      480
CGTGGGGGCC GCGGGGTCCC AGGCTACGAA ACGAACAAGA CATGCTCGT TTGTGGCAGA      540
CGATGTACCC GTCCAGCAC GCTCAAGAAC ACATGCTCAT CCACACGGGC GAACTGCTTT      600
TCAGTGCAGT TGGCCCGGGT GCTCCAAGCG GTTCAACGTC AGGAGCAATA TGAACCGACA      660
TGTTGAATCC CACAAGGCC CGCTGATGAA GGAAAGCAAG AAGAAATCCA GTTCTCCC      718

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(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1523RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

GATCTTATCT AAACCGCTCC GCGATGATGC TTGTTAGCA ACGGAAGCCC GCATTTCAAA 60
GTCAACATCA GCGGAAGCTT GGATAGATGA GAAAATCACA GGTGTACAT GCGCGAGAG 120
CTGAATTGGA TTCACCGCTT TGCTATCAST GGGIWAGAGG CGTTCACITG GCTGTTCTGA 180
ATTTGAACTT CTGGAGCTAT WCGAGGGGTT ATGAGCAAGT CCAAGTTCCC GCGTGAAAAG 240
CTGATCCTGG TAATACTCGG TGTAATCCAC GCTTTTCTGC CAGCAAAAAG CTGGCGAGTT 300
TGGAATCTTT CCTTTATCGG CGACGTCOGT GCGTACATGG CGTTCAATGG TATTTGCTGA 360
TGTAAGTGTG GGGAGAAGTC GTAGGGAATG TCTAGATAAG GTTGACGCTG AAAAGCTATT 420
ACGTTGCAAT AGCTGCGGTT GAGAATGGTG TACTTGGGCA CAGCAACCTG CTGCGCTGCA 480
TCTGGGTGAG CTATTAAAAA TCTCGGCCAC CGAATAGAAG AGCATCTTTG GGTGAGCGCG 540
ATTCAGTTCC ATGAGATCAA CAAAGGATAA AATCGGAGG TTATCAAGGG AGAATTGTGT 600
ATCATAAAG AGCCAATCAT CACTGCAGTT GCTATATTT GGATTATTGT GATATTGCOCT 660
CACAGCAGTG TTTATCCGGT CTTTTTGGCA GTCATATACC ACAATGGATT GT 712

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 649 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1523UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

20	GATCGACAGA ATGAGCAGAG CCATTCTGAG AAAGCAAACA CGGCCCATG CGTTCTGGG	60
	ATCCCTGCCA CAGAGCGAAA TGGGCCGAGA AGGTTTGTAC TCGCGATCA AGGATCATCT	120
25	GGCCTTAGCG CCATGCGACG TAGTAAAAGG ATGGCATGGA TGCTGGTGG AAATGCGGTG	180
	CGACTGGCGC AAGACATGGA TTTTATCAAC ACCAGCTCCA AGATATTCTG CCAACACAC	240
30	ACTTCGGAGA CGAATTGCGC AATGAACATG GGTGAGAACA GTACATTATC CCATTCTCTG	300
	ATGAACGCAA ATATTATAGG CTCAGAGTCA AGCAGGGCCA TTAGCAATCC ACCTATGCCA	360
35	TCTGAAACTG AGGAACGTTA CAAAAGTGTT TTACAGAGAC TCGGTAAACA TGTCCCTGGG	420
	GGTAGAGGCC TATCTCAGCT TTATAATGAG TTTTGGAGG ACGAGGCGAT CCTCTACGGC	480
40	TTAGGTGGTG GAAGTGAATA TGTTGAAGCA TACTGCGATA GTTTGGATCA AACAAAAAAC	540
	AATGTGAGCA TCGAGACTGC GTATGAATCT TCTTTGCTAG AGCGCGGGG CCAGCAGGTT	600
45	TTTCTGTCTT TCGCCCAACG CCGAAGATA GAGCTACTGA GGATCATGT	649

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 660 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1524RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

5	GATCTTTTGA AACAAAGTGAA TTTCTGGAAA TCGAAGTGGC GTGACTTTGA CAAAATTAAAG	60
10	CAGGACTTAC TGGCCAACAT GCGGACGAAA GAGACGGACT TCAACAATCG ATGCACCGAC	120
15	TATGAACGTA ATATAGTTGA ACTTCAGCGT CAACTATCAG AAAAGTGGCA CGCTACAAAC	180
20	GAAAGCTCTG TCACTTCAAC CTCTGCGGAT GTACCTGGAG AAACCAAAGA ATATATTGAG	240
25	TCTCTCAAGG AAGTCAACCG TAGACTGGAA GAAGATATGT TTGCTGTTTT TGCGGGGAAC	300
30	ATAGTGTAC TGGAGAACAT CGGCTGCTT CTTTCTAGAG GCGCTGACAA CAAGTTACAG	360
35	ATTATACGCG TTAAAGGTTT AAGGAAAAAC ATAGATGATA GTATAATAAA GGACAGCAGC	420
40	CCTGTAATAA ATTACATAT GGTGAAGAGC ACAGTTTCC AGGATGTGAA GAACTTATTT	480
45	GACGAGCTTC AACTGAGCCA AGGTGTTAAC GACCAACTCC ATTTTGTAG TAGCTGGAA	540
50	CGCTTTTATG AAGAGGATCT ATTTCACACT TCCGIGATCA AGAGGTTAC CGATGTAGAG	600
55	AACCTGGCTA AGAGCTCAGA AAGGAAAATA AGGCTAAAAA AAGCGTATTG AAAGACACCA	660

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 671 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1524UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

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5
10 GATCTATCGA AAGTGTGAAG CTCTAGACA AGTTGTCCA TCCAAAAC GGGAGAACCT 60
    CTTTGTGCTA CCGTATCAAC TACCACTCCA TGGACAAGAC TGTTACCAAT GCGAGGTCA 120
15 ATGTCTTACA AGAGCAGGTC AGTCGGGAC TAGTCAGGCT TTACAACGTT CAATTGAGAT 180
    AGCCCAATCA GCGGAGACT AATAAACTTG TATATACAGC TTTGGGACA TCGACCCAT 240
20 GTAACGTATA GTATGATATC TGCTTACTCA TATGCACCT GAATGCTAGC AGACTTCGAG 300
    AAATGCCITTA ATACGCAGCA TATCGATAA CTAGTGCTTA AAGCCAAGTT CTGGATCTT 360
25 CACAGCTAAC CGTTTTCTTT TGCTCTGAT GGCAGCTACA AGAATAGCAA TCCTTTATGG 420
    ATCTGAAACC GGTACTGCAC AGGATTTGCG TAATATACTG TCCCACCAAC TACGTGTTT 480
30 TCATTACAAG CATACGGTGT GCTCTATTGG AGAATATAGT GCCAGAATA TCCTGCGATG 540
    TCAGTACCTA TTTGTCATTT GCTCCACCAC CGGCGAGGCT GCGCTGCGC AAAATGCGCG 600
35 GCAGTCTCCG CAGGCAAAG TGGAAGGTAC ACCATGGAGT GTGCTCAAAA GAAGCTCTCT 660
    CCCACCAACT C 671

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(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1525RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

5	GATCTTCTCT CGCTGGAAC TGGTATGCGT CCAAAATTTT AACTTAACAA TTTTTCACCT	60
	TGACCTCGCC AAGCATCTAT ATCAGTGATG TCATCTGAC CAACCTCATC CCAAATGCAG	120
10	GCCATGGCT GCTGCAITTA CGGCTCAGT GCGCGCTAG AGAACTAGCG TTACGCTTTG	180
	GGGTITACTA GCAAGTGGC GTGCGTGGG ATTGCAATG TGGGCGGCA CCTTATCCAC	240
15	GCGACACAGA AGTGGGTATT TTGCTTGT TACATAGATG TCCAAAACA GTACGCGCAA	300
	AGCACCAAGC AAGCTTCAGC AAGACTCAGG GAGGTGTTAG AGGCGATAAT CCAATCTGTG	360
20	CTGAATGGAG CAGGCGACGG GACCAAAGTG GATATTTGCA GGCGAAAGTG AGACGATGGC	420
	AGCGCAAGAG GGCAATGGAG TAAACGGGGA CCTGGACGGC GGCATGCAGA AGACGTTCAA	480
25	CCCCGTCAAG CCGCTGGAAT TCAACGTGAA TTTGGCGGTT TACCGGGGCA AGGCGGGGCT	540
	CGGGGAGACC CTGAAGTGGC GCGCGGCGG GCAAAAGCTC AGGCTGGAG GAGGAGACAG	600
30	ATAGCGAAGC GAGCGGGAGC TCCAGCGGG GCGGGGGAG TGCAGACAG TCTAGTCTGG	660
	AGCCCCCGAA GGTGGACCG TCGTTGACG CTTGGCGGCT GAAGTGTGCG CC	712

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1525UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

5	GATCATCGCG ATTTTCGGTG GCGTTGATGA GAAAGGCCCT CACTTATACA TGCTTGAACC	60
	AAGTGGGCGT TACTGGGGTT ATAGAGGAGC CGCTGCCGGA AAGGGCAGAC MAGCCGCTAA	120
10	AGCGGAGCTG GAGAACTGA TTGGGAACGA TAAGTCAGAG CTGTCAGCTA GCGATGCACT	180
	GAAAGAAGCG GCTCGGATCA TCTAAGTGGC CCATGAGGAT AATAAGGAGA AAGAATTCGA	240
15	AATTGAGCTG AGCTGGTGCT CCGCTTCGGA GACGGATGGC TTGCACAAGG AGGTACCAAA	300
	AGAGCTATTT GATGCAGCGA TTGAGTTTGC GAAGAAGGAG ACOGGTCAGG AGAGTGATGA	360
20	TGATTCAAGC GATGACAACG CATCTGGAGG TGAAGAGTCC TCAACAAAGA AGGATGCTGA	420
	CGGIGATGTC CAGCTTTCAT GATAACAGCC CGGCATTATG TGGAGGTTCA TTTCATGACA	480
25	ATTGACGGAT GTTACTAAGT GTATATTAAG TTAATCCACC TATATAAATT AATAACATGC	540
	AAAGCAATTT AGAATTTGTC GGAAAGCAGG TTAAAGCATG TCTACTCTCC TTAATCTTTC	600
30	GCGAAGCTGT ACATTTTCTT CTCAAGTGAA CGAATTCCTAT CCACCGGCTG CGTCTGATTC	660
	TAATTTCTTA CGTTGGCGTT CTGTGTACCA TTTCGGCGTC AGC	703

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1526RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

EP 0 866 129 A2

	GATCTGGCCG CGACCTTGAG AGGCGTCTGT ACCTTCTTTC AGCACAAC TA TTGTGGGAGC	60
5	TTGGTTTCCA AAGTTCATCC TGAGCTCGGT GGTGTTTTCAG ATATGGTGGG TGATGGCCTC	120
	GTCACGGTCT GTCAGCTTCC TGTACCGACG ATGACGGCAG TTTTGGCCAC TAGGCCATTT	180
10	TTTTTTTCAG CTCTAAGATG GCAGACGGCA AGGAGAATGC TCCAGGACAC CGGATAGAGC	240
	TCCAATCTCA GCAAAACATC GCCTACTGGC CCATTGCTGC TGCTGCATAA CACTTCTATG	300
15	GCCTAGTTTG TGCACTGGT CGGCGCTTCA CATTGTATCT CGTGAATTGC GTACCGGTAC	360
	TATATTACGG TTGTGTGGCC GAGCGGTCTA AGGCGCTGA TTCAAGTGTA TGCTTACAGC	420
20	TGTTACACAGC TGAACACTCA GGTATCGTAA GATGCAGGAG TTGGAATCTC CTGCAACCA	480
	ATATTTTTCG GGGGTTTTT GGGCGCCAG CGAACTGAA CCGCACACTA TTTCGTGGTA	540
25	CCGTTGGAGG TAAACTGTTG GAATCCGACA GTGGGTACC GAAACCATCC CAGCCTCTTA	600
	TTACTAAGCT GGATCGTCA CTGCAAGCG TGATATTGGA ATGTTCCCA CGTATTATTA	660
30	CTAAGCCGCC ATCTTCCCG CCATGAGGAG GTACCGAAA ACCAATCCCC AATTGCAAT	720
	ACTAA	725

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1526UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

EP 0 866 129 A2

	GATCGTCACC AGGTCCCGG TCTTCGGGAA CGTCTTGCCA TGCCCTGGCG ACAGTCTGTC	60
5	GATCTTCACG TTACCTTGA TTACCTCOGA CATGCTCGTT GCTGCTCCCG TGCTTGCCCG	120
	AGAGTGATCA AGTGGTGTG ATTAAGGCC CCAACGCCAC CCGCTGGCC GGGTAACACG	180
10	TGCCCCGCGG CTCGCCCCG TGCGGCTGTG CGGCCCGGCC GCCCCATGCA CCGGCAACCG	240
	GGCCGGTGCA CCGGTGCGC GCACTTTGCG CCGCCCGCGG CCGCCACTGC CCGAAGCGGT	300
15	AAACTTAGTA CGCAACCGCC CAGCGCCCGT CATAGCATAC GGACGCCAGA CCGGGTAAGG	360
	CCGTAGCCCA GTCGGGAATG CCGGCACGAT ACCTCTTTAG GCAGGATACT ATTTTAAGGC	420
20	GTACAGGGCG GCAGCCCATC GTGCAGGCTG CAGTAGCAAG CTGAGACAGG CTGGGCAAGT	480
	CTAGACCTGG GACACAGCCC GCAACCTAGA GCGCGCGGTG GCGCGAGGC GTCAGACATT	540
25	TTGGGTGCGA GGGCGGTGG CAGCAGGACA AAGAGCCCG AGAGAAGCAA ATGCMCAACT	600
	AAACGGGGAG GAAGGGCAGC GGATTTCTTT TTGGGCTTCT GTGCGAGGTG GAAATTGTAT	660
30	AAATAATGGG AGCGCGGCT GGTCTTGCG GCTGAGACTG T	701

(2) INFORMATION FOR SEQ ID NO:831:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 705 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1527RP

50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:
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55	GATCTTGCTG CTATCCAGAA ATGGGAAGTT CTTAGACAAC GGGGAATTAA GCGCCTTTTC	60
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EP 0 866 129 A2

CAATATTTTGG AGCGTCGTGT CATAGCTCGG AAGACGCAGC AGAAGCCCCC CCAGTAGTGT 120
 5 CTGTTTCATGT TCGCTCATGA AAGGTGTCTC TATCAAATCT AGCTCCATCA TCGCAGAGTA 180
 GTTATTATCT TTCTTCCAAG ACAGACGCAC ATGCCGCAAC TTOGTCAGGA TTACAGTAAA 240
 10 ATAATGGTAG AACCGGGGAC TCACAGAAGC GACGACCGCT CGAAATGAAG TCGGCCCGTA 300
 GAAGATOGTG CGGCCCTGCT TCTCTATCAC AAGATGGAAC TCGGAAAGTC TGTTCACGGG 360
 15 GGACACCGTG CCCATAACGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT 420
 CCGCGCGAGC TCAGTCTCAA GCTCGTCGAT CCGTCGCAGC AGCTCCACAT TGGGGGTGGA 480
 20 GCTGAACAGC TCCCGTGAGT TCACGTCTGT CGTAAACTCA GACAGGTACA CACACTCGGG 540
 CAGGCCCTTC CCAATACATG TATAGCACTT CGGCCGCGCC TTGTTGCACT TGACGGCGCG 600
 25 CTTGCGGCAG AACACGCAAG ACTTGCTGAC CTTCCGCTTG GTTTTCACAA TCTTGCCATC 660
 GGACTCTGCC ATCCCGCCAG CTTCAAGCAA AATGATTAGG CTATA 705

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1527UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

GATCGCGGAC GTGGAGCACT GGCCGGAGAT GCGCGCGGCC ATCCTGGTGG TTTCTGGGGA 60
 55 CCGCAAGGAC ACGCCATCGA CGAGCGGTAT GCAGCAGAGC GTGCACACGT CGGACCTCTT 120

CAAGGAGGCG GTCCGGACGG TGGTGCCGCG GCGGTACGGA AAGATGGGGG CCGCGATCCG 180
 5 CCGCGCGGAC TTCCGGACGT TTGCGCGCCT GACGATGCAG GACTCGAACT CGTTTCACGC 240
 CACCTGCGTG GACTCATTTC CGCCGATCTT CTACATGAAC GACACTTCGC GCGGATTGT 300
 10 CAAGCTGTGT CATCTGATCA ACGAGTTCTA CAACGAGACC ATCGTGGCGT ACACGTTTGA 360
 CCGGGGTCCG AACCGGCTGC TCTATTACTT GCGGAGAAC GAGGCGGGC TCTCGGCTT 420
 15 CCTCTCTGCC GTCTTTGGCG CCAACGACGG CTGGGAGACC ACGTTCTCGA CGGAGCAGCG 480
 CGCCACCTTC GCGCGCAGT TCGACGAGTG CGTGCGGGC AAGCTTCGGA CGACCTGGA 540
 20 CGACGAGITG CACAGAGGAG TTGCGCGCCT CATCTTCACG AAAGGTGGG CCAAGGCGCC 600
 AGGACACTAA ATCTCGCTC ATCGACCCCG AGACGGGCTT GCGCGTGAC GCTATTCTCC 660
 25 TGCTATTTTC TGCTCTGTAT ACCCTGCCAG AACCGGCTAT ATATATAGAA TATGCATT 718

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 701 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1528RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

50 GATCACTGTA TCGAATTTGA CACCCAAGGA AGCCAAAACA TCGTGGGGG ATCCCGACAA 60
 TGTGGAACAT ATGATATCGC TTTCTGCAAG GATGCGTGCC TGAGCTTTCC TCTTATCAA 120
 55 TTCTCTATTT CTATAATTCA CGCAATCCT TTCCCTCAGC TCATCGCGCT GCTTACCTAG 180

CTCATTAATC TTCTTGCTCA AGTCCCTCAA CTTTAGCTGT ATCTTAGATA TCTCATCAGT 240
 5 TGAGAGTTTA CTAGTCGGCG AACCATCCTC TTTATTCATC ATATCCCTGA GCTTTCTCCT 300
 CTCGCTACG GCGTCATGAA AACTCTGATC TAAGTTCGGA TCGTGATTTA TTTCGTACGA 360
 10 CTGATTCAAA GCTCGCTTGT CAACCAGCTC TTCCAACGTT AGGTCTCTGA TAGCAGCGTT 420
 AACTGCATCT GATTTACCAA TCCGCACTAA TTTTGGTTTG AACAACTTGC CGTCAGTATC 480
 15 GACCAAACCT TCTCTCAGAC GCAACACAAG CTCGTCAACG GCTGCATTAC TGGGTGCACA 540
 TATCAGAACT TTTTGTTTCT GTAGTAACAT CTCAGTAGAG GTAGCGTTCG ATTCTGTGGG 600
 20 ATTTCTGATA ACATTGATG GTAGTCTTTT TCGGCTAGTT AGGAAAAAGC CGACGACACC 660
 AAGAATAGTC TTAGTCTTAC CAGTACCAGG GGGTCCCTGG A 701

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1528UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

GATCCAGCAT TTCCGGGTAA ATCGCGGTAT TCCGCACCG AAGGTGGGAA GCTTCAACGA 60
 50 GTTGATCTGC ATGTGGGGGG CGCAGATGGT TCTTCCACTG CTGCGAGACT TTGATGCCTG 120
 CAAAGTATCA GATGCTGTTA TTCTGGCGAT GTATGAGATA CTGCTGAATC CGCAGATGCT 180
 55 CCGGTGCTCG CCGGAACTCA AGTACTACTA TGATCTAGCA TTCAAGGGCA TGTATGAGAC 240

EP 0 866 129 A2

GGGACATGAG CTTTTAGACC ACACAAAAGA ACAAGGTATC AATCTGCTCG TACCTGGAGT 300
 5 CGTATATTCA CAGATGTACG GCTGCCCTGA ACAGAGTTCT TGGGCAACAC GTCTCTTGCG 360
 GCACTTCTTC GAGAACGAAT ACTCAATCAC AAATGAAAAC GTGACAACCG AACTGCTTGA 420
 10 CGAAATCACC TATCATTTTA TTCAGTTACA GTTGAGCAGG AGCAACAGCT CGTATTTGAG 480
 CATGATTGGA CTATTCTGGA GCAAGATGTG CCGTTCTTT GCGCTGATGC ATGTTGATGT 540
 15 CTTAAAGGAG TACTTTATTG AGCTCAAGAA TATTAAGTCA TTGGGGTCCA CGACTAATGT 600
 TCATATTGAA TCTGTTTTC AAGTATTTTA TCACCATCTC ATAATGCAGG TAAGATCAAA 660
 20 ACCGTTGGAT ATTCTGCTCC GTATTTTGAA ATTATCCTGG AAAAACTAGG G 711

(2) INFORMATION FOR SEQ ID NO:835:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 722 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1529RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

45 GATCAAAAAG AAGGCGATTG CTATGGCGAC GGTGACTGCT GCTACCGCGG TCTACGCTCT 60
 ATATCCTTCC TCTCGATGT TGGTTGACAG CTCGCGTTG ATCAAGCTAG AAGGCACCAT 120
 50 TTCTCTCAGT AGCAAAGGTG CTAATAATGA TACTGATGTT TTCATATTAC CAGAAAAACA 180
 TTCTGCTGTT CCGGGCTACA ACACAATCAT TCGTTTCTC GTACCGGCGA TGAATGCCCT 240
 55 CAGGCTTTAT GGCAGGCCGA AAACACTATC GCGAGCAAG GATGACACAA ACTCACTCCT 300

EP 0 866 129 A2

GTTTAGTCTA CCAGCGCTTC CACATGTGCA CTACTTGCTG GTCTAGGATT TGCTTCCATT 360
 5 AGTGAATTCA GCGTCTGGCT CATGGAAGAC GCAGGAGTGG CGGAGACAAA TCAAGGCTCT 420
 ATTACAACGG AGGGTAGCGG CTGGCTATCA GGGATGTGGT TCAAGCTCCG GTCTATCCGG 480
 10 CGCTCTGTCC TCCCTGTCTC TGGGTCCATT GAGTCTACT TCTTTGTGAT CGCCGCATTT 540
 TGCTCCGTCC ATTGGGTTTT CGCTACTGA GTCCAACTAC ACTTTTATGT CAAGTCACTC 600
 15 AAGAATAACT TCACTACATG ATAATATCCA GAGACCATAT TGAATACCGT GGCCAGCACA 660
 TCCGATAATA CWTGCAACC AAACAATATG CTATCTCCCG CAGGCTTGC CCTGATGCA 720
 20 TT 722

(2) INFORMATION FOR SEQ ID NO:836:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 691 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1529UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

45 GATCCCGCTC AATGCCAAGT AGAATGTTTC TGGGGGAGC CCATACAGTA CCGCCTCCTC 60
 CTCATCCCGG CTCTCTGCT CCACGTCTC TGTGCAACA TCTAGCAGTT TCCGATAAC 120
 50 ACTGGGGATG GTCATGCTCA CGGCTCCGGA TATCACGATC AGCACCAAGG CGCATACTAG 180
 AGACTTGAGC TCAGGCCGGG CCAATTGGAA CAGTCTAGC ACATCCTTGG CACCTGATGC 240
 55 GTTGCCCGTC GCGGTGACA GCTCGAGTCT TTCTTGGTGG GGTTTCTCTT CGTACTTGC 300

EP 0 866 129 A2

COGAGGGTTT GCTGTTGAGT TTAGCCTCGT TTGAATTCCT GTGATGCGC TGAACGAAAA 360
5 GGGGTGCGT TGATGTAGAT GATTGAACGG CGGCCATCGC TGCATCCCAA TAACAGGCCT 420
CGGCACCTGC TTAACAGCTA GCGATAGCCA CATATATGTT CTCCTGAGG TCATATTCCC 480
10 AGTTTCTTC TAACCTCACC AGCCTGTAG GCTCTGAG TTGCTGTAA GTGTGAATT 540
TCGCATCGG ACTCATTTTT CATGGAGAAT AAATAATTGT ATTACAAAT AGAGATGCAT 600
15 GCGCAGCTAG TCGAGGCCAG CTAATAACA GCTCTGGAG CTTTCAGTT GTAGCGCAC 660
GGTTTTCGGC TCATGTGAC TACAACATTT T 691

20 (2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 714 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1530RP

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

40

GATCCTCTG CTACAAACAC ATACCTAGAT TTCTCATATT TTATACTGAA TACATATAAT 60

45

ATATCATTTA ACTGTCTTCA TTCATGAGAC GTGCTCTAAG TTCTGTGCTG CTCAACTTGT 120

TTTTCCACTT GTCAGCCTCT TCGCCCCCA GTAGGTTTAC CACATGCAGG GCTAGCTTCC 180

50

TCATTCCTTT GCTCTCAGC GTATCGTTGA TTGTCTGGC ACGGCCACA GTTTCCTCAC 240

TCACTACCAG GGCTTCGATA CCAGGTTGCG TACCCGTGGG CCGGCACAG TCATGTAAG 300

55

CAAATATTTT GATTTCAGC CCGGTTTCA GCTGTGAAG GAAGCTGCAC AGTTATGCG 360

EP 0 866 129 A2

ATCGTTGCTC GAAGGACTGA AGCTGCTCCC TGTATTTCCT GTTCGGCAGC AGTTCTTCAT 420
 5 CTGTAATCCC CACGATCAGC CGGGACGCAG TCACGAGCGC GGCAACACTG AGCAATATTT 480
 TATGTCCGTC GTGTAAGTGG TCGAAAGTGC CTCCCAGCGC GCTAACAGCG TACTTGTCCTC 540
 10 TACCGCCACT CTGACCGGG CCCGCAGCGG CCATCGCCGG ACTATCAAAC AGCTCTATCT 600
 GCGTGTGGG GAAAGCATCC TGCAGCAGGC GATGCTCAG GAATACAACG TCCCACTTCA 660
 15 TTGGGCTGTA CGCTTCCATA CTGACGTGTA ACAAACATT TATCGGGGTC GTGT 714

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1530UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

GATCCTGGGA CGACATCGAC ACCATTCTTA TCGGTAACGA ACTTGTGAAC AACGGCCAGG 60
 CGACCGTGGA CCAGATGGCT GGTTACATGA AAAGTGCCG CAAGTGCCCTC GCTGAGGCCG 120
 45 GCTACAAGGG CCAGTTGTT TCCGTGGACA CTTTCATGCC TGTAATCAAC AACCTTGGTC 180
 TATGTGACCT ATCAGACTAC ATGGCTGTCA AGCCCCACCC ATACTTCGAC TTCCACACTT 240
 50 CTGCTGCTAT GGCCGGCCCT TGGGTTTTCG ACCAGATCCA GAGAGTCTGG AGCGCCTGCA 300
 ACGGTAACAA GAAAGTTGTC ATCACCAGGA CCGGCTGGCC TACTCAGGT CAGACTTACG 360
 55 GCAAGGCCAT TCCATCCAAA GCCAACCGA AGATGGCCTT GGAATCTATC AAGGCCACTT 420

GTGGTGATAG CGCTATCCTA TTTACTGCTT TCGACGACTA CTGGAAGCCA GATGGGGCTT 480
 5 ACGGTGTGGA GAAGTTCTGG GGTATGCTAT AAGTTGCCGT GTGCTTCTTT ATGAOCTGTC 540
 TCTTTATTTT GCTCGGAACC CTTACATGCA GATGGGGGGT GCGGTGTCAT GGGCCTGCAG 600
 10 CCTCCGGGCC TGCAAGTTTC TACATGCCC TACTTTAGCT GCCACGGGAC TTTTGAATTT 660
 CTTTGGCAGG TGGTACTGCT GGCATCCTTC TCATAGAACA CAGTGTGCC ACAGGG 716

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 723 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1531RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

GATCTGCATC CTCGTGATGG AAAATACGGC CATGCAGCTA ATTTTGGAAT GGTTCCTGCA 60
 40 TACCGTAAGA GAGATGGCTC CAAATCATAC CCAGTTACTA TCCTGTGAC TAACTTTTCA 120
 AAGCCGACAC CTACCAGACC TGCTCTTCTG AAGTTGGGAG AACTCACAAC GTTCTTTTCAT 180
 45 GAGTTAGGCC ACGGCATACA CGATTGCTG GGTTCCAATG ACTTGGAGTC GCTCAACGGG 240
 CCTGGGTCCTG TCCCATGGGA TTTCGTGAG GCGCCCTCTC AGATGCTGGA ATACTGGACG 300
 GCACGGCGTG ACGTTTAAAC TATGTTATCC AAGCACTACG AGACAGGTGA GAAAATCCCG 360
 AAGTCGCTGC TGGATGCTG GTTTAGTGTT GCGGGCTCA ATTCAAGATT GGCCAACCTG 420
 55 GGCCAACCTGA AACTTGGCTT GTTCGACATG TATGTGCACA CCGCGATTG CAAAGGAGCG 480

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GAGGTACCGA AATTATGGAA TGATCTCACC AGAGAGATCG GGCTCATGAA CTTAAAAAAC 540
 5 TACACTAGCA CCGGCTATGA CTCCTTTTGA CATATTATGG CTGGATATGC TGCTGGCTAC 600
 TATGGCTACC TTGGTGCCA GGTMTTGTCT GCAGATATGT ACGACACAAA GTTCAAGCCC 660
 10 AACCCATTCA ATGCTACGGT GGGTGTGGAA TACAGGGACA CTATTTTAGC TACCGGTGGA 720
 CTT 723

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1531UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

GATCCAATCC TGGAGGCGGG TTAAAGTGCT CCTCAATGCA GCGCAGCCGG CACTGGAGTA 60
 TGGCACGGAA ATCGCACTCT GGAGGAGGCG CGTGGTTGGG AACTGGATCG TCCACCTCGC 120
 40 GCAGAAAGGC CGTTTCGAAG GCGCAGGCGA GGACCGGAAT GAGCAITTAAT AAAGAGGTAA 180
 CGTGCATGCT GTGAAGAGTT TCACTTTATG CGTTGCATTC CTCCCCCCT GAAGACGAAA 240
 45 ACACGGCGCA CATGCGCTAT ATATACCCCT CGTGTCTACT ATTGTGCGCT GCGCGCTCTC 300
 ATGTCAGTTT TTACTTTTGT ACCCGGGGAA CCGACATCT GCCACAAGC ACCAAGGCC 360
 50 AGTGACCAGC TCTATGCGC TTGCTCTGCC AATAACCAGC CCGCTACTAG CCGAGCATTT 420
 TGCCTTAGTC CACCAGATAT TCAATGTGA TGSTTGCTCG CCAGCCTGG GCTGGGACAT 480

EP 0 866 129 A2

AAAGATCGGA AGCTCCTGTG CAAACTGCA CAGCGCGCCT TCGAGAATAC TCOGCAGGGA 540
 5 CCCCCCTCC CATTAGTCCT TGGCAGTTTT TTGCTTTGTC CCGCGATAAT GTATCTAAAT 600
 ACAGAATATC GATTACGGCG AATAGGCAAG TTTTGTGGTC TGACATGCCG AGTGTCAGTT 660
 10 CATGATTACA TAATGTGTGCG TGCCATATCT GT 692

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1532RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

GATCTKTGA AAGAGTAACC AGGATCAAGC CTGGGTATA GCCAGCGAA TATGCATATG 60
 35 AAGTCTTTCT GCGTGGGCTG TTTCAATGAC TTCAGTGATA TCGCATGCC AGTTTCTATG 120
 TCAAACCTGC GCGACTGCAG ATAATCAAAT ATCTCCTGCT GCAACACTGC CTGGTAGTTT 180
 40 TTGTCACGGA GAGGTGCGG GTGCGGGTA CTCTGCAGCG CACCGTAAGC TGACGGACCC 240
 CCGCCGGGAA CAATCGAAGG CCGCTGCGAA GATCGCAGAC TCCGCGGAG AGACTTTGCG 300
 45 ACCTCGGGCA CAGGTCTTGA AAGAGAGCTC CCGCGTTCC GTGCCAGACT CTTGTTTATC 360
 ATGTCCGTAA GAGCAGCGTT CGTGCCAGGT ACGCCCTTCT TGTTCGTGTT TCCACCAATT 420
 50 GATGGAATTT GAGACGTGAA CCTCTGCGGA TTCAAGCTAT TGAGCACACC ATTGGCACCA 480
 CTTGAGCCCC TTGCTCTGC CATCCCTAAT CGTCTATCC TACGGGGGCG TAATAAGTTA 540
 55

EP 0 866 129 A2

CTACCAGACT CTGGCCCTCA TCTGGGACTG ATGTTATCGT CTGCAGCCAG ATCCTGTTTG 600
 5 TGACCCGATC GAAATCATCG AGTACGAATA ACCACGTGAC CATTATTCAC GTGATGAATT 660
 TGGCGGTCC TGTTCGCGAC TCTTACTCCA GGTTAACCAT GACTAGATGG GCATACCTCA 720
 10 GA 722

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1532UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

GATCATCTGA ACGCTCATGA ACAGTTGCGG GAACATCGTG TOCAGACTA TGCACTGCTG 60
 35 GATGTCTTTC TGGCCGAAGT ACGCGGGTC CGGAGCAACA ATGTTGACCA GCTTAGCAAC 120
 GACCGTGGCC ACACCGCGGA AGAAGCGTGG ACGGGTGGA CCTCCAGCA TCTGCTGAC 180
 40 GCCAAGCACC GACACAAAG GCGCGGCTG CGCCTGACC TOCAGTGGG TGCGCGCGG 240
 GTACATTTCC GCGGGAGAGG GAGCAAAGAG CACGTCCACA CCGGCTCTT CCAGCAAGC 300
 45 GCGATCCGCT GCCAACGTCC TGGGATAGCG GTCAAGATCT TGGTTGGCG CAACTGGA 360
 AGGGTTTACG AAGACTGAGA CAACAGTAAA GTCGTTTTC GGCACGATC TCCGACGAG 420
 CGTCATGTGT CCTCATGTA GGCAGCCCAT CGTTGGCACA AACCAATCG TCTGTGCTT 480
 55 GCAATCTACC GTCTGCTTGC GCCATTGCGA GACTTCCTGG ACCTTATTGA GCACGTGCAT 540

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GAGGCGTATC GCTTTGATGG TTCAGCCTTC AAGTTTGTCR GTGTGCATCT CACAGATTAA 600

5 GGAAGCTTGC GCACACTAT 619

(2) INFORMATION FOR SEQ ID NO:843:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 564 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1533RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

30 GATCACGAAC TCCATCATTA CAAAGTCCAT CGCGTGGATA CGAAAACAAA ATGCACAGCC 60

GCTACCGACC TTCCGAAACC TCGAGAAGAT CAACCAGCCG CCAAGAAGCG CTGACCATGC 120

35 GTGGGAGTAC ATAAAATCGT GAATTATTGG GGTGTATGT ACTATATACT ATCGCTCTGC 180

CGCCCAATGA TGGTTACGCC TCTTGCACTG GCATTCCTGGG TGACGAGGTT GTCTCCGTAC 240

40 ACCTCTACTA TTTCCAGGTT GGGCGCACAT TCGCTGATAT GGGCGAGCAA TTGTCTGTCA 300

ACGCAGCGGA CGAACCTAC ATTCACTTGC TGCAAGTTTG GACAGGACAT TAGCTGGAAC 360

45 CCAGCTGCCG TCAGGTTCCT GGCTGAGTTC AAGTTTAGCT CTTTGAGGAA TTTGGAACAT 420

GGATTCAACC ATATCTCCGC AATTGATGCA TCATCCAGCT GATGGCAGCG CCTCAAGTTG 480

50 AGGTAGTGAA GTCGGGGAAG CTGGACCGAA GAGAAAAATG TAATGAATCC ATCGGACGTA 540

ACCTGGTCCA ATTCCTCTAG GGAT 564

55 (2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1533UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

GATCCGGAGA CAGACGTGTA TCTGAGTTCT ACCGCTGGGC GCTGAAACGC ACGTCGTTAG 60
CGCACATCCT GTGTGCTTGC ACCGGGCCAG AGCAACCAAG TATTCCTATA TTCGTGAAAA 120
CTGCGGTAAT AACCATGTAG AAGATTCGCG GCCCGAATAC CGTTTTCACC CCAATATGTC 180
CGTCATGTGA GCTATTGGAT CGAAGAGTTT TTAATGACGT ATCCCTATC ATAAAGCGGT 240
GCTGGATTAT TGGAGCATGC ATCTGGTICA GCTGGGGCGT GCCAAATATA TGGTGCAAGA 300
AGAAACTATC GTACCAACCC CGTCTGTCTT GACCTGTGTC CTCTTAATCG GCATGACTAA 360
TATGGGGTAT CCTTAAACCC TTTAAGATGT TACCTCGGT CTCAGGCGG GTTGTCTAGT 420
TTACAAGAGT AAATACCACC TTGCCCTGG GAGGGTTCTT ACTTTACAGT AGGAAAGAAT 480
CGATACCACT GGTGGGGGGA TTGGTATAT TTTGAAAGAT GGATGGAATG GAGGGCTCCT 540
TATTGACAGC AAAGCCACTC CGACAGAATA CCCACACCTT GGATTGGAA GCTGCGGATC 600
GACAGACAT GGTACGTAA TCGAATTGTC CTGTGGGGC GCCCTTCGG TTAATCAAGA 660
AGAACAACCG CGGGCACGC AGGGAATAT TGAATTCAGT GCTGCCAAGC CTAATTTATG 720

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1534RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

GATCCACATT GGAATATGGG TATGGGACTT GATGGTTGAA CGCTTCGCTT CAACCACTGC 60
AACATTGGCA AACCGTTTGA AGTCTGGAT GATTTTCTCC TTCTGGATCG CAGTCAAGAT 120
GTGGCCGAAT CGTTTTTTCGT TGTATAGGOC TTGCTCATCC TGTGCTTCAT CCTCATCAGA 180
CGCTAATGGA ACGTCTGGCA CAATCTCGAC GCCATCGCAG GATGCGATAC TCAAGGTATT 240
GAGCATGTTT AAGGCATGTT CCGTTGCTAC TTTAAACCCCT GCATCAACTT CCTCTCTGTT 300
TTTCCATAGG CGAGGGACAT CGTTTGTATC GTAACGAAAC TTACTTTCAA AGCGTTCTCT 360
CAGTATAGAA ACCACATTGT CTTCCTTCAA ATACTGGTGG ATAATATCAT ACAGAATAGT 420
CCATGCATTT GACCGGATCT TCAGGTATAA AGCATAATTG TCCTCCTCGA TGAGGTGAG 480
CTGGAAGTCG TAAGCGGTAC TTTCATCGGT GACATCCCTT AAATTGGGTA GTTTATACTT 540
TAGAACTGAA CGGCGGAAAA CATCATCAAA GTGGTCCATA ACAAGTTGCC AGACGTTATC 600
CTGTGGATGG GAGAGTAAGT GGACAATATC GTCTCTAGTA TGTTGAATT GGTACTTTTT 660
CGCCCTCAAT ATAATAGCTT TCATCTCCTT ACCACGCTCT CTTTCGCTA GTTCACTATC 720
TTCTCCA 727

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1534UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

GATCAGCGTG GACTTGATCA TGGTGTGTCT CGTCCGCGCG TGTGGTAGGC GGGGGACGCT	60
GCTGCTGTCC TTTGTGGGGC CCGCGGGGGC GGCGATCAA GATCGCGCAC CACGGTCGCC	120
GGCGGGGGGG CTCGAAGACA CACGCGCACA GCAGCGGGCG CGTCCCGGGC AATGCAGGCG	180
GCACAGCTAT CCTCGCGGCT CGTACCGGTG GCTGCCCTCG GGCGGATTGC GCTGCTCAGC	240
GGTCAGGTGA CCCGAGATAT GTTGCAAACC AAGCCATCGA TGGGCATAGG AACGCATTAC	300
CAGCGGATTC GAAAACCCCTC ACAACCCGCC ATCTGCTGGT ACGACCAACG CAAGTCGCTG	360
GCACTGGTTG CACAGTGGTA AGGTCTTCTG TCAAAATTAC TCTGCCAGGG CCGCTCTCAA	420
AACCTGTCAA GTGCAGAGCG ACTGACAGTC CGTCAAGATG CGACATTACA ATGCTCTGGA	480
AGCTCTCCAG TAGGTCTCTG CCGCGGTGCT AGACAGTCAG GGGCAGGCTT CATCGACAAA	540
GACGCGCAAG GATGTGCGAA TTGTTTCGCA CAGTCCACTC TAGGGTCGGA CCGGAAAAAC	600
AGCGCTACTC TGGGTTGACT GGGGCGAGAC TGGTAGCCGG CTGGTGGCC TCAATGAGGA	660
CAGACCAAGG TGATCATGAT AC	682

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs

EP 0 866 129 A2

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1535RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

GATCTTGCTG CTATCCAGAA ATGGGAAGTT CTTAGACAAC GGGGAATTAA GGGCTTTTTC	60
CAATATTTTG AGCGTGGTTT CATAGCTGG AAGAGCGAGC AGAAGCCCCC CCAGTAGTGT	120
CTGTTCATGT TCGTCATGA AAGGIGTCTC TATCAAATCT AGCTCCATCA TOGCAGAGTA	180
GTTATTATCT TTCTTCCAAG ACAGACGCAC ATGCCGCAAC TTCTGCAGGA TTACAGTAA	240
ATAATGGTAG AACCGCGGAC TCACAGAAGC GACGACCGCT CGAATGAAG TGGGCGGTGA	300
GAAGATCGTG CGGCGCTGCT TCTCTATCAC AAGATGGAAC TGGGAAAGTC TGTTACGGG	360
GGACACCGTG CCCATAAGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT	420
CCGCGCGAGC TCAGTCTCAA GCTGCTGAT CCGTGGCAGC AGCTCCACAT TGGGCTGGA	480
GCTGAACAGC TCCCGTGAGT TCACGTCGIG CGTAAACTCA GACAGGTACA CACACTGGG	540
CAGGCGCTTC CCAATACATG TAGAGCACTT CGGCGCGGC TTGTTGCACT TGACGCGCG	600
CTTGCGGCAG AACACGCAG ACTTGCTGAC CTTCCGCTG GTTTTCACAA TCTTGCCATC	660
GGA	663

(2) INFORMATION FOR SEQ ID NO:848:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 649 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1535UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

15	GATCGCGGAC GTGGAGCACT GGCCGAGAT GCGCGCGGCC ATCTTGSTGG TTTCTGCGGA	60
	CCGCAAGGAC ACGCCATCGA CGAGCGGTAT GCAGCAGACG GTGCACACGT CGGACCTCTT	120
20	CAAGGAGCGC GTCGGGACGG TGGTGCCGGG GCGGTACGGA GAGATGGCGG CGGCGATCCG	180
	CGCGCGGAC TTCGGGACGT TTGCGGGCCT GACGATGCAG GACTCGAACT CGTTTCAAGC	240
25	CACCTGCCCTG GACTCATTTT CCGCGATCTT CTACATGAAC GACACTTCGC GCGGATTGT	300
	CAAGCTGTGT CATCTGATCA ACGAGTTCTA CAACGAGACC ATGTGCGGT ACACGTTTGA	360
30	CGCGGGTCCG AACCGGTGC TCTATTACTT GCGGAGAAC GAAGCGCGGC TCTCGGGCTT	420
	CCTCTCTGCC GTCTTTGGCG CCAACGACGG CTGGGAGACC ACGTTCTCGA CGGAGCAGCG	480
35	CGCCACCTTC GCGCGCAGT TCGACGAGTG CGTGCGGGC AAGCTTGGGA CGGACTGGAC	540
	GACGAGTTGC ACAGAGGAGT TGCCCGCCTC ATCTTACGA AGGTGGGGC AGGGCCCAAG	600
40	ACACTAAATC CTGCTCATC GACCGAGAC GGGCTTGCC CGGCTGAC	649

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1536RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

10

GATCATTGTGTT CCTTGCAGCA CAAACATCCA CAGCTGTCCG ATTTGCAGTT GCAATCCGGA 60

GCAGCAGCTC CTTCGCAGCA TTTCGAAACG CCAGGCTCTC CCACCTCTTT CGCATGTTCT 120

15

TCTGACATTT TTGTTTGTTT TAAATCGTGA TTTTGAGTCG ATGGTTCCGA GACCGGCGCA 180

GCTGACTATA GGGGGGACCA AGACCCCTTTA TATATTTTCG CAACCAGATA CATTAATGCG 240

20

ACGCCAAAAC ACTATCAAAA ATAAGGTATA GCCTCATTTT TATTGTGACC CATGGGACAT 300

GCTGTAATCG GATTATCTTA ACTAAGCTAG TATTATGTCG GTATCCTTTT ATTAATTACA 360

25

ATCACTGCTG AGTTCCGGTA TCGTGCAACT GCACACCGAG CTCATCAGTG GTTTCGTTCC 420

CGCGCAGATC ACGTGCTGC GACATGGCGA CTTCATCCAC TGGCGCCCAG CTAAGTGGTA 480

30

TATGACATTA TGGCCGAGAG GTTAAGGCGT GAGACTCGAA CTAAATTGAG GGATCTCTTG 540

GGCTCTGCCC GCGCAGGTTT GAATCTGCTT GATGTGTTA TTTTGTGCTT GCGCGGCTA 600

35

CGGGGGGCTG TATTTGCTTG TTGCTATTTA GATAAACCAG ATACTAACT ATGGGTAGAA 660

CTCGCGGTAC TTCCCGTAGT AGTAGGCTGT GCCGAAACCG CCGAGGGCCG TGAGCAC 717

40

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 710 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

55

(A) ORGANISM: PAG1536UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

5	GATCAGCTCG GTACTGGAGA AACAAAGGCTA CTGTCCCTTG CCTTGACGAA GTTACGCGAA	60
	ATCGAAAGCA GCAGCAACAA GCAACATAGC AAGACCGCTA AATACATTCT CAAGTCATTG	120
10	GAATAAGCTC TAAAACTACC GATACGTATA TTTACTGCGT TAACGTTTAT ATACATATAT	180
	CTAGGCGTGC GTATGGGTGT TGTAAGTGTA CATCTAACCA AATAACTCCA CTATAGCTGT	240
15	AGTACATGGC ATTCCCTTGT AAGCAACTTC AGGTTCTGGA CTACCCAATT GCTGTCCGCG	300
	ATCCAGCCT TGGGGTCGTG GCCCTGTGTT GACCTCAATT TAGCGAAGAC CGACTGTAG	360
20	TGCTCTCAT ACTGCTTGAA TTGCGGAATG ACGCGGTTAG AGTCGAAGTC AACATACAG	420
	CCGTATCGA CTATCTGAA GAGGACATCG TCCACCGCA GGAAGAAAG ACTCAAATC	480
25	AGCATACT CGTTCATCAC TCTCACTTA ACATTCAGAA TGCTAATGCC ATTGTCCGCT	540
	AGTTGCTCT CAAATAAAAT CATGTGTCG TAGAAAAGAA TGGGGTCCG GCTCGAAAAG	600
30	CTTCGCCAGA GGCAGCTCCA CGCTGTGTC TCTGACCATC GCCCTGCCAT CTATGGTGCC	660
	CTGGTAGAGC GTCGTGTACG TCCAGTCGTA CTGGTGGGAT ATGTTTAGGG	710

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1537RP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

5	GATCTCCGTA CTTTAGGATG GCTTTATAGA GGGCACGAAT TTCCCTTTGG CCTATAGAGT	60
	TCAGGTGTGT GGATTTCGCA CGTTTTTTGG AGCGTGAATC CTCCTTGTGG CTTAAGCTCT	120
10	GAGCTCCATC TCATTGACG CTATTTTTTA TCTTATTCAG AGCAACATTC CTACGATTCA	180
	TCATTGTCAG TTGTTCCCTGG ACATACTCTT CATCCTTCGG CTTCGTCTCT TCGTCTTTGA	240
15	GTTTGGGTAG CTCGTCTTCC GGAATGATAT CATCCCATTC CAGTCAGCT TTATAATCGG	300
	TGACTTCAAA CTGTTTTAGG AATTCCTCAC CTCGAGATG AGACTCTCCC AAATCTGGTG	360
20	TGGTGACGTG ATCTTCCGCA TGATTCAAGA CATCATCCAA GTTCAAATCT TCAAGCTTCT	420
	TTTGATTATC ATGCGCTTTG AACATATTGC CTGCACCAA CTTGAGAATC TCAGACAGCT	480
25	CTCCTGCACT AGGTTCCGCT TTGCTCTTGC TCGTATATTT ATTCCCATCT GTAACACCTA	540
	ACGAGATGAT AGCATACTCC AAGATCATCT TTTTGGGTGC TCTTTCTAAG ACTTCTTCTT	600
30	CAACGGTATT CTTAGACACA AAACGGTAAA CCATAACATG ATTCTTTTGA CCAATTCTAT	660
	GCGCGCGAGC CATTGCTTGG AGATCGGCCT GTGGATTCCA GTGGGAATCA AATATGATCA	720
35	CAGTGTCTGC CGTCATC	737

(2) INFORMATION FOR SEQ ID NO:852:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 716 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1537UP

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

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5      GATCTAGACC ACCCGGGCTC GTTACCGGA TACGAAGTAA AAGCAGTCGG GAGCGGTCTT      60
      CTGGCAACGA CGTTTCTTTC TACACACCTC CTGGCACAGG ATCCAGCATC CTGCCGCATA      120
10     ACGTCAACGC CGCGTTGTG ATGGTTCCCA GGTGCCACTG GCGCCAAGCG CTGCGTGAGA      180
      AACAGCAGCG CTGCACTTCG CTGCTTCGGG GAGGCTCCTG GGAGTGGTCC GGGGGTTTTC      240
15     CCACCGCTCA AACTAGCGGG GCGTGCCTGT GCGGGCTCT CCATGCAACT GGGGCGCTCC      300
      CATGATGGCG GGGGCTTAC CAGGGTGGTG TTGGGGCTGC CTGGCTGTGC GTGGCCACAC      360
20     GATGGCCTGC TGGAGGAGCT GAACCTGCTT CCGTGGTGCA AAGGTGTGTG CGACAGCGCA      420
      CCTGGTGCA AGCTGTGCCT GCGGGGGCGT GTGATTGCT GCGTCCGGG GTGCAACTGT      480
25     GGTGACAGCG CTTTGCAGGC ACGTGATGGT TGGTGCGGG CCCAGACGTG CTGGGTGTGT      540
      CTCAGACAGC TTTTCCGGCG GCTGCGGGC CGCCGTTGCC GCCATATGAT TGATTCCGTC      600
30     TCGATTAGTG CATGGTGGTC AGCTTCAGA TGGCCAGGCT GTACTTGTGC TTGCCCCGGG      660
      CCGGCAGGCT CTTTGGCTGT GCGGGTGGT CTTGCTTGT GGGCTGGGC CGTTCT      716
35

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(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1538RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

EP 0 866 129 A2

GATCCCTCTG CTACAAACAC ATACCTAGAT TTCTCATATT TTATACTGAA TACATATAAT 60

5 ATATCATTTA ACTGTCTTCA TTCATGAGAC GTGGCTAAG TTCTGTCTG CTCAACTTGT 120

TTTTCCACTT GTCAGCTCTT TCGCCCCCA GTACGTTTAC CACATGCAAG GCTAGCTTCC 180

10 TCATTCTTTT GCTCTCAGC GTATCGTTGA TTGTCTGGC ACCGGCCACA GTTCTCTCAC 240

TCACTACCAG GGCTTCGATA CCAGGTTGCG TACCCGTGGG CCGGCACAG TCATGTAAAG 300

15 CAAATATTTT GATTTCAGC CCCGGTTTCA GCGTGTGAAG GAAGCTGCAC ACGTTATCGC 360

ATCGTTGCTC GAAGGACTGA AGCTGCTCC TGTATTCTT GTTCGCAGC AGTTCTTCAT 420

20 CTGTAATCCC CACGATCAGC CGGGAAGCAG TCACGAGCGC GGCAACACTG AGCAATATTT 480

TATGTCCGTC GTGTAAGTGG TCGAAAGTGC CTCCAGCGC GCTAACAGCG TACTTGTCTC 540

25 TACCGCCACT CTGACCGGC CCGGCAGCGG CCATCGCGG ACTATCAAAC AGCTCTATCT 600

GCGTGTGGG GAAGCATCC TGACGAGGC GATCGCTCAG GAATACAAG TCCACTTCA 660

30 TTCGGCTGTA CGCTTCATA CTGACGTTGA ACAAACATT TATCGGGTC GTGTACAGCT 720

TCTGCTTCAG AAG 733

35 (2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: PAG1538UP

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

EP 0 866 129 A2

GATCCTTGGG ACGACATCGA CACCATTCTT ATCGGTAACG AACTTGTGAA CAACGGCCAG 60
 5 GCGACCGTGG ACCAGATGGC TGGTTACATG AAAACTGGCC GCAAGTGCCT CGCTGAGGCC 120
 GGCTACAAGG GCCCAGTTGT TTCGGTGGAC ACTTTCATCG CTGTAATCAA CAACCCCTGGT 180
 10 CTATGTGACC TATCAGACTA CATGGCTGTC AACGCCACC CATACTTGA CTTCCACACT 240
 TCTGCTGCTA TGGCCGGGCC TTGGGTTTIG CACCAGATCC AGAGAGTCTG GAGCGCCTGC 300
 15 AACGGTAACA AGAAAGTTGT CATCACCGAG ACOGGCTGGC CTACTCAGGG TCAGACTTAC 360
 GGCAAGGCCA TTCCATCCAA AGCCAACCAG AAGATGGCCT TGAATCTAT CAAGGCCACT 420
 20 TGTGGTGATA GCGCTATCCT ATTTACTGCT TTCGACGACT ACTGGAAGCC AGATGGGCCT 480
 TAOGGTGTCC AGAAGTTCTG GGGTATGCTA TAAGTTGCCG TGTGCTTCTT TATGACCTGT 540
 25 CTCTTTATTT TGCTCGGAAC CCTTACATGC AGATGGGGGG TGGGGGTGCA TGGGCCTGCA 600
 GCTCCGGGC CTGCAAGTTT CTACATGCC CTACTTTAGC TGCCACGGGA CTTTGAATT 660
 30 TCTTTGGCAC GTGGTACTGC TGGCATCTT CTCATAGAGC ACAGTGTGCC ACAGGGTATC 720
 ACTGG 725

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1539RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

EP 0 866 129 A2

GATCAGACAT GGTGTTTTGC GGCCCTCGCT CCTGTGGGT GGGGTCACCG CAGTTCAGTG 60

5 GGCCAGCATC AGTTTTGGTG GCAGCAGAAA CCCTTAGGAA TGTGACTTTC TCTTCGAGG 120

AAGTGTATA GGCTAAGGTT ATACTGCCAA CCGGGACTGA GGACTGCGC TTCGGCCAAG 180

10 GATGCTGGCA TAATGGTTAA ATGCCGCCG TCTTGAAACA CGGACCAAGG AGTCTAAGT 240

CTATGCGAGT GTTTGGGTGT AAAACCGTA CCGTAATGA AAGTGAACGT AGGTGAGGGC 300

15 CTCTTTAGAG GTGCATCATC GACCGATCCT GATGTCTTCG GATGGATTTC AGTAAGAGCA 360

TAGCTGTGG GACCCGAAAG ATGGTGAAC ATGCCTGAAT AGGGTGAAGC CAGAGGAAAC 420

20 TCTGGTGGAG GCTCGTAGCG GTTCTGACGT GCAAATCGAT CGTCGAATTT GGGTATAGGG 480

GCGAAAGACT AATCGAACCA TCTAGTAGCT GGTTCCTGCC GAAGTTTCCC TCAGGATAGC 540

25 AGAAGCTCGT ATCAGTTTTA TGAAGTAAAG CGAATGATTA GAGGTACCGG GGTTGAAATG 600

ACCTTGACCT ATTCTCAAAC TTAAATATG TAAGAAGTCC TTGTGCTTA ATTGAACGTG 660

30 GACATATGAA TGAAGAGCTT TAGTGGGCCA TTTTGGTAA GCAGAA 706

(2) INFORMATION FOR SEQ ID NO:856:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 743 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1539UP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

55 GATCACTACG TGACATTCCG TACGGAATGG CACTCCAATG CCGACAAACC TCTTCCTACC 60

CCGTGA CTTA CCCC GATGTG CCAACTACCA CACATCTGGG CCATAGCCCC AGGCATCTGG 120
 5 CACCAAATGT ACTCGATATC GTTATTACAT GTCTAGGCCC TCAGGTGCAT CCACCATCTG 180
 ATATCATGTC TGCTCTAGGC TATATATTTT GGTGCGGGCC ATATCTACCA GAAAGCACCG 240
 10 TTTCOCGTCC GATCAACTGT AGTTAAGCTG GTAAGAGCCT GACCGAGTAG TGTAGTGGGT 300
 GACCATACGC GAAACTCAGG TGCTGCAATC TTTT TTTT TTTT CCTCTCTCTG CAAGCTGGCC 360
 15 GCCAACACAG GTCACCCCTAG TATGGCTCAC ATGCAATTCA GATATCTACT TCTGACTGGT 420
 CTGGTGGGGC ATGGCCATCA TTGCAAACAG TGTCTCGCA TGGGACTTTA ACGACCTGGC 480
 20 GATAATAATC AGAGATGTC TACTTATAAA ACATCAGGCA CAAAAGAAA GGTGCAGCGA 540
 AATGGTATAT ATAGGTCTTC CAGATCCAAC ACCGGTACCT CCTACTTGGC CGTATCTGGC 600
 25 TCTCCGTGGC GCTTGCCGCT GAGATGCTGT GGGCCCGAAA TGTACTCTCA AATGGGCTTG 660
 TTCAGTGGCC CATAAGCTC ATAAGCTCAG TGGCCCGGAT GCTTAGTAGT AGCTGGGCGG 720
 30 CTCTTCATAC TGCTGTCTGT ATA 743

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1540RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

GATCTTTTCT TTGTCAAAGT TCAACACCTG TAAGCCGGCT CTAGATACCG CTCTAGAAAG 60

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GGCCACATAC GCTTGGCCCT TTTCAAAAAC ACGTCTGAGA TCCACTTTCA CTTTGTTTAG 120

5 TGTTTGGCCT TGAGATTTAT GAATGGACAA GGCCCATGCA AGCATGAGTG GCAATTGAAC 180

TCTCGTTACT AGAGGCTTCT CATTTTGTGTC CTGATAGCC CATGCTCTT CTGAACTAA 240

10 AACTGTTCTG GTGGTATTGT CGGCTGGAA GAATGCACT AATGGCACT TCTTACCCTT 300

TGAGCTCATG TGAACCTCCT GTAAGAGCTG CTCTTCCGT TCTAGATTGG CCTTCACTTC 360

15 AGGATCTGTG ACTTCTCGAT CATCCTTTAA GAAATOGAAT ATGTGTGTC CCAAGTGGTC 420

TACAGTGICA TCTGTGTCTA TCGTCTAAA CTCTCTCGC AGAGCTTCT TGACCATGCT 480

20 TGTGCGGGTC TCCTTCTTGG GCTCCTCATC CTCATCAAGC TCGGGGGGT TCCAGTCGTT 540

TTTGGCTAAT GCATCCCGAT ATTTCTCCCA TTCTGCAACG TCAAGATCAT CATGGCGAAC 600

25 ACTTTGATAG AACATAAATG TTGCCTCATC GATGAAGTCA ATGACCTTC CCAGTGATCC 660

GTTTACGAGT GTATCATCGA AGTTCTTAAT GTTCATAACC TGTGCGCGA CTTTAA 716

30 (2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 643 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: PAG1540UP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

GATCTCCTGC GCGAAGAGCA CGCCCTGCGC CCATCCGGCA TAGGGGCCCC ACTTTTGTAT 60

55 GAACATTTCC CGCACAAGCT CCAGCTCCAT GTTCAGTTTC TTGCGCACAC TGGGAAGGTC 120

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CTTGTATCGC GCTTTCAGCG CAGCGATCTT CGCTGCOGAT GCATTGAACT TGTAGTCTCT 180
 5 TTGTGOGATC CTGTTGATGT GCACGTCTAC AGGCACATGG TGTCCATCT GCATGCCCAT 240
 GAGGCAGACG CAATCTGCGA CCTTOGGACC CACCCCOGGA ACCTOCATAA ACOGCTGACG 300
 10 GATCTCCTCC CGCGATATCA TGTCTAGCCA GGATTCCAGG TGTTCACTAT CGCTCATGTG 360
 TGCCGGTTTA CTTGAATCCA TCCATTCTGC CGCAGCCATG ATATACTTGG CGCGATACCC 420
 15 AAACCCCAAA TCCCGCAGTG CGTCTCGCT AGCGCCTTC ATCAGCTGCT TGCTGGTGGG 480
 GAATGAGTAG TATGGAGTAC CGTCGAGCTC GCGGAGGAAG CTCCCGTACT GCGAACACAG 540
 20 TGCATGGCAC ATCTTCGTGA TGCGCCCGAT ATTGTGTGTG CTAGAGCAAA TAAACGAGCA 600
 CAGTGTCTCC CAGGGTCTCT GTGCGAGTAT TCGCAGGCCA CGA 643

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1541RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

GATCGAACAA CCATACTTTA GCGCCACACG ACGTTCCCC TCGGGGATAT CCTGCCGCC 60
 50 CTCTACAAGA TTGGATTCAA TCATCACCCC ACAAATGGCA TTCTCAOCTT TACTCAGCTG 120
 CTCATAGATA TCTTGGGCGA CTTTCGGCTG GTTCGGGTAA TCCTTGTGTG AATTTCATG 180
 55 CGAGCAGTCA ATCATAATCC TCCGCTGGAC CCCAGCGCTG TCAACTAGCT TGCATTGAC 240

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CAAGTCCTGC TTAGCCTGTT GTACACTGGC AGCGTCATAG TTTGTGCCAT CTTTACCACC 300
 5 GCGTAGAATG ATGAAGGTGT CCTCGTTACC TTCAGTCCCA ACAATGCCAG TCACTCCAGG 360
 CTTGTAACC GAAAGAAAGT AATGAGAGTG AGCAGCGGCA CGCATAGCGT CAATAGCAAC 420
 10 CTGTAAGCAG CCATCTGTCC CGTTCTTGAA TCCGATCGGG AACGATAGTC CAGAAGCCAG 480
 CTCACGGTGC AGCTGCGATT CTGTGCTCCG GCGCCAATG GCGCCAAGG AGAAGCAGTC 540
 15 GCTTAAGAAC TGCGGCGATA TGGTGTCTAG CATTTCGCC GCAATTGGAA TGTGCTCCAC 600
 CAGCTGCGTG TACATCTCCC GCGAGATACG CAATCCCTTG TTTATTGGA ACGAATTATC 660
 20 GATGTCGGG TCGTTGATGA GCCCCTTCCA CCCCACCGTG GTCCGCGGTT TTCCAGATAC 720

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1541UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

GATCAGCTGA TGAAGATTGT ACGTCATCAC TGCTATTTAA CACAAACATA ACATAATTCA 60
 TCCGCGATAG TTAAATGTTT AGAATTCCCG CTGTGCGCGC GCGGGATCGG GGTTC AATTTC 120
 CCGTCCGCGG AGCTTTTTTGT GACATTATTT GAAACGGTTG TCGTTATAAC CGTTCCGATG 180
 55 GAATGTGGCA GGACCCTGTA ACGGCGACGT ATCCTGCAAC TTCCGCGTGT TGTGCGGTCT 240

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ACGCCAGGGC TTGGGCTTCC AGAAATTGGC TTTCCCGAG CCCGAGTTTT TGTGACCCAA 300
 5 TATTTGAGCT GCTGATCATC AAGCTCTAGT CGCACACAGG GGGCCCGAGT ATCCATTGAC 360
 AAAGGTGGC GCAACATCCG ATCGCCGGT CCTTTTATAT ATAAATATAC ACTAATGACA 420
 10 CATGCGAATA CCCGACTGCC GTGGATAGG GACGTTTGAG GCTCATAACC CCTCAATACA 480
 GATAACAAA TTGGAATATA GGAGAAGAAA TGTTCGAGAG GCTAAACTT AGGTTCGGC 540
 15 GATGCAGAAG ACTCAGAGC AACCGTTTAG CAGACGTTCC ATACCCGAAT CCCACGTTGA 600
 ATTCCGCAAT CATTTCCAGA ATCGACACAA TCACGGTGTC AATCTCGGGT CGCTATCGTC 660
 20 CTTGAGAAGT GGATATCGAG TCGATGTTCC AATGTGGCGG CGAGACCGAG CATGCGGGGA 720
 TCAGGAAGAT GA 732

25 (2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 614 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: PAG1542RP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

GATCATGTGG AGGAACTCGG GCAGCGTCTC GGAGCCGGG TAGTGGGCTA CTGTGGCGGC 60
 GCGGGCAGCC GACTGCTCGG GGTATTCTGG CGCCGGCGCA GCGGCGTGTG AGCCGATGCT 120
 50 GCTTCGGGG TGGCGGGCGG CGAAGGCGTC TGGCGGGCGG CGACGGGCGC AGGGCGAGCC 180
 CCGTTCGGAG AGCGCGAGCA CAAGGCAGTC GAGGGCGAGG AGCATGAGG TGGTGGCGAT 240

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GGTGGGGGCG TTGAGGCGGT CCTGGACGAC GCGCTCGGC AGGTGGGGG GCTGGAAGAC 300
 5 GGTGATCAG TGATGCGGC GCGGGCCAG CGTCCAGCG GGATGCGCG TGACGGCGAT 360
 GAGCGGCTG GCGGGTGGG AGCGCGGCT GCGCAGGTAG GCGCGAAGT GCAAGAGCTC 420
 10 GTCAGTCTCG CCGGAGTGG AGCAGAGCAG CAGGGCGTC CCGTGGCGA CGATGCGAT 480
 GTGCGGTGC ATGGCCTCG TGGGTGGAA GACGCGCGG GGGATGCGA ACGAGTGGCA 540
 15 GGTGGGACA GTCTTGGGA TGATGCGAA GGAATTGCG CAGCGACGA ACACGAGCTT 600
 GCGCGGTCC GCGA 614

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1542UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

GATCATTTAC CTACGCATCG GCGTCCGCG CATTGCGCA GACGGATCG TCGAGACGG 60
 45 CTACCTGGAA CACTACTACG AGAACCGTA CCGCGCGCC CTCTGGACG GCTGCGGTGT 120
 GCAGCGCTG ATAGGACTCC ACGCGCTGCC GCTGTAGCA GTCATGCGC TGTGCGGAC 180
 50 CCGAGCGGTT TGCGTCTCG GGAGCTCCG GGTTCGACC GCTGAAAAA GGAGGGCAC 240
 GCTGGTATAT AAACGGCACA CGAGCCATCC GCGTCAGGA ATAGCGTGAG TCGACAAGAT 300
 55 GGTGCGGAA CACGGTCTA AGGACCTCA GAAGAAGCT GTGAGCTTTT CCAACATTGC 360

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CCTGGGAGCG GCGTTGAATA TGTGCGAGGT CACGACGCTT GGCAACCGC TTGAGGTCAC 420
 5 CAAAACGACC ATGGCCGCAA ACCGGCAGTT CCGCTTTTTC CAAGCGGTGC GGCACGTGTG 480
 GTCCCGTGGG GCGGTGTTCG GCTTTTACCA GGGGCTGATT CCGTGGGCTT GGATTGAGGC 540
 10 GTCCACCAAG GCGCGGGTGC TGCTGTTTGT TTCTGCCGAA GCGAGTACC AGTTTGGCG 600
 GCTTGGTCTC AGCAACTTCG GTGCAGGCAT CCTGGGCGGG TGCTGGCGG CGTA 654

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 714 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1543RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

GATCCCTTAG CGACTCTCTC CACCGCTCGA CGAGGCATT GAGCTCTTAC GAACTGCACA 60
 AACCTACTCG AACTCTGTTT CCAGACTTCT TTCTGTTTGT CTTCAACTGC TTTCGCATGA 120
 40 AGTACCCCCC AGGCTATTTT TCTTACCGC CTGGTGTGTTG TCTATATAAC CGTTTGTATT 180
 TTTGATAAAA AACTCAGCTC TTCTCTTACG GCAGAAATAT ATATCCAGTC CTTAGGCCA 240
 45 TCGGAAAATC TGCTTTTFTA CCGCTGTTTC TOCCAGTCTT AGCACTGGCA GAAAAAAGAT 300
 GTATGGCGTA TAGGCGCTGG CCGCGCGGAA AAAAAAAAAA AATAGAAAAA TAGAAAAATA 360
 50 AAAAGACGTG GCGCGCCCG CCGGCAGACG AAGAAAAAAT AGGCGCCAC CCCTCCAAGC 420
 AGACGACAGG CGAGACATAA TAAATCCCA CACCAAGGGA AGAAAGTCTT GTGCAGGCTC 480
 55

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COGGCCTCAT ACGCTGCCAT TCTGTTCAT COGGCTTGCA AACCCAGTAG TGGCATGTCA 540
 5 AAGCATTGCT CCGACGCTCC GCTGCCTTGC AGTCGACATC CTCTTCCTAA CCCCAGCCAG 600
 ACTTCCATA CTTTGCACTT CACATAGCAT ATCACTTTTC AGATCACTAC GTGACATTGG 660
 10 GTACGGAATG GCACTCCAAT GCCGACAAAC CTCTTCCTAC CCGTGACTT ACCC 714

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1543UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

GATCCGTAACT TCGGGATAA GGATTGGCTC TAAGGATCGG GTAGTGAGGG CCTTGGTCAG 60
 35 ACGCGGCAAG TGTGCTTGTG GTCTGTCTC GGGGGCTTGC TCCTGGGGAC GGACTGCTTG 120
 CGTGCTCTGT CGTAGACGGC CTGGGTAAAC CATCTCTGGT CGTCGCTTGC TACAATTAAC 180
 40 GATCAACTTA GAACTGGTAC GGACAAGGGG AATCTGACTG TCTAATTAAA ACATAGCAAT 240
 GCGATGGTCA GAAAGTGATG TTGACGCAAT GTGATTTC TG CCGAGTGCTC TGAATGTCAA 300
 45 AGTGAAGAAA TTCAACCAAG CCGGGGTAAA CCGCGGGAGT AACTATGACT CTCTTAAGGT 360
 AGCCAAATGC CTGTCATCT AATTAGTGAC GGCATGAAT GGATTAACGA GATTCCCACT 420
 50 GTCCCTATCT ACTATCTAGC GAAACCACAG CCAAGGGAAC GGGCTTGGCA GAATCAGCGG 480
 GGAAAGAAGA CCGTGTGAG CTTGACTCTA GTTTGACATT GTGAAGAGAC ATAGAAGGTG 540

TAGAATAAGT GGGAACTTCG GCGCCAGTGA AATACCACTA CCTTTATAGT TTCTTTACTT 600
 5 ATTC AATTAA GCGGAGCTGG AATTCATTTT CCACCTTCTA GCATTTAAAG TCCTATACCG 660
 GGCTGATCCG GGTGAAGAC 680

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1544RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

GATCTCAACA AGATCAATAG GCATATCCTG CCGGCTAGGG ACACCACTGA ATTTTATGAC 60
 GAGAAGGCGG AAGAGTTGGA CCGCAGTGTG AGAATGGAAG AAATGGCCAT TCGGATGGGC 120
 AAACGGCGCA AGTGGCTGAT GAAGCACTGC GAGGGCGATG TGCTAGAAGT TGCATCTGGT 180
 ACTGGTAGGA ATATAGATTA CCTAGACTTG AGCAAAATCG ACACAATCAC CTTTCTGGAT 240
 GCGTCTAAGA ATATGATGAA GATCGCCAAT AAGAAGTICA GAGAAAAATA CCCACACTTC 300
 AAACAAGCTG CATTCTAGT TGGAAAAGCA GAAGATTTAG TGGACCTGGC GACTGGGCAT 360
 TCGCCTCAGC AACAGAATCT GGAATTGGTC AACTCTCCTG AGCAGGTGAT CCCGGAGTCC 420
 AAGCCCAAGG TTAAATACGA TACCATCATC GAAGCCTTCG GTCTGTGCTC TCACCATGAT 480
 CCTGTACGGG CATTGAAAAA CTTTGCAGAA TTGCTAAAGC CTGGCGGAAG AATAGTTCTG 540
 CTTGAGCATG GCAGAGGGAC CTATGACGTT GTGAACAAGA TTCTAGACAA GAGAGCCGAG 600

CACCGTCTCG AGACCTGGGG CTGCAGATGG AACTTGGATA TTGGCGAAAT TCTAGATGAC 660

5 TCTGATCTAG AATGTCACC GAAAAA 686

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 683 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1544UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

GATCAAATTC CAATCTCCGT CAGCGTCAGG CAGCCCGGTT ATGTGTGAA CTCTTCGCTG 60

30 CTCTCTTCT CTTCGCTGAA CCCGCAAGAA AATTCACCT CACCCCGAAC CAGAGGCGAA 120

AAACTGAAAA TGAAATAAGG CGCCGGCTTC CGAGGACGTT GCGGGCTGTT GCAGCTCTAC 180

35 TTGCAATACC CGCAATAGGA CTACCAGACC TTATTAGACA CTGTAATATG TGGGCAGCAG 240

TAGGTGCAGT CTACAAACTT TTATAGCGCA GCGGGCGTA TTAATCTTTT CTGCTCCCGC 300

40 GTCCGCGATA AGTTGTGACT CACAGTCCCG CGGACCGAAC GTGCGACCGA GTGCGGCGAA 360

TAATGAGTAA TGTCTATGT ASTGGTGTCT AGGGGCTGA AGGCTATGCT CTGGGCTAGC 420

45 TGAATGTCA CGCAGACAT GGGCTTCGTA GGTGCCACTT TGCGCAGCAG GTGGAACGAC 480

AGCGCAGTCA TGGCAGGAT GTCTGCGCTG GTGTGCATTA TCTCGAGCAC ACCGCGGTGT 540

50 ATGCGGGCGT GCAGGTCTGC TGGCGCGGCG TGGGCTGTT CGGGGCTGTA TTTCTCGAAA 600

CAGTGACAGT GGATGTAGGG CAGCACCAAW TGCTGGGTG CGAGCGCGGT OCTCCGAGAT 660

55

CCGTGGGCGG AGTACAGCCC GGC

683

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 714 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1545RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

25	GATCATTAAAT CAGCCATGCG ATACCCGGGC AAGATGACCA TTAGCTCCTG CTTTCGACAG	60
30	AAACAACGGA CTATGGGTAT AGAACTTGAT GATAGAACGT TGAGGCATTT AAAAAAGTGG	120
35	CTAGACCGGG CTTTAGATCC GCGTACGACA GACGAGAGCG TCACAGCCCT TGTAAGGAC	180
40	TATGTACTAC AGGTACTACT AGAGTGGGAC ATGCGAGCTG TGAAGGGCCG AAAGAACGAG	240
45	TTCTGGGAGC AGATGAGCCA GTACCTGGCA GGTATGGTCA AGGACCACAG CTGTCTAGAT	300
50	GGGTGTGTTT ATCAGCTAGT GGACTTAGGC GAGCCTCCCG CCGGGAATAG TTGCGGGCGA	360
55	CAGCTGCGTG TCCTGAAAAT CCCAGCGGAC CGGCTTGGCT GGGAAACCTT GCGTGGGAG	420
60	TTTGCGGCTT TTGGAGCGGT CACCAGGGCG AGGATTGATT ACGTGCATCG TGAGGCATTC	480
65	TTGGAGTATG CGGATGCGGC CAGCGTCGTC CGATGTGTGT CCGTCCGGAA GGCATTCTTC	540
70	GGGAACCGGT TCGTTGAGGT GCAGCCCTGC TCGCGAGGCG TGGGAATCAC TAAGCGGTGT	600
75	CGAAGTCTGG CCGCCGATC ACGAACAAC TGTGCCCGAG CATGGATCAT CTGGGGTGCC	660
80	TCCGCGAACT GGTGTGTCTT TGGATCGTGG ACGTGGCCCT CCGCTGTCA TCCT	714

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1545UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

GATCATCTTG CAGGGACCGC WCCACGTGGC GTAGAAGTCC ACGAACAAGA GCTTGTCGGA 60
GCCACCGCG GACTCAAATT CAGAAAGGGA CTTGATTTTC GACACATTG CGTTCGTGT 120
GGCTGACTGT ACCTTGTTGA TACGCAGTAC CCAGGAAGCC GGGCGGAGCC CCGCCTTTTA 180
TACCCGGCGC CTGCGGTCA CGTGTACCA CGTCCGGGT CTCCTCTTA TTCCGCTCA 240
GGAGATAAGG ATGACAAAG CGTCTCGCG CGTCCGCAT TGAAGTCTT GACAGCAATG 300
GAACCTCTGC TATAAGCGT GTCTGGGCG CAGCCCTTCT CAATGGTCCG TCTCTCTGTT 360
CGCTTTGTTG AGCCAGGCG CGGTTTGTG TACGTTTCG ACGGGTTGG ATCTCCAACG 420
CACGGTCGAA TAACGAACAT GAAAGCCAGT TGTACAGTAG CTACACCCCA GCAGACGAAG 480
CATCAGCAGG CAGTTGAGAG CCGGTACGAG AAGTTCGGT ATAGAGCACA CTOGAGACCA 540
TAGAGGTCAT CCGCTAGGCG GTACTTCAGG TCAGGC 576

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

EP 0 866 129 A2

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1546RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

15	GATCTTGCTG CTATCCAGAA ATGGGAAGTT CTTAGACAAC GGGGAATTAA GCCCCTTTTC	60
	CAATATTTTG AGCGTGTGTT CATAGCTGG AAGACGAGC AGAAGCCCC CAGTAGTGT	120
20	CTGTTCATGT TCGTCATGA AAGGTGTC TCATCAAATCT AGCTCCATCA TGCAGAGTA	180
	GTTATTATCT TTCTTCCAAG ACAGACGCAC ATGCCGCAAC TTCGTCAGGA TTACAGTAAA	240
25	ATAATGGTAG AACCGCGGAC TCACAGAAGC GACGACCGCT CGAAATGAAG TCGGCCCCGTA	300
	AAAGATCGTG CGGCCCTGCT TCTCTATCAC AAGATGGAAC TGGGAAAGTC TGTTCACGGG	360
30	GGACACCGTG CCCATAAGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT	420
	CCGGGCGAGC TCAGTCTCAA GCTCGTCGAT CCGTCGCAGC AGCTCCACAT TGGGCGTGA	480
35	GCTGAACAGC TCCCGTGAGT TCACGTCTGT CGTAAACTCA GACAGGTACA CACTCTGGG	540
	CAGGCCCTTC CCAATACATG TAGAGCACTT CGGCGCGCC TTGTTGCACT TGACGGGCGG	600
40	CTTGCGGCAG AACACGCAAG ACTTGCTGAC CTTCCGCTG GTTTTCACAA TCTTGCCATC	660
	GGACTCTGCC ATCCCGCAG CTTCAGCAA AATGAGTAGG TCATATTATT TACCTGCTGG	720
45	TAATCTTGAA TAATGCTCAC T	741

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 707 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

EP 0 866 129 A2

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1546UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

GATCGCGGAC	TGGAACACTG	GCCGGAGATG	CGCGCGGCCA	TCCTGGTGGT	TTCTGCGGAC	60
CGCAAGGACA	CGCCATCGAC	GAGCGGTATG	CAGCAGACGG	TGCACACGTC	GGACCTCTTC	120
AAGGAGCGCG	TGCGGACGGT	GGTGCCGCGG	CGTACGGAG	AGATGGCGGC	GGCGATCCGC	180
GCGCGCGACT	TGCGGACGTT	TGCGCGCCTG	ACGATGCAGG	ACTCGAACTC	GTTTCAGGCC	240
ACCTGCCTGG	ACTCATTTCC	GCCGATCTTC	TACATGAACG	AACTTGGGG	CGGATTGTTC	300
AAGCTGTGTC	ATCTGATCAA	CGAGTTCTAC	AACGAGACCA	TGTTGGGGTA	CACGTTTGAC	360
GCGGGTCCGA	ACGGGGTGCT	CTATTACTTG	GCGGAGAACG	AGGCGCGGCT	CTGCGGCTTC	420
CTCTCTGCCG	TCTTTGGGCG	CAACGACGGC	TGGGAGACCA	CGTTCTGGAC	GGAGCAGGGC	480
GCCACCTTCG	CGCGCAGTT	CGACGAGTGC	GTGCGCGGCC	AGCTTGGGAC	GGACCTGGAC	540
GACGAGTTGC	ACAGAAGAGT	TGCCCCGCTC	ATCTTCACGA	AGGTGGGGCC	AGGGCCCCAA	600
GACACTAAAT	CCTCGCTCAT	CGACCGGAGA	CGGCGCTGOC	CGCTGACGCT	ATTCTCCTGC	660
TATTTTCTGC	TCTGTATACC	CTGCCAGACC	GCGCTATATA	TATAGAA		707

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1547RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

GATCCTCCGC CTACACCAGA ATATTTCTGG CCAATTAGTT GTTCACCATC GCCCCGAACG	60
TTGGTGAAGC CAOGGCCATA CGCTGCCATG CCGAGTGCAA TTTTCTTGG GCTGACCTTA	120
AATTGTTGGG TCATCATGAG TATGCCATCA TGTGCATTCA ACTCATCAA GTTGTCATA	180
CCCATATCTT CATACCGAG CTTATCTAGG TGGGATTGT ACGGGAATT CGTAGCATTG	240
TACAAGTTGC TATGGTAGCC TGTTCGCTCT GACCATGCAC CGTGGTAGTC GTATGTCATC	300
ATATTCCACA TGCTGAGATA CTGTTCATC TOCTCAACG GGAAAATGCC AAGTGTCTGA	360
GGAAAGGCGG GTGCTGCCAT GCTTAAAGTG AAGGCGGTT CTGTAGTCCC GCGGGGCCCC	420
CAGATATTGT CTTCCAATTC GTCCATCTTG TGTGCAAGC GGCTACACAT TTCTAGATAC	480
ATCTGGGGTT CGTAGCCATC ATCCTTAGGG AACTCCAGT CAAGATCTAT CCCATCGAAG	540
CGTACTCAA ACATTGCGTC GATGCGGAG TCGATGAAGT TGTTAACTT CTCCTGTCA	600
CGCACAATTT TATGGAACGG CTCCGATTG GAACAGCGC CAACGGGCAT CATGAGCTTG	660
AAATCGGTCC CTGGCGCGT CTTGAGGTAA TTAAGCTTCG CCTATTGCCC	710

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 608 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1547UP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

10

GATCTCTGAG GGTTCOAAGG CAAGCCCGCC GGAGCTTGCC CAAATTGTGT CACCCGCTCT 60

CGAGTAGATG GTGGCCTTGT CGACCTTCCC GGTTCCTAAC AAGTGTGTCAG TGTAGGCTAA 120

15

AGCTCTAGTT AGTACCCACG AACGGGCCAC GAGCAGAACA CGTAAAAACA CATACTTGC 180

CAAGACATGA TGGTTCCGG ATGAAATCTG AGTTAGTGCT AACACTCGCA GATGCTCTGG 240

20

TGAGTGAAT CTACGTATCA ATAGTATTGA TTTGTCAATA AATATACCTT GGCTTTTGT 300

AATCTTTTTA TATAAGGGT TCCGATCTGC TGACATCATA GCACAAGAAT TAAGTATCCG 360

25

GGTAACGAAC TGCCCGGGTA ATGGGGGCA CAGGGCAAGT GCGGGTAAC GGCATOCACA 420

TACCGCAGAG ATGCACTGGC GGCTACATAC TGTACACAGG CTCGCAGCTA CTCGTGCTCT 480

30

GAGTCGAGAA CAGCCACCTT GCGAGCTTG AGAGCGACCT CTTTCATCTGC GCGGGGGGCC 540

GGCGGGGCAG CAGCGTACTT GCGTGGCCC TCGGTGTICA GCTGCTGCAG ACGCGGGGCG 600

35

TTTAGGTC 608

(2) INFORMATION FOR SEQ ID NO:873:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 706 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: DNA (genomic)

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1548RP

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

```

5      GATCATCATT GCTCGGTTAG CGATTGCCGG CAATTTTACA GCTGGTTCAT CGCTAGGCGG      60
      TAAGGCGACC GCGGGTAGTT TCCGTCTCTA CCGGTCCGTG GTGTTTGSTT TTGCATCGGG      120
10     ATGGACAACA TATGCTGCAG ACTACACTGT CTACATGCCC AAAAATTTCTA ACAAATAACG      180
      CATCTTTTTC TTCATGATTG CCGGTCTTGC GACCCCGTTG CTGTTCAAGT TGATTCTTGG      240
15     AGCTGCTGCC GGGCGCTGTG TGCACACAAA TCCTACGTGG GCGAATATT ACAAAAAACA      300
      TTCCGTGGGA GGTCTGTGCT TTGCTATACT GGCTGAAAAC GCTCTGGGCG GGTITGGGCA      360
20     GTTCTGCTGC GTTGTAAGTG CCATGTCCAC AGTTGCAAAC AATATTCCAA ACATGTATTG      420
      CATCGCTCTC AGCAACCAGG CGCTGTGGAG TCGTTTCGGG CGTGTGCCAC GAGTGTCTTG      480
25     GACCCGTGTC GGCAACGCAT GCAGCTTGGT CATTCGAATC GTTGGGTACT ACAAGTTTGA      540
      GACCTTCATG ACCAGCTTTA TGGATTCAAT TGCTACTAC CTCTCCATAT ACATGTAAAT      600
30     ATGTGTCACT GAGCACTTCG TCTTCCGCA GGGCTTCGGT GGTTCACAGT CAGCCACTGG      660
      GAACGTCCCG ATCTTCTCTC AGCTGGTTAC GCTGGCTGGG CTGCGC      706

```

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 590 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1548UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

EP 0 866 129 A2

GATCGACAGA TTACAGTTAC AAGCGAGAGT TCGGCTTATT TAAGGAACAG AACCTATAAC 60
5 ACATTTGAAG CTOGAGTTTT GGCACGCCAA GACCGATTTC CGGATTAACT ATCTTGAAGT 120
TTGCACTCAG ACTCAAGAAC TACTATTACG ATACTATAAC AAAGACGATG ACTAGCACAG 180
10 CCGACCACAA GCAGCCCAATT TCGTTGAAGG TTAACGGGGC TCTATTGAC GTCGACGGGA 240
CCATCATCAT CTOGCAGCCC GCGCTAGCGG CCTTCTGGAG GGAGTTTGCC AAGGACAAGC 300
15 CGTACTTGA TCGGAGCAT GTCATCAGTG CCACCCACGG CTGGAGAACC TACGACGCCA 360
TCGTACCTT CCGCCAGAC TATCTGAGTG AGGAGTACGT GACGAGACTG GAGGCGGAAA 420
20 TCCAGACAA GTACGGCAAG TTCTCGTGG AGGTTCGGG CGCTGTTACG CTCTGCAATT 480
GCCTTGAACR AACTTCGAA GGAAATTTGG GCGTTGGTA CTTCGGGCC CTTCAGATG 540
25 GCACCAAGTG GTTCGATGTC CTCGGCATCA AGCGTCCTAG CACCTTCATT 590

(2) INFORMATION FOR SEQ ID NO:875:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 736 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
40 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1549RP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

50 GATCTGCTTG GTCTGACCAC CGAAACCGA CTGCTTACGG TCATATCTTC TCTTACCCCTG 60
AGCAAACAAG GAAGCCTTAC CGCCTTTGTA CTGGGTCAAC TTGTGCTGGG TGTGCTTGCG 120
55 GCAGGCCTTG CCCTTGCACT AAGTCTTTCT GTTCTTTGGA ACGTTAACTG CACAGTTAG 180

EP 0 866 129 A2

TATACGTCCT CTGGGAGT CCTTTTGA TGTGAGCG CGCGTCAGA AGGCGCTGCT 240
 5 GTAGCGAGCC GTGGCCCCCT GCGGCGCTC CGCGCTTCC CTCGTCATA TTGAACATAC 300
 CCATTGCGAG AAGTAGCTTC TGTGATGCTC TGTGCTTACT ATCAAGCAGG ATGACACCG 360
 10 GCGTTGAATC CTGAAATTTA CCATGTTTTT CGCTTCGGA GCTCGGCGCG CGGCGCGGC 420
 GGCTGCGCG CCGGAAGGTC CAGTGCTGCC CGCGCTCGT CGCCCGAGTT CACCGGGGC 480
 15 ACCACGCAGC GTGGTGATC ACGCATGTGC AGTATGTGTG GGTGTGAAT AAATAGATGT 540
 ATGGGTGTAG TCACATGTTT GTCACAGGCA CTCTCGCG GCTAACGCTT CGAGATTGGC 600
 20 CAATGCGTGT GCGGCATAG GCGATGGCAG CCATGCGTTG AGCTCTGCGC GGGGTAGAG 660
 CCCAGTCAT TAGACTGCG CACTGCAAGC GTCTGACCG CAGGTTTTAA GCTGGTGTGT 720
 25 GGCGCTGCG TACGTT 736

(2) INFORMATION FOR SEQ ID NO:876:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 707 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1549UP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

GATCCATGTA TAATCACCCC ACAGCACCTT TTGCAGGTTT TCGCGCTTGG CCCCCAGCTT 60
 CTGCTCGTAG AACTTCGCAA ACAGACTGAC GTTGAACCCC CACCCATCTG CAGCAGAGGC 120
 55 AAAAATCACA TTGTTCCGGG ACGGGTCGAA GTATATGTCC GCATCATCCC GCTCCACATA 180

CTCGGCCTGG GCGTCTGCT CCAGTTTCTC TCTCCACGAG AGGTATCCA GCAGCCGCTC 240

5 CCGGCCAAAG AAGGACCCCA GTACAGAGTT GACCTGTTC ATCGTCTTGG ATAGATGCAC 300

GTAGGCCTCC TGTGGGCTCA GCTGGAGCTC CGTGATCAGC CGATCGATCT TGTTCAGCAC 360

10 CAGGATTGGT CTCAGCTTCT CCGTCCAGCA CTGCCGCAGC ACGTAATCG TCTGGGAACA 420

CACACCCCTCG ACCACGTCCA CCAGCACGAT CGGCCATCA CATAGCCGG AGCCCGCGCT 480

15 AACCTCGCTG GAGAAGTCTA TGTGGCCCGG AGAGTCGATC AGGTGATTA AATGTTGTT 540

GACCAGGGC TCGCTGCTCC CTTCTGTTT GTGAAGCACT CCGAAGTTAC AGAGAAATCG 600

20 CACTGGACTC CATCGTGATG CCTCCAGCT GTCATCTGG CCGGAGTCT AGGAATCGCA 660

CTTTCCCGC TAACCGCTGT GAGATAATAC CGTTGGATGC GAGGAGG 707

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1550RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

GATCGAGTAC ACAAAGTACA TGGATGCTGC CAATAACTAT AGTCTGAAAT CAATGCGTTC 60

CITAGCGAAT GCAGATGAGT TGGCGCAGCT GGCATCATTT AACTCCATCA GCCATTATTT 120

ATTGGCTGAA TCGCCATCTG TCCAGACACT ACAATTTTTA TTAAGCTCAT CTAAATTGTA 180

CCCAAAATTA ACGAAGGAGA ATCAAGAATC TGCAATTATC GAAACACTGC TGTCTCTCAG 240

EP 0 866 129 A2

TGAATTACG TTGCTGCAG ACTTCTCTCT CCAGGCAGGT TTCCAGGTG AAAAATCGGT 300
 5 CATTTTGAAG TACTTTTGGC GCTTTTTC AAAGGCACCA AATGGGTCCA GGGACCGGC 360
 CAGAAATGAC AAAGGCGAGG AACAACTTTC GCTTACTGCC CAAAAGGAC TATTATTATC 420
 10 TTGAGACTCT TCTTGATGTC GCAGACGCT TGGCAAAGTA TTGCTAAGC TACTCAGTG 480
 GACAACCCCTT CAGACCATCG CATATATTGG ATCTCAAAGA TGATCCATTC AGAATCATAA 540
 15 GCAAACCTGCT AGAAACGAAT CCCAGTCTGT ACCGTGAGGT TGAAACGACT TTGAAATCC 600
 TCAAGCAATT ATATGAAGGA TTGCACTGC AGCCTCATGA TCCAAAGTAC ACAAGTGAAT 660
 20 ATACCCGTTT GCTAGTCTGT CACATTGATT GTGCATTGGC AAATAT 706

(2) INFORMATION FOR SEQ ID NO:878:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 736 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1550UP

40
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

45 GATCTCCTCC CGGATATCA TGCTAGCCA GGATTCCAGG TGTTCACTAT CGCTCATGTG 60
 TGCCGGTTTA CTTGAATCCA TCCATTCTGC CGCAGCCATG ATATACTTGG CGCGATACCC 120
 50 AAACCCCAAA TCCCGCAGTG CGTCTCGCT AGCGCCTTCC ATCAGCTGCT TGCTGGTGGG 180
 GAATGAGTAG TATGGAGTAC CGTCGAGCTC GCGAGGAAG CTCCCGTACT GCGAACACAG 240
 55 TGCATGGCAC ATCTTCGTGA TCGCCCGAT ATTGTTGTTG CTAGAGCAA TAAACGAGCA 300

EP 0 866 129 A2

CAGTGTCTCC CAGGGTTCCT GTGCGAGTAT TCGCAGGCCA CGATGTGTTT TCCGATGAA 360
 5 ACGTGTGTCT GCTTTCTGCC ATTCTGCTAA CAAAGCCTCT AGGTTCACCT CCATCCGTAG 420
 GTAGCGCATC AGCCATTGTC GTGCGGCCCC GCTGCAGTCG TCATCTTTAT TCCCAGCTAC 480
 10 GCTGAATTCA ATACTGCACT GATCGGGCTG CTTCAATACA ATAATACGAT AGCCCAGCTT 540
 GTCATTTAGT AGCATGCTCG CGAATAGTA CCTTTTCTCA TGATTCCAGA TCCACCTGAA 600
 15 CGCTTGACCA CATTGCAATA CATGGTCCAG GACTATTTCT CCTTTGGGA ATATCAATCT 660
 GTTAAACTTC ATAAGTGTG ATACAGCACT GACCTGGCTC TAATAATCAG CGTCAGGCG 720
 20 CTGGCTCGAG CATGTT 736

(2) INFORMATION FOR SEQ ID NO:879:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 702 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1551RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

45 GATCTCACGT GAATGGATA TCTGCTCAAC GGCCAATTCT CGTATATTCT GACGAGATCT 60
 TTGGGTCAAT TACGTGCACT TTGGCCGAAG CCTTCGCAAG AGCTTCTAAG ATACAGAATG 120
 50 CTGCCAGGTG CATCTTAAAA AGCGGGTTTA CAGTGAAGCC TCCGTCTTTC AGGGCACCAG 180
 CCCCTAACTG TACATAGTTT CTGTTATGTA GTTTGCCTTT CCTCGGATG CTGCTCTTT 240
 55 GTGGAACAAA AACAGGCGGT AGAAGGAAAT TCCCGTGGGT CATCGGTATC GGACGGCGTC 300

EP 0 866 129 A2

TGCCCTGGATC TCGCGAGTAG CTTTATGAGC CATTAGTGAG GAACGCCAGT TTOGACGACA 360
 5 GATTTAGTCT TTTCGTGTTT CCTGCAAACA GGCTTGAAT GTATCAGGC GCTGGCGCAG 420
 CGACAGGCGA CACCGCTTCA CATAGGGAGA GGCCACCCAC TGAACACGG GTGCACTGTC 480
 10 AGGGGGGCGA GCGTACTGCC TACAATGGTA TCGTCCGCAA ACGGCAGGC AACCGGCAGA 540
 GCGGGCATTT AGATCTAAAT TTATCAGCC ATGGACGGAT GGATTTACGG CAGCGTGTCG 600
 15 CCGCAGCAG GGCACGCCA GACTGCGAGG TGGCAAATAA TTCACATAG AACCTGCATT 660
 ATAAACATCC CAAGTCATTA AACTTACTAA ATATTGTTGC GT 702

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1551UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

GATCCCGGTG AAGCTGGCA ACTGCACGGT GCGCTACGAG GACCCGGGG GCGCAGTGA 60
 GCTGGCGCAC TACGACTACT CGAGCGAGCT GGACCGGTAT CTGAAGGATA TCGAGGTGA 120
 45 GTACGAGGTG CTGGCGTACA ACTGGCCGAC GTTCTGCGG TACGTGCAAG AGCTGGAGGA 180
 GGGGAGTTT CCGAGTTCT TCTGCGAGCT GCTGCGGTAC GCGCGGAGA ACGAGGTGTA 240
 50 CCGCGCGAAG CTGTGGGCGG GGCTCGTGAA GGAGCGCTCG ATGCAGGAGC TGATCAGCG 300
 CAGAAAGCGC TCGTCACTCA CGCCTGTGTC GCGCGAGGA GGAGACGAG CGACGGCAGG 360
 55

TGGAGGACGA CTGGCACAGC AAGCTCGACG AGCGGACCG CTTCCTGGGG CTGCGGAGCA 420
 5 AGCTCGTGGC CAAGCGTGCC AAGAAGACCA AGGACGGGCT GTGGACGGTG CTGTGGGAGC 480
 GCTTCCAGAG CGACGCTAAG ATOGAGAAGA TGCGGGGCGG CAACGAGGCC GGCACGCCCC 540
 10 AGGCGGGGCG CGACGAGCTC CTGACGCGCG GCGAGCGCTA CGCGCTGGAG CAGGGGCGAG 600
 GCTTCCTTGG CGCTGTGGT CCTGTGCGG GAGCGGGCGC CGGCCCTGGC CGTGCCCTGC 660
 15 AACGAGCTTC CCGATGAATA CTGCATCACC AAGACTGACT TCGACGGCT CGCTAGCCAC 720
 GGCATCCCGG TCGAG 735

(2) INFORMATION FOR SEQ ID NO:881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1552RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

GATGTGGC TCATGCCACC ACAACTTCCA CGTCCACTGC ATCTACCACT GGCTCAACAC 60
 45 CTCACGTCC AAGGGCTCT GTCCGATGTG CAGGCAAGCG TTTTCACTCC GGGAGGGCAT 120
 CCGCATTAAC GAGCCCCACC GCGACAAGTT CGAGAAGGTG TTGATGAAG CGGCCAGCA 180
 50 GAGCGTGGTG AGCGTCGGG GCGCCAACCC GGTGGGGCG GACCAGGACG ACGTCATCAT 240
 CKACCAGGAG TTCATCCGCT GACACTAACT AGCCTGTGTA CCATGTAAA AATAATGCTT 300
 55 CCAACCAGAT TCGAACTGAT GATCTCCACA TTAGTAGTGT GGCGCCTTAC CAACTTGGCC 360

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ATAGAAGCAA TACGAGCGTC TAGCGGACTG CGCCGGGCTA TATGCGCGG GCGTGACCGC 420
 5 GACGAAACGC TGGCGCCCAA ATACCTGATC CCAGGTTTCC AACGCTGGTC ACGCAACTTC 480
 TGCCACGTGC ACTGCACACC ACGCCAGCAC TATATAGCCC CGCACCGGC AGGCGTTCCTT 540
 10 GCCAGGTCAC CGCGTCCAGC TGTGCTGGCA GCATTCCACC TGAAAAAGTT TCACCAGCAG 600
 AAAGACTTTT CCACTTCTCA ATAGCACTTC TATCCCTTAT TTCTCAGCA GTTTTGCAAT 660
 15 GAGCTACACT ACCAGACAGA TTGGAGCTAA GAACACCTTG GACTACCGGG TGTTCATCGA 720
 GAAGGCGGCA AGGTGCTCTC GCGTTCCAC GACATCCCAT TGTACGGGA NGAGAGAACC 780
 20 AATCTTCNAC ATGGTGGTGG ANAT 804

(2) INFORMATION FOR SEQ ID NO:882:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 490 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1552UP

40
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

45 GATCTTGACG ACACGCCTGC GCGGTAGTC CGTGCGAGTG CAGACTGGT CGCGAATAA 60
 ATAGCTTTGT GCCAGGCGGT CGCGAGGCG TTGCGGACT CACCGCATAA AAGAAACAG 120
 50 CTGCGCGCGC GCGGCGCAA AGCAGCCAGG CGCAACGGC GCGCGCAAA AGCAACCGT 180
 ACACAGATA TGGCAGATTC ACRTACATAT TATACATAGC CGGCGCGGC ACGCGGCTCA 240
 55 GCGCGGAAG CCGTACAATG TGCGGCCCTG GCGCTTGAGC GGTACACGA CGTCGAGCGA 300

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GGTGACGGTC TTGCGCTTGG CGTGCTCGGT GTAGGTGACG GCGTCGCGGA TGACCGACTC 360
5 CAGGAACGAC TTGAGCACCG CGCGCACGTC CTGCTAGATG AGGCGCGAGA TCGCGTTGAC 420
GCCGCCACGG CGGGCCAGGC GCGCGATGGC GGGCTTGGTG ATGCCCTGGA TGTGTGTCGG 480
10 GAGGATCTTG 490

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1553RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

GATCCGAGG TGTACACGT TCACAACTG GTCCGGGTAC ATCATGTTGA ATGCTTGA 60
35 CTTCCTCCGC GTCACCAGG TGTGGTCGG GAAATCCATC GAGCTGACCA TGCAAGAGTG 120
CCCCGAGAAC GTCTTACCA CGTGTTGCT GTTTGGGTCC AGCAGGTGA GCATCCGTT 180
40 CTGCCGCGCA ACCGCCATCA GTGGTTGCT CGACTGCATC AGCTTCACTT TCGACGAGTA 240
CTGCACCGTG TTGCTCAACC GCGCCCTTAC CAGGTCCACC GCCACCAGC CACTCGCCAG 300
45 GTTCGTCCCC CGCAGTACA CCGTGTCTG CGAGTTGCTG CCGTAGCACA TCGCCCGCAT 360
GTCGCATAGT TGTGCGATGT CCGCCGACGT TACGTGCACT TTCGTACGC TCGCCCGTT 420
50 CGCGAAGTTC AATGACTGCG CGCCAGCGA CAAGACGCC TGCTTGTGGC TCAGCAACTC 480
CACCACCGGC TCTGCCCCGA TGTGTGCGT GTGCCGCGTG TATAGCGAGT ATGACGGGTC 540

EP 0 866 129 A2

GTACGACGAC ACCCGTCCGT ATGIGTCCCC ACCCAGATCA GATTGACGTC CTGGTCAAAC 600
 5 GCCATCTTGG TCGCGCTCTT CTCCTTGGCG TCGTAAGCCC AATACAACTT GCGCAGGTGC 660
 TCGGTGAGCT CCACCGGCGA CTGGTATGAA A 691

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1553UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

GATCCGCGCT GTGTGCCCCC ACGCAATGCC TACCTGTTC A CTGTCTCCA GGCTCCACAC 60
 CCGAATCGAG CGGTCATCCG AGCATGATGC AACCAGTGGC CCGTCGTGGC TCACCAACGC 120
 GCAGAAGATC GAGCCCTCGT GGCCCTCCAG CCGCTGCACC ACCGCCCCCG TTGTGAGCTC 180
 CCACACCACC ACCCGGCCCA TCACCGTCCC CGCGCACACA TACACCGCAT CGCCCAACCAC 240
 CTCACCGAC CCGAGTACA GCAGGACCG CTCACCGCG TTGATGCTGC GCACCACAG 300
 CATCTCCAGG TCCATCTCCA GCACGCTGTT GTAGCAGGTC AGCAGGTAAC ACGAGCGCCC 360
 GTCCGGGCTG AACGCGGCCC CGAGCACCCA CTCGGGGTTC ATGTACTCGT GATACTTCAG 420
 GTTCCGGCGC GTCATCACGT CCTCCAATC CAAGATGCTC ACCGACCGGT CCCCATATGC 480
 AATTACCCAC CGTCTCTCA CGCATATCCC GTGCACCTTG TTTGCTGGA AAACCCGGCA 540
 GCGGTCAGC AGCACTCCG CGGATACTC GTATACGTAG ATTTCCGGC CGCACCTGC 600

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TAGGCACCTC CCGTCCCCGA GAATCCGCAC TGCAGTGCAT GGCGCAATGT CATTGACCTT 660

5 ATCCAGCGAC ATATTCAATG TTAAATCGAC TATGATCCCG ATCTAATG 708

(2) INFORMATION FOR SEQ ID NO:885:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 705 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1554RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

30 GATCAAACTA GGAATTTTGT ATAATACTGA AGAAGGTCCC ATATTCAAGT CTCTATCCAG 60

CGATGATGAG GAAGTGGGTG AGATTGTGCT GCACGACCTG ATGAACAATC TOGATTTTCAT 120

35 AACTATGGAT CATCTGACA GATCGAGAAA CCAAATCAT CAAGATAGAC CGATGATGAT 180

CAAGAACTAG TTTGAGATCC CTCTGCTACA AACACATACC TAGATTCTC ATATTTTATA 240

40 CTGAATACAT ATAATATATC ATTTAACTGT CTTCATTCAT GAGACGTCTG CTAAGTTCTG 300

TGCTGCTCAA CTTGTTTTTC CACTTGTCAG CCTCTTCGCC CCCAGTACG TTCACCACAT 360

45 GCACGGCTAG CTTCTTCATT CCTTTGCTCT CACGGGTATC GTTGATTGTC TGGGCACCGG 420

CCACAGTTTC CTCACTCACT ACCAGGGCTT CGATACCAGG TTCGCTACCC GTGGGCCCCG 480

50 ACACGTCCTG TAACGCAAAT ATTTTGATTT CCAGCCCCGG TTTCAGCCTG TGAAGGAAGC 540

TGCACAGTT ATGCATCGT TGTGGAAGG ACTGAAGCTG CTCCTGTAT TTCTTGTTCC 600

55 GCAGCAGTTC TTCATCTGTA ATCCCCACGA TCAGCCGGGA AGCAGTCAG AGCGGGGCAA 660

CACTGAGCAA TATTTTATGT CCGTCGTGTA AGTGGTCGAA AGTGC

705

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1554UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

GATCACTGAG GAAATCAAAA CCTGAGCAG CTTCCTGTG TTGGGTTGT ACGGTGTGGA	60
CTGTGCCCAA GTTGAGACTG TCCTCCAGGC CAAGGCTCCA GGCCAAAAGC TCTTCCTAGG	120
TATCTTCTTC GTGACCAAA TTGAGGCGG CGTGAAGGCC ATCAAGGAGG CTGTTCAGAA	180
GCATGGATCC TGGGACGACA TCGACACCAT TTCTATCGGT AACGAAGTTG TGAACAACGG	240
CCAGGCGACC GTGGACCAGA TGGCTGGTTA CATGAAACT GGCCGCAAGT GCCTCGCTGA	300
GGCCGGCTAC AAGGGCCAG TTGTTTCGGT GGACACTTTC ATCGCTGTAA TCAACAACCC	360
TGGTCTATGT GACCTATCAG ACTACATGGC TGTCACGCC CACCCATACT TCGACTTCCA	420
CACCTCTGCT GCTATGGCCG GGCCTTGGGT TTGCAACAG ATCCAGAGAG TCTGGAGCGC	480
CTGCAACGGT AACAGAAAG TTGTATCAC CGAGACCGGC TGGCCTACTC AGGGTCAGAC	540
TTACGGCAAG GCCATTCCAT CCAAAGCCAA CCAGAAGATG GCCTTGGAA CTATCAGGGC	600
CACCTGTGGT GATAGCGCTA TCCTATTTAC TGCTTTGAC GACTACTGGA AGCCAGATGG	660
GCCTACGGT GTCGAGAAGT TCTGGGGTAT GCTATAAGTT GCGTGTGCT TCTTTATGAC	720

CTGTC

727

(2) INFORMATION FOR SEQ ID NO:887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1555RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887

GATCATACAC GCATTGCAGG TATACATTAT AGTGCTCATA ATTATGGGAT TGCAAATAGA 60
 ATGGGGCCCT TACCGTAGTA CTGTCFTGGT AATGCAGCGA CGCTCAGGCT TAAGAAGCTT 120
 TTTGTCTTCC GGTATTACT AACAAATAA TTCTCTGAG CACAGGGAGT AGAGATGAAT 180
 TACATAATCC ATATGGACAC CTGCTCACCT TCCAGCGACA TTAACATTTC CTTATGAATG 240
 CCAATAATG GTGCTTAAAT GATGTGCTTG GTGTAATGCG CATTATAAAA TGTATGTGGA 300
 TTATATATTG TTTGTAGCAT CTAGTAAAC CATGGTAGCG AGGTCTTTGG CCATACCCCTT 360
 CTGAAGAGAG ACATAGCAAC AGTGTCTTGT GCAGACAGTC TGGCGTCGAA TGTTCGCTTG 420
 AAGTAACCAT GAGTACCAAG ACTCTCCTTA ATGAAGCCAG AGCGTCCAGA TTTCTGTAAT 480
 AGTGGGATCG ACTTGAACCA CTCGACATCT TCTGGCCTAA AGAACATATA GCGCACTGTG 540
 ACGACGCGCT TGTGGAACCT GAATGGATGG GCAGTTAATA TGATTCTCTT GGCCAATATC 600
 CGTGTGTGGT CTGCGTTCAG GAACGTGCGG TGGCCCAAGA ACGTCAGGCC CTTTGGATCA 660
 GAAGGGTTTT CTTTGAAGTA GATGGCCGGT GACTGGGTCA GGTCCAAGGG AA 712

(2) INFORMATION FOR SEQ ID NO:888:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 689 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1555UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

GATCTGGGAA ACAAGCATT CCAACTAGTT GGAATGGCTG GCAATTAGCA GCTGGGGCAA	60
GGCAGATAAA GCTAACTGTG GCATAGTTTC CGTGAGTTTT GATTGGTTTT CTCAAGCAGG	120
AATACTTTGC TGGCCGCCAC GGNCGCGGTT TTTTACTGTG CAGGCCAGCC CGCGGCTGTC	180
CGGGTAATGC CTGGCAGACC CGCTCTAGGG CACGCGAAT CGCCCGTGAC AACGCCTGCC	240
GCCGCAAGAT GAGCACCTAA AGGGCCGGCA GCTCCGCTA GACAACCTGA TGGTAACGTC	300
GTATTGTAAT ACTTAACCTA TACAGGGTTT ATTGATTATA TTAATCAGAA ACTGCGGTGA	360
GACCCACAGC CCGCCCGCCG AATTGTGTAC AGTAGGGGGC AGCGGGCCGC CCGCGCTCT	420
TAACGGTACT TGTGGAAACC AATGTGTTG GCCTTCTCTC TGAAGCACTG ACGGCAGATG	480
TTCAAGCGGT ACTTTCTGAT CAAACCAGAG TGCGAAGCGC ACACGGGGCA CTGGCGGGAG	540
CCCTTACCGT AGTTTCTTGG GTGGGAGAAC CAAACGTTTT CGTGAGCCAT CTTGTCTGCA	600
ATGGGTTAGT ACTCTGTCTG ACCGCTTGA AACGCTCCG CCTGTGTGA GCTGCCACA	660
CGCTCGGCGT CTGCGGGCTC CTCATTGCC	689

(2) INFORMATION FOR SEQ ID NO:889:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 700 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1556RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

GATCAACCAG TCGGCGGAGT CCTATACGAC CGGCATCAGG CTGGTGTTCG AACTTCTCGG	60
TGACCCCTCG ACGTACCTGC CTAAGGATAG TTTGCCGCCA GAACACCTG ATGAGGGCTT	120
CACGAGTGCT TCTGGGTCGG AGCTGCAGCG CCGCTTTGCA TTCAAGTGTC AAAATCCAGG	180
AGTCACCTC GTAAATGACT TCACGGTAGA CGTATACCG GCGTCAACCT TCCAGCTGCT	240
CAATGATAAT ATCTGCTTGT GTTTTGATAT TCTGAGAAGG CAGAAGTGT GGCACACCGT	300
CTTATATCTT ATTTCCCAAC TTTTGCTGCA TCAAGGCCAG GATTCTGGG TAGGAGACGC	360
CCAGCACCC GCAGCCCAAC CCGGCTCCA CCGCCGCCA TCAAGCAACA AGGGCTGTGG	420
CCGAGCAAGT GCGGCGGAGT CAGCCACGCT AGGGGACGAA AATATGCACC AACTTACCTT	480
AACGGAAATT ATGAACAAGT CTGTGATTCC CGAAGATGAC CGATGATGGA TGACCGCATT	540
GAGCTCTATG TTAACGAGAA CTACGTCTAT CTGGGGACCA GGAGGGTTC AGCTTCTATA	600
ACGATCCGAT TGAGAGGTGG GAGGCGTTTG TAGAGTCACT AAGACAGATG CTTACGTAGG	660
TATATAATTC TCATCTCAGC CTTGGTATGT ATGCGCTTGT	700

(2) INFORMATION FOR SEQ ID NO:890:

(i) SEQUENCE CHARACTERISTICS:

EP 0 866 129 A2

(A) LENGTH: 718 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1556UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

20	GATCCGATA ACGTCCACAT AAGGGAGAGA CTAGAGGCTT TGACTGCCCA GCTAGCCAAC	60
	CCAGGGCCCC AGCAGGCTCA GCAGCAGCCT CAACAGCAAC AGATGCAACA GCTAGAGGG	120
25	CCAGCACCCA TTATGTTGCA GCCAACATTG CAGCAGCAAG ACCAAACAAA TCGTTGAAT	180
	AACAAACCTG CGTTCCTACG GTCTCTCC CACGGAGTTG CGGTTGCCG AACAGAGTCC	240
30	GCAGGCCACA CACCAATGTC AGGACGGCCT CAGCCGTTGC AGCAGTTGAA CAATAACGGA	300
	AGTATCCTGG AACCGTCATT GTTGCCGCAA AAGAGGCTTA TGGAGGGTGG AATGGATACA	360
35	TTGGTAAATG CCATTTCGCA GCAGGAGTTG CAGCAACATC AGAAGAAACA TATGCTTCT	420
	CAGAACCATC CTAGTTTGGC CCTGGCTACA GGACAGCCGC AGCAGTTACC ACCCGATGCC	480
40	GCTCCCATAA TACCGCCCGA AAAGAAAGGT GCGCTCTCC CCCAGTTCA GAAACTGAA	540
	CCAGAGCATG CGGCAAAAAG ACTGAAGCAC GAGCAGAATA ACGTTAAGA GCAACCGGTC	600
45	CGGTCTCGAA TATACCTTGG ATTACGCACC CAGCTTCCAT GGAACATTCT GGTCCGGGAG	660
	ATCAGAATCA CATCTATCT GGGCTTCAG TCCAGCAAC CCAGTGTTA CTCGGTA	718

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid

EP 0 866 129 A2

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1557RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

GATCAGGCGA GACATTGCGT AGAAATATCA ATTGGTTCCA GAGGAGATCT GTCTCTGGT	60
CATTGTAGAG AAGCGGCCAG ATATAATTGT CCAAGTGAA CTGTCITTTT TGAGAAAACA	120
CGCTTTCATA CACAGCGTCC GACTTTTGGG CTAGACCATA AGCAAGGTCT ATAACTTCCG	180
TGGCAGTATA ATTCCAGACC GCGGTGGTT GCGCGGGAC AAGGGACTCC CAGTACCCAA	240
GTAAATCCTT CGTCATTGAG CTTTTTTAAC ACAGAGCCAA CTAAGATCGA CATGGTAAAC	300
GACGGATTGA MTTTGTACC ATTTTATAG GAGACCAGAT ACATTTCAG AAGCAACAAC	360
CGCAATCGTT TTAATGGTG CAATCAGTGC CATTCTGCA GCTGGGTCCA AACTCTAGAT	420
TTACAAACC CGCAGGAAT AGCTAGTGT GAACCAGCGA ACATGTAAGG AGTTTCATTT	480
CCCCACACTA TTGAAACTA CTGCGGTGAA GCGAGGTGGG GCGCATTAAC CGCCATATAA	540
CTGTGGGTT TGATAACAAT TATCTCATAT TGCTTTTTT ACGCACAAAT ACATCCACTC	600
ATAGAGAGCA TTACGCCAAT GCAGTCAAAT ATAACGAGA ATTTGCATAT CAGTACGTGG	660
AATCGCAGCA GTTGCTGTGA TTTTACTATT GATAACGGGC GCAGCATAAG GGCTGTGTTT	720

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1557UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

GATCCGCGGA TTTGGGCACC ACAGGGTAGT GTGGCCGCAT CAAATGATGG CACACAAGCG	60
ACGTGGGTAC TCAGCCCCCT TATTTGATTT GAAGAACAGA TTGATTAGGT CTGATCTTAT	120
AGCTCTGGGC AAAGCGGGGC GCCTTGGGCG CTGTGTGGCC GCGAAGTATC GCTTAGGAAA	180
ATGCTGGTGA ATGTATATTA TACGCTGACG GGAGCATTGC AGTCAGGTGT CATGTATGGA	240
CTTGCTTGGC ATTAACTATC GCAGCAGCCA TCTGATGCTT ATGCACATCA ACTAGCACAG	300
CAGCCATATG ATGCTTATTC ATACCGGCGG CCTATCGCCA TCTTCTTCAT ATAAAGGCAG	360
TGTTGTACAG ATAGGTGCAT TGTCTCTGA ATTCCAAAAG CTCATCGCGA GTGCAGATGA	420
AAGATCTCGC TTCTTTGGTC CCGCGCGAGG CGGCACCATC GTGGAATTTC AGTCACAAG	480
ATGTTATTAG TCTTAGCCAT CAATTGATCA ACCAAACCGA GGCGGTTTAC CACAACGTGT	540
TACAAGAAAA GCCACCAACA ATTGACAATT ATATCATGCC TCTAATATAC CATGAGGAGG	600
AAACAGACCT GCTATGGAAC CAGTTGGTGT TTCTCCGCAA TGTTTCGCC GATCCGGAGA	660
TTGCTGAAGC GTCGAAGAAC GCAACATCCA TGCTGGACGA CTGGATTATT GGCCTTACGT	720
CAAAGT	726

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1558RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

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GATCTATTTT GCGACTTCC CTTATCTACA TTATTCTATC AACTAGAGGC TGTTCACCTT      60
GGAGACCTGC TGGGTTATC AGTACGACCT GGCATGAAAA CTATTCCTTC CTGTGGATTT      120
TCAAGGGCCG TCGTAAGCGC ACCGGACCCA GCATAGATGC TGGGCTCTTC CAGCCATAAG      180
ACCCCATCTC CGGATAAACC AATTCGGGG TGATAAGCTG TTAAGAAGAA AAGATAACTC      240
CTCCAGGGC TCACGCGGAC GTCTCCACAC TCAGTTACGT TCCCGTGAAG AATCCATATC      300
CAGGTTCCGG AATATTAACC GGATTCCCTT TOGATGGTGG CCTGGAAAAT CAGGCCTTTG      360
AAACGGAGCT TCCCATCTC TTAGGATCGA CTAACCCACG TCCAACGCT GTTGACGTGG      420
AACCTTCCC CACTTCAGTC TTCAAAGTTC TCATTGAAT ATTTGCTACT ACCACCAAGA      480
TCTGCACTAG AGCGGTTTC ACCAGCTTT ACAGCTAGG CTTCGTCCT GACCTCCAG      540
CCTGCCTACT CGTCAGGGG TCATATTTGC CCTGACGGTG GAGTATAGGT AACACGCTTG      600
AGCGCCATCC ATTTCAGGG CTAGTTCATC GCGCGTGAG TTGTTACACA CTCCTTAGOG      660
GATTCCGACT TCCATGGCCA CGTCCGGCT GTCTAGATGA ACTAACAC      708

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(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1558UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

GATCGGGTGG	TGTTTTCTTA	TGACCCACTC	GGCACCTTAC	GAGAAATCAA	AGTCTTTGGG	60
TTCTGGGGGG	AGTATGGTCG	CAAGGCTGAA	ACTTAAAGGA	ATTGACGGAA	GGCACCAACC	120
AGGAGTGGAG	CCTGCGGCTT	AATTTGACTC	AACACGGGGG	AAACTCACCA	GGTCCAGACA	180
CAATAAGGAT	TGACAGATTG	AGAGCTCTTT	CTTGATTTTG	TGGGTGGTGG	TGCATGGCOG	240
TTCTTAGTTG	GTGGAGTGAT	TGTCTGCTT	AATTGCGATA	ACGAACGAGA	CCTTAACCTA	300
CTAAATAGTG	CTGCTAGCAT	TTGCTGGTTG	CGCACTTCTT	AGAGGGACTA	TGGGTTTCAA	360
GCGATGGAA	GTTTGAGGCA	ATAACAGGTC	TGTGATGCCC	TTAGACGTTT	TGGGCGGCAC	420
GCGCGCTACA	CTGACGGAGC	CAGCGAGTAT	AACCTTGGCC	GAGAGGTCTG	GGTAATCTTG	480
TGAAACTCCG	TCGTGCTGGG	GATAGAGCAT	TGCAATTATT	GCTCTTCAAC	GAGGAATTCC	540
TAGTAAGGCG	AAGTCATCAG	CTTGGGTTGA	TTAAGTCCCT	GOCCTTTGTA	CACACCGCCC	600
GTOGCTAGTA	CCGATTGAAT	GGCTTAATGA	GGGCCTCAGG	ATCTGCTTAG	AGGAGGGGGC	660
AACTCCACCT	C					671

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 622 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1559RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GATCCAGAAT CCAAGTTGCG TGTTCGTAGC AACCGCCGCG TGCGCAGGTT ACGAAGCAGG	60
CTAAGGAAAA GGGGCTGGA TGCCGAGCAC ATCTCAGAAG TAGTACAACG CATAAAGGAG	120
AAAAGCAAGC CAAGCGCTGA AAACAAGACC GTGGGTGAGC GGAATCCCTC ATCCGCTGCG	180
GTTGCTGATC CTAAGAAGCG GGTAGTGAT GTCCCAAACA ACCCGCCAAA CAAAGTATTG	240
CTGTACAGG ACCTGCCAAC AGACATTACC GAGCAAGAGC TGGTGGATAT ATTTGCAAAC	300
GATAAGTTGC TCCAGGTAAG ACTAGTCCAA GTCCGGCAAC TGGCGTTTGT AGACTACGCC	360
GATGTACAGA GCGCTACGGC GGTCAAGAAC AACTGGGTA CAAATTATGT GATCAAAAAT	420
CAAACAACCA TCATAGGGTA TCGAAGTAC ATAGGGCGGT GGGGATATGG GTTCTTACCA	480
GTGGGTGGGA ACCCGACAGA TCATTAGGT AACTACATAA TGATAGTATT TACMAGACTC	540
CTTAAGTGC ACGTGCCTCG ATGTCATTTC CCAAAGAGGA CTGTTCTCAT AGCTGTGAGC	600
AACGACTCTT TGCTGCGTCC TT	622

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 643 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1559UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

5	GATCCGATGA CCGTCATGTT CTTCTACAAG AACAAAGCACA TGCGATGCGA CTTGGGCGWG	60
	GGGAACAAC AACAAAGATGA ACTTCGTGCT TGACAACAAG CAGGAGATGA TAGACATCAT	120
10	AGAGACGGTC TTCCGCGGGG CCAGGAGAAA CAAGGGGCTG GTGGTGTGCG CGTATGACTA	180
	CAACTACAAG CGGATACAAT AGAACATTTT TTGCAGCTAG TGTTGTCCCA CGATAGAAAG	240
15	TTTATACGCA ACCCGGCACA GGCGCGGGT TGCTTGGCTC CACAGCTGGC GATGGAGCCT	300
	TGGGTAGGGC CCTGCTGGCC ATTATTCCTC TGA CTGACC TTACGCTAT AGATGGTGTG	360
20	TGGGCTGTTC TGGCGTGAT AGTGAAAATT TTTTGGCTTT ACGCTCCACC GGGTTCAGGG	420
	CTAGGCAGCA GGATAAGTAC WTAGGTCTTT CTGCTTCAGG CATTATATAA CCTCAAGGGA	480
25	GCTTTTCAGA CCTTTTAGGC CAATATATCT CCAAAGTGTG GGCATCTGGA CTATTAAGCA	540
	GGAGGTTCTA TTCCAGCGTC ATCAAGAAAT CTGTGAGAAT AAGAACCATG GCCTCAGAGG	600
30	ATGTGCAACT GGCCAGGAAG GCTGTGAGT TTAACAGGGA GAA	643

(2) INFORMATION FOR SEQ ID NO:897:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 139 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1560RP

50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:	
55	GATCGCGCGG AGGTTCTGTG AAAACCTTCC ATGCACAAAC CCCACACCAT GCTCCCGCTC	60

GTCCTCTTCA AACTCCTTCG CACTAATGGT GCGTCGTCC ACGACTTTAT CATTCOOGTC 120

5 AAACACTAAG TCAGGGATC 139

(2) INFORMATION FOR SEQ ID NO:898:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1560UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

30 GATCOCTGAC TTAGTGTITG ACGGGAATGA TAAAGTCGTG GACGACGGCA CCATTAGTGC 60

GAAGGAGTTT GAAGAGGACG AGCGGGAGCA TGGTGTGGGG TTGTGTCATG GAAGGTTTTT 120

35 ACAGAACCTC CGCGGATC 139

(2) INFORMATION FOR SEQ ID NO:899:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 688 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1561RP

55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

5	GATCCAAATA AGCGTCCGGT CCATACAAAT GAAOOGTTGA GTGAAGCTAC TTCGCTCGGT	60
	CGCGTATGAT TACTCGCACC AGGCTCTGGA TGACGCGGG GGAGATGGCG CTGCTGCTAC	120
10	GGCAGCCAAT ATATACATCT TCTATAGGTC TAATTCAITGT CCGCTTTTTA AAAAATGGCT	180
	TGGTCAATT TGTATGTAGT AGGCTATGTA ACGGCTCAGT CCGTGGACTC GCGAAGCGT	240
15	TCTTGGATGG AAGCAAAGAG CTTTTGGAAC TCTGGGTGGA CCTCGGCTC GCGCGGCTG	300
	GGCTCGAAGA ACTTGGAGGA CGAAACGGCG TGTTCACGT CGCGGTTC CTCCGACAGC	360
20	ACGGCCCACT TGGCGCGGT GGACACGCTC TTTTGTGCTT CGTGAAGTA GGACACAAAC	420
	GCTTTCATCA TATCGTAGGT CTTCAGATG GGCAGAAATG CGTGTAGGT CGAGTAACCG	480
25	TTCTGCTGCA AGAAGTCTTC TTTGATTAGC GTCCGACAT CCAGTAAGAT CTGTCTTTG	540
	TCAGAGAGCG CGACTTACC GACCAGCTGA ACAACTTGCT CCAATTCTC GCGTTGGAG	600
30	AGGATCTCTT TGATACGCTC TCTCAGGACT GCGAACCGG GTAATTGCTA TCATAGTATT	660
	TGTTTAGGAC GTTGGTGTTC CTTCAGT	688

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1561UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

	GATCGCAGTC TGTAGTTGCT GGTACTGGAG TCTTGACTGC TCTATGCTC TTGCTTGTC	60
5	TAAAAGCGAA GGAGACTCGG TTACTTGTAT GTTTTGCTGA CCTTCTGGTG GCAAAAGGGG	120
	TGGGGCGCGG GGTCCGACAC TATTTTGGAG CGGAATCAGC CTGAGTGTTC TTTTGTTTT	180
10	CACCAAGGGC GGGTAACCTG GCGCCAGCGG CTGGCCGGCG AGGTGATGGG CCATGAGCAC	240
	AGCAGGTATC GCGGAATAT GGAGTGTCCG GGGCGCGCT TATGTAGACC CAGCAAGGTC	300
15	CCCAGCCATC GCGCGGAATT GCGCTTTTG TAGAGTCCCG CTAGGCGCGC TGCCGCGGGC	360
	GTCAGCGCT GTGACACAGA CAAATAAAAT TGGGCAAGCG CGAGACACAA GTCCACAAAG	420
20	CGGCACTGC ACGAAGCTAT GCACGCATTC AAGGAAGACT TACCCATAC CGTGGGTTTT	480
	GCCCTGACA ATGAGGAGAT CACATTCCCC AACTACGTGC CCACGCATGT GCAATCGTTG	540
25	CCCCACAGT CCAACGGGAT CCGACAGCTA GTCATAGATA AGCAGAACCA GCGCGTCTC	600
	CCACATATA ACCGCTACT CGACCGCATG GAGGACGGC TCGTGGCTG GCGGCGGCC	660
30	GCCAGCTCC ACGTGGGCTC CTGCTAGCA ATCCACGGCA CGCACCGTA C	711

(2) INFORMATION FOR SEQ ID NO:901:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 720 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1562RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:	
55	GATCATTTGA GTGCAAAGG AGAAGTAGCG CTTTTCACAG TACGTGGGT GTGTGGACAT	60

CCTAGGTA CT GTTGACATTC ATGTGGGTCA GTCAGATTAC AAGTACACAA AGTCGATATG 120
 5 ACAAGCCACG TGACCATATA TCCAAGACGC CCCCCAGCGC ACGCCTGCTC TGTGCATAGG 180
 ACTGGCTACC TACCAGTTAC AATGGGGTTT GCAACTTAAC TGCTCTAATC CTCACACGCG 240
 10 GAGTTATATA TGTGCTATAG GGCATGCTCC CGGGGCGCAA TTCAGGGCCA ACGCCTGOC 300
 ACCATGCCAG AGCAGCCATA CCAAGCGCTG CAACAGGATG CGATATCTCG TTCTATATAT 360
 15 ATACAGATAT ATATATATAC TGTAACAAAA TCCTTAGCGA TCTGCTGTG AAAGGCCGGT 420
 ACTTAAATCA TATGCTGTC TTCTTCAGCC CCGATCGACA AAGCCCGCCC ATCGTTCCGG 480
 20 AAGCTTGAA GCTCGGGCGC AGAAGAGCTC AACTCGAGTG CCGCGCATAT AAAGCCGGTC 540
 ATGAAGAGCA TTGTAAATGC GCAAACTTGG AAAAAGCCTG CTGGCAAAAG CATCACTGCC 600
 25 AGGAGGAGTT GTAGGAGGCG GCGACCATG TAACTATAGT AGAAGGAGCG GTATTGTGTA 660
 AGCAATGSTA CTGGTCGGAA TTGAGGTAT ACCAGCAGGA CGGAGAGTGG AAGGCCGAAA 720

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1562UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

GATCTGGCGT GCATATATAA CGTATCTGCG CTCACGCGAC CTGGTGCGGA CTCTTTTAGC 60
 55 CGGCTACTAA CTCTGTAGCT GTTGGGGCTG CCTGCGGCGC CGCCGGGGGA GCTTGGCAGA 120

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ATCCGCGGTT GCGTCACGGC CAGTGCCAGC CGAACAGGAC GCGCTTTTCT AGCAGCAGCG 180
 5 CTTCCGCAGC GGTTTCTTTT TTTTCCAGC TAAGGTGCTG TATTTTCTCG CAGAGGGTTA 240
 GAAAAGTACA CTTTACATCT GAACACACCA CAAAGTCGTT CTGATTGGAG AGGCACGAAA 300
 10 CCAAACAATT GAAAGGTATG TTGAGTGGTA AGCAGACGGT ACACTGAGCT GCGCGTCTTT 360
 TAGCAGCTGG CGGCCACCG CACTTTCTCT TTTCCCGCTC TGTTGCTTCT TGCGCGCCCC 420
 15 CTTGGCCTGG ATCTCGAGAG CCGGGAGCT ACCGCGCGTC CCGCGCCAGC CTGGGCTTCC 480
 CAGCGGCGCA GTGGTCAGAG CCGGTGCGC ACCGCAGCG GCTTCATGGG CGGCTGGGG 540
 20 CTCTGTTTAC AGGGATCGGT CAGTGCGGT GTGAGGCTAA GCGGTGGCG AG 592

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1563RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

GATCTCGCT ACTTTGACAA CATCAGGAAG GCGCTTGCTG CAGGCTTTTT CATGCAGGTA 60
 45 GCGAAGAAAC GCTCGGAGG GAAAGGCTAC ATTACTATCA AAGACAACA AGACGTGCTC 120
 ATCCACCTTA GCACGGTCAT TGGCCAGAT GCAGAGTGGG TAATCTACAA TGAATTGCTG 180
 50 CTGACTACTC AAAACTACAT ACGGACGATC ACCTCCGTCC GTCTGAGTG GTTGATTGAA 240
 CTCCGACCTG CGTACTATGA CTTTGATAAC TTCAAAAAG GTGATATCAA GCTCAGTCTG 300
 55

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GAACGGATTA AACAAAAGAT GGATGCAATC GAAGAGCTAA GTAAAGAGCA ATCCAAGAAG 360
 5 CATAGACAGA GCCGCGGTA NITCGTGAGC TTGTTGTAGC TAAATATCTC TCTGATATAG 420
 CATGTACACA ATAATAGGAC TTTTGAGCTG TCCTTCGTTA CTTCGGATTA GCAAATTATC 480
 10 GCAGAAGTTA GCAGGCACCG CCGCCCTTGT TGGTGGCCTT GCACGAAAGC AGCTGGTGAT 540
 GTTCGGGCTC GCTAAAAACC CTCATTTGTG CCTATCATAT GCCAGCGCT ACAGAGTCTT 600
 15 CGCATCATCA TGTTTGAGAA GGACGAGATA CTCCACTTG ATGAGGCCAG GTCCCAAAG 660
 ATAAAGGAGT TCCTGAGCCT CTCCCTCGG CTGATCACCG AATCCATCGA AAAGAAAGAA 720
 20 TATGACTCCA TA 732

(2) INFORMATION FOR SEQ ID NO:904:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1563UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

GATCGGTTGT CTTCGGACGC TGGTACAGGG CTGGGATGCG CGTCTGGGCG TGGCGGTGCA 60
 45 TATCGGAGAT ATGGCGCCGT GCCCGTACGG CAAAGAATCA GCAAGACACT AGCGTCTGGC 120
 50 ATTCTTTTTC AATGCATTAT TTAGCTTTTT TTTTTTTTTT TTTTITAGTA TAGACACAAT 180
 ATAAAGTAGA GTTCGTCATC AGTAGCGCTC GTAAGGTTAG GGGCGGCTT CAGGCCATAG 240
 55 TAGCATCTCC GTCAGACTCC TGGATTGGCG CTTCCTCTAT GCCGCGGAT TCCGCAACTG 300

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CGTAGGGTCT TTCGTTAGCG GACTGGTTCC CACCGGGCC ATGGGCAGGC CACGAGGGAG 360
5 CTCCGGTAGC AGCCTGTGAC TTGTCTGGCA GCGAGCGGCC TGGTGGGTGC TGAAGAAGC 420
AGTGGGCGTT GCGACATTGG GCGCCGAATT TGCAGGGCTC GTTGATGGGG TGGCCGAAAA 480
10 AGCAATCTAT GCGCGTGCAC GCAGCGCCCT CGCGGCACAT AATGTGTGAA CGCGCATGGC 540
GGTACTTACA CCGTTTGTTC GTGCACTTGA CGCGAACTT ACACTGCTGG AGCGAACGCT 600
15 CCGCTGGTGC AAACGCACCG GCTTGAAGG ACGTGGCGCA GCAGCAATAG GCTGAACATC 660
TCGTATCTTG GACAAGGAAG ATGCGCCTTG TCGCAGTCCT CTGTGCACAG GTTAGGT 717

20 (2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 688 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: PAG1565RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

GATCACATGT TTTCGCCAGA GAGGGACCTG GCGTTCAGAG AGCGATGGGC CGTTATACCA 60
45 CTGAGCCCTA TTAGTTCCTG GATTTGTGTT TCCAGCAGCT GCGCATGGGG CCGGATTCCG 120
TCAAGTGTGA TTCCGCAGAT GTTGGTTTTG GCTCGATAAG TCATAAGGA AGCTGCTCTG 180
50 TTAGTACATG TCACATAGGA GGCTTCCGCA TTGGGCCATG GCATCCAGTG GCGGGCTTGT 240
GGCGGACCG GTATTCCAGT AGCCGTCTGC GAACGTATT CAATCATCTT TGGCCAGCG 300
55 GTATATAAAG CGGCTGATGA GCTTGGATGC AATGGGGTGT AGCTGGGAG ACTGCACCGA 360

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AGATGTCTAG CAAAGTTTCA TTCCTATTGA ATTGGCAGCC TGCGCCATAC CACATTGCGA 420
 5 TTTTCTTAGC CCAGTCCAAG GGCTACTTTC AGCAGGAGGG TGTGGACATT GCGCTGCTCG 480
 AGCCACAGAA CCGTCCGAC GTGACGGAGT TGATCGGTGC GGGCAAGGTT GACATGGGCC 540
 10 TAAAGGCGAT GATCCATAAG CTGGCCGCTA AGGCACGTGG TTTCGCCGTC ACTTCTGTTG 600
 CATGCTGCT GGATGAGCCG TTCACCGGG TTCTGTACCT GCGTGGCAAC GGAGTCACAG 660
 15 ATACTTTCAG CTCTCTTCAG GGAAGCG 688

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 558 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1565UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

40 GATCCCTTTC ATACAGGTCA ATATTTTATG CAGAGACAGG GGCTGGACGT TGTAAAGGTC 60
 TTTCATCCAG ATATGCTAAG AGGCGAAATT TCATGCACGA GTATGATCAC AAAAAATGAC 120
 45 ACAGCCAAAC AAATTGCCAT TATTTTAGA GGATCTACAG TGATACAGGA TTGGATTATC 180
 GATGTTCTAT CCACCCCTAT TCCATTCATT CTCGCTCTTA CCCCCTATCA GCCCGTCAGT 240
 50 GGAGCTGCAA AGTGCCAGG GAACTGTCTC ACGCACACTG GCGTCTACGA TCAATTTAAA 300
 AAAGCATTTA AGGATATTTA TGCTGTTTTT AAGCCGCTAA AAGACACACA TCCGGATTAT 360
 55 GAGGTGATAG TTA CTGGTCT TTCCTTAAGT GCGCGCTATG CTCACTTTAT GGGTATTGAA 420

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TTGCAACTTC TGGGCTACAA GCGTCATGTT TGGCGCTTTG GATCATTGCG TATAGGCMAT 480
 5 AAGGACTTTA ACGATTGGGT GGATGATATA TTTCGGTGG AAGACGTTTC GAGAAGAATC 540
 CCAAATAATG AGATGCCC 558

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1566RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

GATGCGAAA CACAACGGC GCGGCGCGT AGCGCGCGG GCGCTGCTG AGGACGTGCG 60
 CGACGCGCTC GCGGCGCACT ACGGGGTAGG AGTACATCAA CCGTACGTG GAGGACGAGT 120
 GGGTGTCAA CAACGCGGGC GCGCTATGG GGCAGATGCT GATTCTGCAC GCGTCTGTGA 180
 GCGAGTACCT GATTCTGTTC GGCACGGCG TGGCACCGA GGGCACACG GCGTGCCT 240
 TTGCGGATGA CTACTTCACG ATCCTGCACG GGGAGCAGAG CGGGCACTG CCACACGGCG 300
 TGGAGCGGGA GGTGTACACG CCGGGTATGA CGCATCACT GCGCATGGG CACGGAAGC 360
 AGTACGGAT GCGTGGGGC TCTTTTGGC TGGAGCTGC ACAGGGGTG ATCCGTGCA 420
 TGCTGCGTT CGGTTTTCTG GACACGTTCA ACAGCACACT CGACGTGTAC ACTCTGGCG 480
 GCACCGTGCA GCTGACAGCG CCGACATGT TCAAGAACTT GGTGTACAAT TTCAAGTTTT 540
 AGCCTAGATA CATAACCACC ACCAATGTCT GGCAGGGCT CGCCCGGAC AGAGCTGCCA 600

GAACCCGACG CTGGGCGAGG TGTACGCCAC GCTGACGGC CACTC

645

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 701 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1566UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

GATCCTCAAG TCTACGAACG CCTCGAAGGT GTTTACGACG GCGTTTITGG CTGATGTCAT 60
CACAGCTGAG GCTAAGGGTG ATTTTGAAGC GAAGTCTGCT GTCCAGGTC ACGTGCAACA 120
GGGCGGGCTA CCATGGCCAA TCGACAGAAC CAGAGGAAC TGTCTGGCGG TCGTGCGAT 180
CGGCTTCATC GAGGCTAAGC AGGACGTCAT TCGGAAGCC AGGGGAAAT GAGGAGGCT 240
TTGACTGGC CGACAAGGC GTCTCTACA CCGCGCGGT CCTGGCATC ACGGCTCCC 300
AACTGAAGTT CACCTCCATC AGGCAACTCT ACGACCTGGA AACAGAGTTC TOCAAGCGTA 360
TGCCAAAGGT TATCCACTGG GAGCCTACCC GCGGATTCG GGACCATTTA GAAGGCCGCA 420
AGAGGGTAAC AGTTTAGTGT CTCTGTTTCG CCGCTGCCC CACTATATGT ACCACTAGAT 480
ACCAAGATTA TGGATAAACT TAACATGGCA GAGTACACTC TCATCCACCT GCCATGTATA 540
TAATGTGATT TTACTGACGA AACTGTTTT AAAGCGGTT GCAGGGTCCG TCGCAGCTCG 600
TATAAATATC TTGACGCCAC CTCGATCTCC ATTGGTGAGG AAGTACCCGT CGAGATACAA 660
TAGTGCCAGC TTGCTAAGG GTAAGCTGAC CACTCTACAC A 701

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1567RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

GATCAATGC CCTTCCCTTT CAACAATTTC ACGTACTTTT TCACCTCTCTT TTCAAAGTTC	60
TTTTCATCTT TOCATCACTG TACTTGTTGG CTATGGGCTT CTGCGCAATA TTTAGCTTTA	120
GATGGAATTT ACCACCCACT TAGAGCTGCA TTCCCAAACA ACTCGACTCG TOGAAAGAAC	180
CTTAGATGGC ACTAGCACCC CCGCCAGACG GGATTCTCAC CCTCTATGAC GTCCTGTTCC	240
AAGGAACATA GACAGGGACT AGCAACCAAG GTACTTTCTT CAAATTACAA CTCGGAGGCC	300
GAAGGCGCCA GATTTCAAAT TTGAGCTTTT GCGCTTCAC TCGCGTTAC TAAGGCAATC	360
CCGGTTGGTT TCTTTTCCTC CGCTTATIGA TATGCTTAAG TTCAGGGGT AATCCTACCT	420
GATTTGAGGT CAACTTTGG GAATACTATT CGCTTGAAG GCCTTGTTTG TGTAGGTTT	480
TTCAAGCGCC AGCTCCACTC CACGATCTGG TCGAAACCTA ATAGCAGTG TAGAACTAG	540
CTCAGACCGC AGTCCGCGCA AGTTCCGCCC ATGGCCAGCA TTTTCAAGTT AACCTGTCT	600
TACGACCGAG TATCACTCAT TACCAAACCC GAGGGTTTGA GAAAGGAAAT GACGCTCAA	660
CAGGCATGCC CCTTGAAAT ACCAGAGGAC GCAATGT	697

(2) INFORMATION FOR SEQ ID NO:910:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1567UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

GATCGTCAGA TACCTTAGTC TCTATACAGC GCAAGACATG GGTGATGGCG GGTTTGTTCT 60

ATGCAAAGTC ATTGGGTTTC CCTCTGCGCG CGCATACAAC ACCTGCTTAA CCTGAACAGT 120

CTCATCCTGG GCATCTAGCG ATCCCATGGG TGAGCAGCGG AGGATTTGGT GGATTACTAG 180

CCAATGGCAA TCCAAACCAA AGAAACCGAC TTGGGGGAAT GCCTCATTGA ATAGCCGGTG 240

TTTCGACACT GTGATTCTCT GAGTGTAAAC TCCTCTTTGG TTGCGGATAT TAAACCTGTT 300

CTGTGAAACA TCGGAGCGGT GTTTAGTGGG AAGCAACTAG AGGAACTCAA AGAGTGCTAT 360

GGCATGGGGG CAGCTGTTGC GAAAGTGTA AAACCCGAGC TCCGGTTCCG TTGACACAGA 420

AGTTACTTTC TGTATCTCTA TCAGTCTATC ACCGAAGGAC CGTGGTGTGC TTTGCGCAIT 480

TTGGGGTTGT TCTTTAAGAT AGTTATCTGG TTGATCCTGC CAGTAATCAT ATGCTTGTCT 540

CAAAGATTAA GCCATGCATG TCTAAGTATA AGCAATTTAT ACAGTGAAC TGCGAATGGC 600

TCATTAAATC AGTTATCGTT TATTTGATAG TTCCTTTACT ACATGGATAT CTGTGGTAAT 660

TCTAGAGCTA ATACATGCTT AAAATCTCGA CCTTTTGGAA GAGATGTATT AT 712

(2) INFORMATION FOR SEQ ID NO:911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1568RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

20	GATCAAGAAA CGGTGCTAT TAGGTTCCCA TGCAAAGCGC ATGCAGCGGT CCTTAATCTC	60
	CACCTTCTCA AATGGAAACT CTCTGGCAGT CAAAGAGCAA ATCTCCATGT TGGTGAAGAT	120
25	GGTCTTCTTA GACTTGTGT GACGGTCCAC CTGTACACAG AGGAACTCTG CCTGGTTCTG	180
	CCAATGGAAG GAGACATCAG TAACCTCCAC CAAGTTGATG GTACGCAGAA CACGGCGGTT	240
30	CGGTAGCTCA ATCAGGACAG CTTTACACGA CTGGTTGTTC GACTCTGGAG TCCAGTATAC	300
	CATGACAGTA GATGGTGGGT CGTTGGGTCT GTTTGACGCC AACTTGATGC CCTTAGGAGC	360
35	AAAGGAGAAG TCCTGAACAT CCTCGATCTT CATCACTTA CCGCCCAACA GCTGGAAGTT	420
	CTTCTCGGTC TCGTACACAG CAATTGCGCC AGGCCAAGA CGAGCGCAGA ACTTGTGCTC	480
40	AAAGGACCAC TTGACCATAG GCCATTGCAG CTGCTGCTGA GCGGCGAGCG CAAAGGTCTT	540
	CACGCAGACA CCTGTTGCCA CATCCCATAT ACATAGCTGG TGGCCCCGCG ACTCGGGCCC	600
45	GAATGGACAA GCGTCGTTAG GTTCATCCGA GACTTCTAGA GGTTCGACG AAAAGGTAAC	660
	CAGGTACTTC TCGGTGAGG ACATGGAGAT CGCCTT	696

(2) INFORMATION FOR SEQ ID NO:912:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 697 base pairs
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1568UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

GATCATCTAC GTGGCCCATG AGGATAATAA GGAGAAAGAA TCGAAATTG AGCTGAGCTG	60
GTGCTCCGCT TCGGAGACGG ATGGCTTGCA CAAGGGAGGT ACCAAAAGAG CTATTTGATG	120
CAGCGATTGA GTTTGCGAAG AAGGAGACCG GTCAGGAGAG TGATGATGAT TCAAGCGATG	180
ACAACGCATC TGGAGGTGAA GAGTCTCTAA CAAAGAAGGA TGCTGACGGT GATGTCCAGC	240
TTTCATGATA ACAGCCCCGC ATTATGTGGA GGTTCATTTT ATGACAATTG ACGGATGTTA	300
CTAAGTGTAT ATTAAGTTAA TCCAOCTATA TAAATTAATA ACATGCAAAG CAATTTAGAA	360
TTTGTCGGAA AGCAGGTTAA AGCATGTCTA CTCTCCTTAA TCTTTGCGGA AGCTGTACAT	420
TTTCTTCTTC AAGTGAACGA ATTCTATCCA CGGCTGGGTC TGATTCTAAT TTCCTACGTT	480
CGCGTTCGTG GTACCATTTT CGGTCAGCT CTTCTATCAT TAATTTTGAA TGCTGATCAA	540
ATGTATCTGA TTCATCCGAG CCTGCGACA CCTGGGATAG ACGTTTGATT CTTCTGTCTT	600
TTTCCTTTAA CAGCAGCTTT ACATGTTTCT CCACTATTGA TGATGTGGCA TTTTGGGATG	660
AACATATAAA TAGAATCCCA TTTCAGCTGG TTTCTTTC	697

(2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1569RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

GATCCGATAT ACGCTGAGTG CTATATTACA AACCATCAAT TTGATGTTAT CTTGGACGTA 60
TTGTTGGTTA ACCAGACGAA AGAAACTTTG AAAAAGTTGC ATGCGCAGTT TGCAACCCCTG 120
GGCGACCTGA AGATTATATG CAACCCCTCA AGCACCATC TAGTTCTCTA TGGTTTCCAC 180
AGATTTAGCG TTACAGTGAA GGTTCAGT GCCGATACTG GTATAATCTT TGGGAATATA 240
GTTTATGACG GTGGACACGG CGAAGATGCA CGCTATGTGA TCTTAAATGA TGTCATGTT 300
GCTACAATGG ACTACATTAA GCGTCAGTT TGTGATGAAG CTTCCTTCCG CAAGATGTGG 360
AATGCATTTG AATGGGAGAA CAAATGGTT GTCAAATCTA AGCTACCGAC TCTGCATGAC 420
TACTTGAATA AGCTGATTGA GGTCACCCAT ATGAATGTCC TGACTCTCTA AGAATCATTT 480
GCCGACCCCG AATGTGTTT CTTAAGCTGC AACTTATACT CGAAGTCCAC CTTCCGCGAG 540
GATGCTCTGG CTAATTGTG TATCGAGAGA GACCCCTACTA GTGGTTCCAT CATCGGAGAA 600
GTTCGCATCC GCTCGAAGAC GCAGGGCCTT GCTTTGACCC ACGGAGACAG TATTGCGCMC 660
ATGGAAAGGT CC 672

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 698 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1569UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

GATCTGCAAT GCTCTTCAAC AATTGCTGC AAGCTATTCT CCTGATGACC TTGOCATCTT	60
GAGTGAGCTT TTTGATTCCA ACAGCAAATC TGAATAGGCC TCTATCTCCT TTAAAAGCAG	120
CGTCGTGCAT GGGGCTTTGG GTTTACATTG GAAAAAGCCC CAAAGAACAA GGTAAATGCAT	180
GCCAAAAGTA GCGTTTAATC CACTTCACAT TTAGATATTG TTACGCAGTG TATCTATACA	240
AAAAATAACG ACAAATAATA TCTTTTAGAG CTGGTTCITT AGACTAAAAT AGGGCTCGGT	300
ATGCAATACC TCAGATGCTA TCTTGATATC CGTGIGGATA TCCTCGATTA AAGCCCTCTT	360
CGTGGGTAG TTTAATTGG GCGGATGTA GCCAAGGAAG CTGAACTTAA TTTTGGGGCC	420
ATAGAAGTCT TCTTCAAAGT CGTTTAAAT GTGCAACTCA ACCGCTCTCT TACTGTGTGT	480
ATAGAACGGG TTCCATCTTA CGATAACAC GATTGGAAAG ACTCCAGCT CTGTTTCCGA	540
CAGCTTGGAG CCAAAGTTGT ATATGACCTC GCTCCCATCA TTTCTGTGAT GGGACCTGGC	600
CTTCTTGGTC CATATTAGCC TTAACCGGC CCAGCCAAA TATACTCTG TGGCCATTTC	660
GTAACTTCC CTAGGCAATT GTTCTATTGG GAACATTC	698

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 688 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1570RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

10	GATCCACAAC ACACACAGCT TGCGACTCT TTTTCTCAA GACAGTTCAC CAGTCCAACA	60
	CTTGCAAAAC CATCTGCTAA CGTTTCAACG ATTGCGCAGC AGCAAACCCA GCCAACCGCT	120
15	CTCTCTCAAT CTCATCTCTA GCAACAACAA GGTTCACAAG CTCAGCAGCA GCTACTTCAA	180
	CAACAACAAG GTTTCACAAGC TCAGCAGCAG CTACTTCAAC AACACAACA GCAACCAACA	240
20	CCACCACCAC CACAACCACA GCAACAAACA CAACAACCAC AACAAACACA ACAGCAGCAG	300
	CAGCCCCAAC CTCAACCGCA ACTACAACAA CAACAACAGC TTGGTTTACA GCTCATCAG	360
25	CCACAACCTG CGCAGGCGCA GCGCAACAA CCACAACCGC AGCAGCAGAC GCAGCAGCAG	420
	ACGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGACACA GCAGCAGACA	480
30	CAACACCAAC CACAACCACA ATTGAAACCA CAATCAGAGC AACCACAACC GGTTCACAG	540
	CAAGTCCAGT CTCACAACCC ACAGCAAGTC CAGTCTCAAC AACAAACACA GCCTCAGCAA	600
35	CTTTCACAGC CTGCCAACA ACAATCGCAA CAACAACAGC AGCAGCAGCA GCAGTCTCAG	660
	CAGCAGAAGC TTGCCAAGT GCAGCTGC	688

40

(2) INFORMATION FOR SEQ ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

55

(A) ORGANISM: PAG1570UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

5 GATCTTCGGG CCGCGGGGCG CGCTGGGCTA CGTGCTGACG CTGTATGCGA ACGGCGAGTT 60
 CTCACAAACC ATGATCGTGA ACTCGCACCT GGGGACGGCG CTGTTGGACT ACACCATTCG 120
 10 GTCGCTGATG GGTATCCATA TTGAGTACAA GGGCCATAAC CCTGAATTGG TGGAGCCGGA 180
 GGGGTTGAGC GCATACGATG TGCTGACGGT GCTGGGCGTG GTCATGAGCG TTGCGGTGAT 240
 15 GGTGGTTCTG GTGACCATCC CGATTCTGGG ACCTGTTCTA CTGATGTTTG TGATGAATGT 300
 AAAGTTTTC AAGACTTCT ACGAGCGGTT CTTAATTCTA CGGGGACTAA ACCAGGTGCA 360
 20 GGGCGTGAC GTGTTCTACC AGCATATCTT ACAGTTTGCA TACTTGGGGG GGTCGTACAC 420
 GGTMTTAAAT TTCGTGCTC TATTCTCAGT CTGGGGCTTT GTGTGCTATC CGTTGGCAAT 480
 25 CAAAATGTGG GCGACTTCCA ACATCATCCA CTTTACAGCG GAAGAAGTGG AGTCCATCAC 540
 TGAATGAAAT CATTCAATTA ACATGTCCAT CTATACATAA AGATAGATAT AGCCAGAATC 600
 30 AATACCCCTG CCATTAGTAA AGTACCATGC TGTCGACACA GCGGAATCCC GCGCAACACC 660
 GGCCTGTTG GACGAAGGCA ACTTGAACG CAGCAGCCAT CCCAGGTTAG TGGT 714
 35

(2) INFORMATION FOR SEQ ID NO:917:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 658 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: PAG1571RP
 55

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

5	CGCAGGCOGT AGGCAACACC GTTGGATATC TGCACTGGC AAAGGTCTTG ACCCGGCAGC	60
	AGAAGCTGCG GCGAACGGT AGTCCACGCA TACAAGTGGC CGCGGGGGTC GATTGCCAAG	120
10	TTGCAACCOCT CCTCTGCCAG CGCCACATCC CGCAGCCGCT CGCCTCAAA CCCCAGCAAC	180
	CGCAACGGGA ACCGGGTGGA GCCAGCGTCC TGGCCAGCC GCGCGCCCCA GTAGTAGAGC	240
15	CCGGCTCTC CTGGCTGGG CGCGTCACC GGGATCTGG GGATCCCGG CAGCTCTTC	300
	TTGCGTTGA TCTCTTCAG CCGTCAAGC GTGTGTGTGT CCAACCGCG GTGCGCGCT	360
20	AGAATCCAGC CCTTGATCTG CGGCCATTGA AGATACACG TGCTGCTAC TCCGATCCG	420
	ACGACCACG CCAGGCCCTG GAACACCGC ATCAGCTTCT GCATCTTCT CACCTGTTC	480
25	GCATACTCT GCTCCAGTG GCGCGCGAT TTGTCACTCC ACTGGTAGT CAGCTTGCTG	540
	CGCTTGGCT TGTATGTGC ATGGTTCAGC TGCTCTTGC ATCATCTGG GCTCATCAA	600
30	ACGCTGCCCC TTGGGCAAG CCTTGCTTC CATAGCGAG GCTTGGCAC TGGCAGCC	658

(2) INFORMATION FOR SEQ ID NO:918:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 657 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1571UP

50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:	
55	GATCAGTGA TGGGATGAAA ACTCTGACAA ATGCACCGG AATATATAAG GCATGGAGCT	60

5 GCGGACTCGG CCAGACAGTG CGAGCAGCGA AACAAACA TCATCCAAA TGGCCAGAAG 120
 ACCAGCTAGA TGCTACCGTT ACCAGAAGAA CAAGCCTTAC CCAAAGTCTA GGTACAACAG 180
 AGCTGTGCCA GACTCCAAGA TCAGAATCTA CGACTTGGGT AAGAAGAAGG CCACCGTTGA 240
 10 TGAGTTCCCT CTATGTGTGC ACCTAGTGTG CAACGAGTTG GAGCAGTTGT CCTCCGAGGC 300
 TTTGGAAGCC GCGGTATCT GTGCCAACA GTACATCACC AAGATGACCG GTAGAGACTC 360
 15 GTTCCACTTG AGAGTCAGAG TGCACCCATT CCACGTCCTG AGAATCAACA AGATGTTGTC 420
 GTGTGCAGGT CCAGACAGAC TGCAGCAGGG TATGAGAGGT GCGTGGGGTA AGCTCAAGG 480
 20 TTTGGCTGCC CGTGTGACA TGGGCCAGAT CATCTCTCC GTCAGAACCA AGGACAACAA 540
 CAAGGACATC GTGTGTGAGG CTTTGAGAAG ACCAGATACA AGTTCOCAGG TCAGCAGAAG 600
 25 ATCATCATGT CCAAGAAGTG GGGTTTCACC AACTTGGACC GTGCCGAGTA CGTCAGA 657

(2) INFORMATION FOR SEQ ID NO:919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1572RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

50 GATCTATTAT TAGAGGTAAT ACATTAAAC TATTATCTAA ATTCTTCTTC TTCTTAATTA 60
 TTCTTAACIT TATCTTATTA GGTAAATTAG GTGAATGICA TGTGAAGTA CCATTTATTT 120
 55 TAATAGGTCA AATTGTACA TTTATTTATT TTGCTTATTT CTTAATCTTA GTACCTATTA 180

TTTCTATAAT TGAAAATATT TTATTTTATT TACTAAATAA AAAATAATAA TTAAATAAAT 240

5 AATAATAATA TTCATTAAAT ACTTTAATAT TAATATTAT ATATTATACT TCTTTATCAT 300

TTAGGAGGGT ACCTCATATT GCTGACTAAC AATAGGGGGG TGAACCTAC GCACCTAAAT 360

10 GATAAGAGTT TATCATTAAA TTATATACTA TATATTATAA GTAAATTATC AAACCATATA 420

TAAGGTATAT ATATTAAGAA AGTTTGACTG AGTGGTTTAA AGTGTAATAT TTGAGCTATT 480

15 ATAAATCTTT ATGATTTCCT AGSTTCGAAT CCTATAACTT TCGTATTAAA TAATTATTTA 540

AAATAATTAA AAATAGTTAA TAATAATGAG AACATGATGT TGGTTCAGAT TAAGCGCTAA 600

20 CTAAGGGACA TTACACATGC CAATC 625

(2) INFORMATION FOR SEQ ID NO:920:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 677 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1572UP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

45 GATCCGTGTA TTTTATTATT ACATTATTTA ATTAAAAATA ATGATTTAAA TAAATATTTT 60

TTATAAAAAA TAATTAGTGC ATTGTTACAT GTTCATTAAA GAATGATTAT TATCAAACC 120

50 ATCAACTAAT TGTTATATAT TTATTAAATA TTAATTTTCRC TTAATTAAGA ATTAGGAAC 180

TTATCTATTA GTCTGGGCTG TTCCCTTTT GATTATTAAAC CTTATOGCTA ATAATCTGAA 240

55 ATATTTAATT TTAGATTAAAT AATATATTCT GAGATTTAAT ATTTTAAATA AAATAAATAA 300

TTATTCCTTA AATAATATTA ATAACATATC CATATATATC TAATATTTAA ATAATCATAC 360
 5 TAACATATGT TTCGTAGAAA ACCAGCTATT TGCAAATCAG ATTTGACTTT CTCTACTTAC 420
 CATTATTCAT CAGATAATAT TGCTACATTA ACCIGTTCAA TCGTTTTTAT ATTTTATTAT 480
 10 ATTTTAAATA TAATAAATAT ATATTTTAAT CATTGATAA TAGTAAGATC ATCTGCTTTC 540
 GGGTTAATTA ATATTAACCTA AATTTAATTT ATTTTAATTA ATTTTAACAT TGTAAATAT 600
 15 TTATATTATT TTTAATATCA TTTTTATTT TAATATTATG CTAATATTAA TTAATGCTG 660
 ACCATTATA CAAAAGG 677

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1573RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

GATCCGTATG GAAATTATTT TTTTATTGA ATTATCTTTC TCCAGAACAT CCAAGAAGAG 60
 45 TGTCAGAGTG GTGGGCAGAT ATGGCTTAAA CTCCTCTCC AAAGATTTAG AAATAGATTTC 120
 GATAACAGAA ATGATTGTAA TTTGCAGTTT AATAAATGGG AAGAACTCTT TAATGACTTC 180
 50 AAATATTTTCG TCAACATATG GCCTGATATG TTGCTTCACA ATTGATACCA TAACACCTAA 240
 TTGTTGAAAA TAAAACTCAA GTATTGATGG AGGACAGCTA CGCATCACAT TAATCATTC 300
 55 TCGAATAATT TGCTTTAGGA AGGAGACGCA GCGGAGTCCC AATGTTTGA AGATGTGCAT 360

CACTGCCTGT ATGACAGCAG TGTGATGAGA AGATAAAGAA GGATCCTTCA AAATTTTCAT 420
 5 TAGAGTATTG ATCAAGACGG TTGGATAATA TTCTTCATTG GAGGGTGACA TACCTTGCAT 480
 TAACAAAGCA ACATCTATGG ATGGGGCATT TTGTTGACG GATATAGGCG TCCTGGATGT 540
 10 TCTTTCAACT TCTCTATGTT TATAAGGGTC CAGAGCTCCC AGAATCCCTA TTAGTCTAAC 600
 TGTTCCTTC CTTATGCTTT GGG 623

(2) INFORMATION FOR SEQ ID NO:922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1573UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

GATCSGATAG GACAGCGAGT ACGACGGCCC CTGTGCGGCT GCCAGGGGCT CGTTGCCAAT 60
 GTAAAAGTCG AGGTCTCCG TCCCGGCTT CCCAGCCAGG TTGTTGACA TCAAAGAAGA 120
 TGACGTAAAG CCCGTGAACG ACGTCGCGA CGTGTGTGTG CCAAAGAATG CAGACCGGCC 180
 AGCGCCATA CCGCTCCGC TCTGGCCAT ACGCTCATA CTGCTACTCT TGGCGTCTT 240
 GGAAGGCTGC GCAGTCGAA TTGCCGTTGG GAACACCCAT GAGGGCGAGT CGTTACCTGC 300
 AAATCCAAT TTGGTCAATC CTGTACCATT GTCCATGACA ACAGCAGGAT TATTGAGGTA 360
 TGACATGCTG TATTCTGGT CTCAAATGCT TCTGGTAGAC TTGTGTGAGC CTTTGGCTTC 420
 55 GGATGGCTTG TCACTTACTG GCTTAAGAGT GCTGGCAGTG GAAAAGGGT CTAATCGGCC 480

TTTCGTTTTTA GGTGATCACC ATCACCAACC ACGGTACACC TGACGAAAGG CAACGCCGTG 540
 5 GCTTGTGAAG CCAGGAGAGC CCTCGTAGGT ATTCCGCGGA GCCAATTGGT GGCCCTCTGC 600
 GTTCCTCGAG CGCTCCTGCT CCATCTGCCC TCTTGAAGTC TTTATGAACC TTGAAACAGG 660
 10 GCATATAGCG ACACGGACTT TCTGCAGGTC TGTAGAGTAG CCCACATCCG GCGAA 715

(2) INFORMATION FOR SEQ ID NO:923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1574RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

GATCCCGAAG CTGGTCTGTT TCGAATTCGG GATATTTTTA GGAAGTACGT TTGTTCCAAC 60
 35 GACGTTGCTT CCATGCATCT TGGGGGGTTG TTGACGCAAC ATTTTCAGTC TCACATTCCC 120
 TGAACAGCTT TGCTATCTAC TAGGAGTTAC TGAAGCTTTT AATGTCGTGT AATAAATCTT 180
 40 TTGAGTTAGA TAATTCGCTG CGCTACAGTC TCATGGGTT TTCATTGGCC AATCCATCTG 240
 TAACTCTAAT TGAAAGGGAG AAGATCCTAT ACAGGAAATT AACAAAGGAG TCTGTGGCAC 300
 45 TAGTTTGGG TGGGGGGTGC GGACATGAGC CTGGGCACAG CGGTATGTT GGGGAGGGCA 360
 TGTTAACCGC GGCTGTGCA GGAGACATTT TTGGGTGCCC GTGACGGCT CAGATTTTGA 420
 50 CTGCAATAAG GATTGCTACA AAGCAAGCAG CTGGAGCATT GCTGATCGTG AAGAACTATA 480
 CTGGCGACGT TCTTCACTTT GGCTGGCAA CTGAGCGTGC TCGGTCTATG GGCATTGATT 540
 55

GCCGCGTGGT TATTGTTGGT GATGACGTAC TGTTGGTCTT ACCAAGGGTG CAGGAATTGG 600

5 AC 602

(2) INFORMATION FOR SEQ ID NO:924:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 722 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1574UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

30 GATCAAAAGC GTGAAGCTGG AGCGTAATGA GGAGCAGCCA GTTGTTTTGA TGGACTGGGA 60
 CCAGCTGTAC GACGTGTCTT CGAACATAAT GGAAGAATTT ACAAGGAAA TGGACGAAAT 120
 35 AGTGGCAGAG CTCAACCAAT CGTTCAAGGT ATGTAGCAGC ATGAACAGC AGGGCGGGCG 180
 GGTTACTAAC GCGATGGGTG CAGAAGCAAT TGCTTTGGCA GGAGGGGGCG TTTACCGTGG 240
 40 ACTCGCACAG AGGCGCCACC CGGTTCGGCG CTGCGGAAAG CTGGATGAAG AGCAAAGAGA 300
 CGCACTGGA ACAGAAGCGG CGGGAGCTCA ATGCATCGGC GGCATCATC AAGAGCAGC 360
 45 TCGAAAATTT GACGCAGGA TAGTCCCGGC CGGCATCGT CATGCAATGC CTTGCTCAAC 420
 ATTACATGGA TGGGTAATTC TGCTATGTA CAAACATAAT TTACGCGAAT TTAGCTTTCT 480
 50 TCCAAGGCCT GTCCTCGGTG TCTGCGCCAT CGGCGGCTTC AGTTTCACTC TCCGAGACAC 540
 CGGCGTCTGA GTCAAACTCC TCCGCGAGT CATCGTCTTC CCACTCCGOC TGGAAATCCT 600
 55 CGTCCACAGA CTCATCGTCC TCTGCAGCAG AACCATGTTA ACGTCTCAT CTCGCTGTCA 660

GAACCAAGGG CTGTTTGTAG GCGCTGCTGA ATCTCTTTCT CTTCGTTTTT GACGCGGACG 720

5 TT 722

(2) INFORMATION FOR SEQ ID NO:925:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 589 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1575RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

30 GATCCAGTAA ACTTCAGCTC ATCGTGAGCA ACCGACGTCA CCCCACCAAG CGCAGGCGAT 60
 ACTCCGGTGG AAATCACCTG AGTATATGCA GTACTCTTGG AACCATCGTG AGCAACCGAC 120
 35 TCCACCTCAC CACGCGCAGG TGAAAGTCCG GTGGATATCA CCTGAGTACG TGCAGGCGAA 180
 CTGCCTGCGG AAATCACATC ACTATCAGCA GGTGAAACTC CAGTGGAAAT CGCCTGAGTA 240
 40 CGTCCAGTAG GCTCGACTC ATTGTGGGCG ACCGATGTCA CCTCACCCCG CGCAGGCGAA 300
 CTGCCTGCTG AAATGCGATC ACCACGCGCA GGCGAGACTC CAGTGGAAAT CACCTGAGTA 360
 45 CGTCCAGGCG AACTGCCTGC GGAAATCGCA TCACCACGCG CAGGCGAGAC TCCGGTGGAT 420
 ATCAGCTGAG TCGGTGCAGT AGGCTCGAC TCATTGTGGG CGACCGATGT CACTCACCC 480
 50 CGGCGAGGCG AGCTTCCAGT GGAAATCACA TCACCACGCG CAGGCGAACT GCTGTGGAA 540
 ATCACCTGAG TACTTGCAGT AGGCCACGAC CCANCGTGGG CAACTGACT 589

55 (2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1575UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

GATCAAATAT CAACTAAGGC ACTAGTTTTT GGTGTAGCTG CTCAAGCATC ACCGGATGCT 60
CAGAAGCGTG TAATTAACTT ACAATCTCGG ACTTCACCAC CCAAATCTGA AACACATTCT 120
CATATAAGGC ACAACGCTTC TAGCGTGTAT CAGTCGGAAA CAACAKATAA TATAACTAAA 180
GATACCGGGA TGTTTTCTGC AGTGAAGTCA GGCTTTCCOC ATATACAACA GAAAACCAT 240
TCAGCAGGCT CTGAACTTGA TGACACTGAC TTTCAGAGAA CACAACTAC CAGCACAGGC 300
CCACTTCCAA CTTCAAGOGA ATATGACTCT GOCCTGTGTA CAGTTCATGG AGGACTTGAT 360
ATTTCTCCAA GACCACCTTC CTCTAGCTCC ACAGATTTCT ACGAGTATCC AACTGGTACA 420
ATAACAGAGT CACACAGAGC GCCTTATAAC GTTAGCCAAC TTCCCGAAAA TAATGGGAAC 480
TCAGCTGCCA CTCGTGTGAT TAAGAGAAAC AGTTCTGTTC TCAGCTGGCC TGGAAAGCGTG 540
ACCAACACCC CAATGGTTAA TCRAGCTACA GTACTCAGCG CCTCGCCGGG AGCGGTTAAA 600
TTAACCGAGA AACAGCATAG TCCGGCATCA TCTTCAGATA TTTCACAGC CAATAAAACA 660
CATTOGAATT CTATTGATCT AAAC 684

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1576RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

GATCTTGTTG AGAAGACTCA ACATCGGCGT AATTGCAGAG CCCCCTGTGA CCATACCGAT	60
TTTCTTGTTG GCATTGCTCA CATAGCTGAA CCGTCTTACA GGACCTTTGA ATTCCACAGT	120
TTGGCCTGGC TGTAGCCAG CAAACCATTT GGATACCTTA CCGTCGACAT AAGATTTGAC	180
AATGATATCG AAATGGCCCT CGGCAAAATTT GTTGGAGATA GGCGTGTAGT AACGCACATC	240
TTCTACACCA TCCAGCATCA CCTTCGCAGC TAAATGAAAG CCAGTAGGTA TATCAAGAGT	300
TTCCACGCTT GAACGGAGCT TGAATCTGTA TATCGCAGCA TTTTGTCTTA GAAAGATCCG	360
TTCTTCCAAT TCTAATGGCG TCCACTCATT TGGAAGAATT GAAGTCTGC TTCTGTATGC	420
TAGTAGCAGG CCGTCACCTA CAAACATTGC CAAAGCTAGA ATGCCTAGAA GGTACCATGC	480
GTTCCTCGCT GACCAGGCGA TAACAAGAAC GCCCAATGTA AAGATGCCGC TGGGGATGAA	540
GATCCCATGA ATGGGATCAT CCAATATCTC CATACCTCTG CGTTGGTCA TACTAATATT	600
TTGAAAGCTC GTCTAGCTA TCGTCTAGTA AGGATGAGAC CGGTAAATAT ATGCTTCCTC	660
CTAGTTCTAT AAGCAGGAC TCTTTGCAAC TGGTGAAGTA TCGTCTAAGG GTCATCATGC	720
ATCTGCCGAA AA	732

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 724 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1576UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

GATCAGGCGG GACGGGTACT TGCAGGAAGG CCTCAGGAAA CCCAAGGGGG GCGAGGAGGG	60
CTTCTOGACG TTTTCAACG AGACGGGCTC GGGCAAGTTC GTGCGGCGCG CCGTGTACGT	120
GGACTTGGAG CCGAACGTGA TGCAGGAGGT GCGCACGGGC GCGTACCGCG AGTGTGTCCA	180
CCCGAGCAG TTGATCAGCG GAAAGGAGGA CCGGCGGAAC AACTACGGCG GTGGGCACTA	240
CACGGTGGGG CGGAGCTCT TGAAGATAT CCTAGACCGC ATCCGCAAGA TCTGGACCA	300
GTGCGACGGG CTCAGGGCT TCTCTTCAC GCACTGGCTT GGCGGTGGTA CCGGCTOOGG	360
CTTGGGGTCG CTGCTTTTGG AGCAGCTTTC TATGACTAC GGCAAGAAAT CGAAATTGGA	420
GTTTGCCGTG TATCCGCGC CACAGGTGTC CACTCGGTC GTGGAGCCAT ACAACACCGT	480
GTTGACCACC CACACCACAT TGGAGCATGC CGACTGTACG TTCATGGTCG ACAACGAGGC	540
CATCTACGAG ATGTGCAAGA AGAACTTGA CATCTGAGA CCTAGCTTTG CGAACTTGAA	600
CAACTTGATC GCCAGGTG TCTCTCGGT GACCGCGTCA TTGCGTTTGG ACGGCTCCTT	660
GAACGTGGAC TTGAACGAGT CCAGACCAAC TTGGTGCCAT ATCCAAGAAT CCACTTCCCA	720
TTGG	724

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 686 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1577RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

20	GATCCGTTTA GAGAAAAACG GTAGCCCGGT GAAATACGCA TTTGAGTGGC CAGAGCGGCG	60
	CGAGCGGTCC GAAAGGTAGA TTTGTCCAG TGGGAAGTTG ACTCGTTTGC TTATTTCGAC	120
25	AATCGACGTC TTCAGCTCCC CGTCTTCCAA CGGGGTGAGC TTGTTGAATA AAGCTGTAAA	180
	AACGGCTGA AGAGCAGTCA GCACCAGATA GAAGAACAGC ATCAGGATAG AGACGTAGCT	240
30	GACGAAGCCA GTCGAGAACT TTTCAATTAC CTTCAACAGC GCATAGGCTG CAGGAGTGGT	300
	AATCATGGAG GAGATCATAA ACACTTTTCAG CTGGTCCGTT AGCCATAGCT TGACCGTGA	360
35	CTTGTGTAAC CCGAATTTTT CCTCGAGCAC AAAGTTGTAG TAATAGCTCC CAAACAACCC	420
	CTGCCACCAG TTCAGCTGTA GGTAGACGAT CAAAAGTAC AGCGACTGCG AGATGGTGA	480
40	TACTGGCACC AGCATGGCGG GCATGCGCTG ACCTACCGCC ACTCCTAGGT TOCACATCCG	540
	TGGCAGCCAG TCGTACTTAA TCATTACCAG ATTTAGTCCC AGGAACACCA GATCTCTAAC	600
45	CATACGGTAG CGTTACTTGG CCGGCTCGTA CGCCTGCGTC TTTTGCATTG TTTCTTTATC	660
	AATAACGCCC TCCAGTTCGC TGGGTA	686

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 699 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1577UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

GATCTTCGAC ACTATGTAGG CCGGTAGAT GAGCAACATT ACCACGAGT CCAGGAOGGA 60
CACAGCGTTC ATCAGGCATA CGTAGCGAT AATGCAGAGG GCCAGCATCG CAAACAGTAG 120
GTCCACGATG ATCGAATGCC GCTCCGCCG GCTAAGATTT ACCCAOGCAG ACCTCATCAC 180
CATAAATATC GCGCCCTGTA CCACACAGAT GATAAGCGG CAGGCGCCCA GCACCTCACC 240
CACAGACAAG GCGGCGGCAT TGTTCGCGC GTTCACGAC ATCAGACTGG AGAACAAGTC 300
GGCGACGAA TTGCACCATG CCAGTAGGAT GGCTGCCAGA ATGCCCTTGT GCGGCGGTT 360
CGGTGGCTC GTCAGGTCA CCACTATGGG ACATAAATAA TCAGAAGGGG AAAGCGCCAG 420
CAACACAAAA CACACGCTCA GATGTAGAAC CGTCAGCACC ACGAACCCAG GGATAGCTTG 480
TTCTCTCGT ATAGATACAC TGGATGTGTG ATCCGTGCCC ATGTACTTGG TGCATGGTCC 540
ATCCTTGAC TCTGCCTTC CAGGTACTTG GTAATAGTAG TGGTAGCCAC CGCAACACTG 600
GTCAAAAAGC ACACCTRAAA CCTCAATATG TAAGGCGTGC GAATGGTAGA TCGTTATTTT 660
AAAATGCAGT GCTTGAGATG AACAGATAGA CTGGTGCCC 699

(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1578RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

GATCATCCTG CTGGAGTTG AAGTCATCTT GCGATTCCCT CATGCATAGG AGTTGGTTAG	60
CACCAAACAT AGGATTCATT CTCAAGTCCA CCTGCGTTAA CCGTCTGTG CTATACTTTA	120
AGTAGTCGAT GAACTGTCTT GTAGAGTGAG CCAGGTTATT AAAATTAAAC CTGTGGGAAC	180
TATCCCGGTC TAGTOGGATG AGATTATCGG TAATCTTATT CACGACACC CAGTCTCTGT	240
TCGATAGACG CTGGCTACCC GCAGCCTCAT TCCGCAACTC CTTATCGATA TCTATTCCAA	300
GGATCTCGTC CAGGAGAATG CTACCATTTT TATCGTTCTG AATGAACTTG CCTCTACATC	360
GAGCAAAGCA TAGGTGTTTA ATGTGGATAT CCGCTAGATC GAACCCAGAC TCATCGCCGA	420
CTTCTCTGT ATCTAGCCCA AAACCATGCA TTAGCAGCTT CAAGACAATC GCCACAAGCT	480
GCGATTGTTT CCATGTCCTG CAAGGAAGCT TTACGACATA TGGGATTGG TCATCGCGGC	540
CATGTTCAAA GTTTTGACG ATTAGCACGC AGCTAGTGA TGGGGTGAAC ACGATCCTAG	600
TAAGGACCGC GACGAAGTCA ACCTTCTGTG CTAAATATC ATTACTGAG AAAAAGCTC	660
GAAGTTCCGC GG	672

(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 737 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1578UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

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GATCTTTTTC TGGTTCCTTT CCTTTAAACA GAATAATAAT TGAACAGGTA CCGTATTATC 60
GCGCATGCT AAGTGCACCT TTGACCGAGA CACTTTAGTG ATATTTATTT TGGTAGTGTG 120
CTOGTATACG TGGGCCACGA CTTTCTTGCC ATTAATCTCG TCCTTGGCGA AGCGTCTCTG 180
GTAGCATCTT AACGCACTCA TTAATGCCAA TGATCGGGG TTGATCGCCT CACGCCCATC 240
CGAAACAACA CAGACACATA TCGTTTCCA GGCATCGGGG CCCAAATAT CAGAACGCTT 300
CCGTGAGTG AAATATTTTA TGTTGTCCAT GACGCTTTT AATGTCCGTG CCAATAATAT 360
GTGTTTTG TGTTACATCG TTATCACGAT CATGATTTCT GTCTACGG GTACAGCGTA 420
TTTAAATTGT CTCACGGTAA AGTCTTTTAG CTGAACTCA GCTGGCTCAC AGGTGACAGC 480
CTGATATCGC ATGAATTTGT ATTGGTTGCT GAAGTAATCT TCTTCATGC CAGTGGCGTA 540
CTGGGACACT AGCTGTTCAC TGACTGGACA ATCAAAGATA AAGTTTCTC GATATAGCTT 600
GAACTTTGCT AATACAATGC GATTTTTAGG CTGTTTGGAC TCGGTAAAC CACTCAGAAG 660
CGTTCTGAG CTGAGATGCG TCAGTCGCC AGAACCTTGG GAACCGGAGT ATGCCGATTA 720
GGGCTACGC GAGAGAT 737

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 663 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1579RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

10

GATCGAAATA CCACTGATCG ACCGCGGTGC CTCGCTTTGC AGCTGCTCG AGAGCCGCTC 60

TCCGAGATAC CCGCAGAGC ATGCCTTTTC CAACACCATC TTCTGTACC GTTCGGGAG 120

15

TGACCCCTACT ATACTTATGA TAATGACCTT CTGTGCTTC AGAGTCCCT CTGTTTCTTT 180

CTTCAGGTAA AGGTGCGATT CTCGGCCAGG CTGTAGTAG CCACGGACCG CAGACGCAAT 240

20

CCGCGTGTTC CACGGCATGG GATGGAAGTA CTCACCGGA GAGTGGCCCG GCAGAAGCAC 300

CGAGTTGTTC ACGCCGACCA CGTACTCGA CTGGTGCTCC AGCGGACACA CCTCGAGCGG 360

25

ATACTCCTTC AGCGGCAACT GGCAGTTCTG TGACCCGGTG TTGCAAGGC TCAGCTCGCC 420

CTGACCCAGC CCCCAGACCC CCGCCATGTC TCCCATGTCC GGCAGTACT CCGTGTGCCA 480

30

GCACCAGGAG TCATTTCGCC GCGCTACCGC CTGCAGCGCC TCTGTCTCA GCGTATGCAC 540

CTGCTTCGCA GTCACTGAT GGTACTCGGT GCTCTGGTGG ATCAGCAGCC CGTCTCGGG 600

35

GGTCTGCCAG AACGGCATCC ATCCCACCAC GCTTTGTAGA AACGAGGTGG TGGGGCGCCT 660

GCA 663

40

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PAG1579UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

5	GATCGCACGG ACCGCGAGAC GAGTTCTCTT GGTTCGTGCG ATTGGCGATG GTAGGCCGCC	60
	CTGTTGCACG TGACCTGGGG ACAGCAGACT TGGCGTCAA ATCAACCTTA GCTCAGCTG	120
10	TGATGACATC AGCCAAAACG GCGTCGGTA AACACCTTC GAGGCGTTCG TCGACTTGAG	180
	GATCAGTTTA CCGTGCTTAC CCTTCCCGTG CGCCTTTTCG AAGGACTCGC GGAGCGTCTC	240
15	AATATCTTGT GAGAGCTGTT CCAGCGAGAT ACCCTCTTCT GGAACGTAGG AAACCTGTGC	300
	GCCCACCGCC AAGGCAGCAT GCGTTGCCAG ATAGCTGAG TTACCACTT GGACATCGAC	360
20	GACAAAGACC CGGCTCTTG TGGAGGCTGC CGACTGCTTC ACAACATCAC AGTACTCCAT	420
	TAGGCATTC AGAGCTGTGT CTGAACGAG CGAATACTCA CTGCCCGGA CGTTATTGGA	480
25	AAGTGTGCT GGAATGAGTA CCATTGGTAT TCTGAAAGCT GGTAGTTCT CAAGGGCCCG	540
	CTCCAATTGA TGCAAGGAGA CGAAGGCTCG AACCCACCAA CAATAACCA GCGTCAAAC	600
30	TTGTAATTTT GGAAGTAGTA GGCAATCATG CCAATGTCTG CATCTTCTGG GACAGTTCTG	660
	TTGGTTCCCA ACTCGGAACA CCGCGAGATT GCCAGCCAAG CATATCTTTC CAGTTCAACG	720
35		

(2) INFORMATION FOR SEQ ID NO:935:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 718 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
45	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1580RP

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

5 GATCCGTGTC GACAAGTTGG TCACGTATAT ATGGGCGGTG TTGAGGCGG TCTGGGTGTA 60
 CCGCCCGAAC CAGCAGCGCT GCCATCTCGA AGACATCATG CTCTTGGGTG TGTACTGCGG 120
 10 CGAGGCGCGG GGGCAGCCGC TCTTGCTCAT GCGATCGTT CAGGCGGTGG CGGCACGCTA 180
 CGGGGTGCAG ACGCTCCTCT GCGAGCAGGT ATTGATCATC ATTGACCGCA AGTTGGCGGG 240
 15 CGGACAGTCA TACTTGATGA TCCGCTGCG AGGGAACGCA AAGCCGCGCA TCTTCACGG 300
 GCGGCGCTTG CTCGACACTA TGCGGCACAC AATACCCAAC ATTGCCGACC CGCGGAGCCT 360
 20 GCGCTCGCC CGGTTCCTCA CTCGCTCAC GAAGCGCGG GGTGCTGAGA AAATCTTCAA 420
 AGACTGGTCC ATCTACTGCG ACAAAATCCAT ATGGCGGACG ATCCCTGATC ACTGGCCAA 480
 25 TGGCATTCTG CGCTACCTCC CGCACTCTG CAGCGCGATG GACGAATCCA TCTTTGAGTA 540
 TTTCATGTC TATTGGAAAA CGCAACAGC AAACCACTCC ACGACAACA TTTTCCACAC 600
 30 CGTCTTCTC AAGCAATTG AAACGATCTT GGTCAAGAGT ATCCCGGCGA CGCATCCACT 660
 TTGTGATTG CCGGGAGCAG CTCATGGACT CCATTATCGA GATGCTTTTC GCGAGTCC 718

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1580UP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

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5      GATCCTTTTC ACCAACAGCT GTCTGGGCCA GCTGGGGCCT GGGATGAACT ACAACGAGGC      60
      AGTGAAAGCG CTGACGAACC TGGGCTTGA CAGCTTTACA CTGCCGGGGG ACGGTGGGGT      120
10     TTCGCTGAA CAACGTGTAC TCTGTCCGG TAGAAGACGG TGCTCAGATG GAGCTGCTGA      180
      AGGGGTACCT GCAGCAGTTG CGGCAGGAGC TGGCCACGGG GCTGCTGGAC CGTGTGTATG      240
15     GGGCGGAAAA GGCACAGCCC TCGAAGTTCT GGCTGGCCTT CACAAGGGCG AAGTTTATGA      300
      ACAAGGCGCT GTAAGGCGAA ATAGGTACGT AGCTGGGGCG GCCAGGAAGT ATTTACAAAG      360
20     TTGGCTGTAT CGCTACGAGG TTTTGGTGGC GTGTGCCTTG TTGGAGCGCA CGAGGAGTTC      420
      AACGGCGGAA GCTCGGAGCT GTTCCGGGTC TTTCAGATC GGGTTCAGCT CAATGCTGAG      480
25     GTGGTGTTT TTGGCGCGGA AGCCTTGAT CCGGGCTGC AGGTCTGTCA GGGCTGGAG      540
      GACAGCTCA TAGTCTGCAT CTTCTTTCAC GGGCTCTTTC TATGTTTGA AGGACTGAAC      600
30     GATGTCTTTC ATACCGGGCT CGACTCTGCT GATCATCTCG ATGGGCTGGC GCAACAAC TG      660
      ATGGCGGTGC CTGTGGGGT CGGTCCTTA ATCATCTGCT GGATT      705

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(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1581RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

EP 0 866 129 A2

	GATCTTAATT TAAAATTTTA ATTAACATA TATAATTTAG AAATATATAA TCTAGAGATA	60
5	TATAATCTTA AAATCATAGG TAAAATACT TAAGATAGTA AGAATAAAAT TAGTAAATA	120
	AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA	180
10	ATTTTATTA TTAAATGAT TATTATCTAT TTAACATAAA ACATTTTAA ATGTTATAAA	240
	ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTAATATT	300
15	AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA	360
	ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC	420
20	TTTCATAATA TTTATTTTAA TTAGTCTAGT AATATTTCTA TTTAATAGTC TACCCTTTAA	480
	TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC	540
25	TAATAATTTA TTATCTAAG TATATAAATT AATTAAATCT TTTTATTAT TATTCTAAAT	600
	TATTATTAAT TAGTAAATTA TATTTATTTA TTTTATTAAC ATAATTTTIG ATAATAATAT	660
30	ATCAT	665

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 732 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1581UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

55	GATCAATTAA TAAATGGTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA	60
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EP 0 866 129 A2

CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT 120

ATTGAGTTTA TATTAAATTC ACCACCTCTT ATTCATTTCAT TTAATACTOC TCTAATTCAA 180

TCTTAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAATTG 240

GTAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAA ACTGAATATC TACATATTAT 300

ATCATTAATA TAATAACTCT TTAATTAGAG TGGTAOCACA AGAATGCTGA AAGCATTAGG 360

GGTGTGTACC TTAGCTCTCT AATTAAAGTT ATAAAATTAT CTTAACTAAT AAAAATAATT 420

AATTAAATA ATAAATAATT AATTAAATTT AAAATGTTA AAAAAAGAA TAAATAATAT 480

GTTATATTTA AATAGATCAA AATTCAACA ATTCCATTT CATTTAGTAC TACCATCACC 540

ATGACCAATT GTTACATCAT TTAGTTTATT AGGTTTACTA TTAACCTTAG CTTTACTAT 600

ACATGGTATT ATTGGTAATA TTTATCCTTT ATTATTATCT TTATTAGTAG TTTTATTACT 660

AATAACTTTA TGATTTAGAG ATATTGTAGC TGAACCTACT TATTAGGTG ATCATACTTT 720

AACTGTAAGA AA 732

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 694 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1582RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

GATCTCAACA CGGTGGTTGG AGAAGTGTGC AACACACGAG TACGTAGTAC CCAATCAAT 60

ACCGACTGAT TTAGACATGA TCACTGATTA GAAAACGAAA TCTCTGGTTT TCGGATAACC 120
 5 GGGAGAAATA CCAATGGTGA TAACCGTACG TAAGGCCAGA GGTACAAAGC TACTCCAATC 180
 TGAAGCTACA CACGCCCAAC CCTTTTATAC AATTTC AATT TTTTCTCTCC CAAACGAACA 240
 10 TGGCAGATAG TAAGAGTCTT CGAGCCCAAT GCCTGTTCGG TTTTFTTTTG TTCTGGAAAA 300
 TTCTACCATA ACGTATGTGG CCGTTGAAAA CTGATCAAAC GGGTCTCGAA GATCTTAGAA 360
 15 TAGAGGCTCC GACAGAAAGG GGGAGGCCGA TTCAAAAAAG ACGCATGAG CCTCACTCGT 420
 GCTTCGAGGC GGGAGAGCCC ATAGGCTTCT TTCCAGGGC CACCGACGGT TTCTGGAAAG 480
 20 GAGCGAAAAC AGAGAATGAA CCGAGGCGGT TGATCTGCAT CTGGAFTTG GCGTAGGCCC 540
 GTTTCAACTG AGCGGGAATG CGTGGATGCG AAACCTACGC GTCCGCACGC AACTCCACT 600
 25 TCCGTACCAC CGCAGCATG TTGGCGATT TTCGTAGGC GCCTTGATGA AAAGCGAGTA 660
 TAGAGCCAGC ACAATCCAG AGCGCGCGCG ACAA 694

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 707 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1582UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

GATCTTGTC TCCGATCCA GATACTGGTC GAAGCGGAG TTCATCTCGT CTACAATCGG 60
 55 CTTCACGAG TCGGTGTAT CTATCGGTC CCCGAAGCCC GCGGTGTCCA CCACGTCAA 120

EP 0 866 129 A2

	CTTCAACACC ACGCGTTTCT CCTCGATCTC CGTCGTGACG GTCTCAATCT TCACTTGT	180
5	CTGCGCGTCC TTGGCCCGCG ACTCGTCGCC GTCTCAACG TCTCAAGCT TCAACGGGT	240
	GAAGTCTCC GCGGTGTCTT CCTTCGCGCT GTATAGCTCC TTGTTGAACA ACGTGTGAT	300
10	CAAGGTCGAC TTCCCCAACC CCTTGGCGCC CACGAGAGC AAATTGAGGT TGAACCCCG	360
	CCGATCGAC TTGGATGCC ACTGCTTGGG AAGGTTTGGG AACCCACGT ACCCGAGAT	420
15	CTTGGGTGG ATGATCCCA GGTCGGCTG GTCTGCCAGC AACTGGCCCG CCGGAGCTC	480
	GCCACCCAGT GCGTCGCCA CATCTCTCTT GTGTCCCGA AGGTCCAACC CCATCTCTC	540
20	CTCTTCACG TTATGTCCG AGCTTGTGTC CTTCGGCTC GCGTCCCGT TGCTCATAG	600
	TGCGCCCCCG TGCTGGTGT CAGGCTCCG GCGTGTGG CACTGTTGT GTTTGCGAA	660
25	TCTCTGTGG AGCTGTAGG TAACATGCTT GTCTGATTT GGTAGTC	707

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1583RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

50	GATCAATTAC CCTGGGCCA ACCATATTTG GATGAATATT TGCATTGTTG CCGATAGGG	60
	TTCCCTCATC GTGTATGTTA TAGACCTTCA CGTCTTCATT AAAAGGGCAT GTGATGACTT	120
55	TCTTGCTGTC GGCAGAGAAG GTCAAACAAA TTACAGATTG TTCTGTACCG GCCAAACTT	180

TATAAACCCCT GAAGTTGTTT AACACGTCAT ATATGAATAC CTTACGATCG CTGGAAGGGT 240
 5 CAGTGGATGC ACTGGCCAAA TACCGACCAT CTGGTGAGAA TTGGAGGTAC CAGATTTCAT 300
 CTTTATTTTC CGAAAGAGTC TTCACATGAC TGAAATTGAA CATGCACATA GAGCCAACGT 360
 10 TATCTTGAAG CAAGTTATAA GTGGTTTTCT CTCCAGAAGC GTTTCCTTCG TGGTTGTGAG 420
 GATCGTCGCT GAAGCTTAAC AGGTCGCTGG ACCGCTGGAA CTGTATAGCC TGTTTTAACA 480
 15 ACGTAATGAG CCTGCCCCGT GGAACCAAAT CATTGGGGTT GATATATTGT GAAATCTGAT 540
 CAAGCGCCAA TTGCGCGAG GCTGCCAGAG ACCCTCCCA TATTTTGTGT GCTCTGCGG 600
 20 ATTCCGCAGG ACACGTCAA ATAGTGTCA CTGCAGAAGA GCTGTGTGG GAGTCATAGC 660
 CCACTCTCCC TGGGCTCCT CCACCATAGA TATGGTCTGT ACAGCCACAG CGAGTCC 717

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1583UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

GATCGACTGG AAGTACACGT CCAGCGACCG GTCAAGGCC ATGTCTGGA CGGACTGCTC 60
 50 GAAGGTCTTC ACGAGTTTCT TGGCGATGCG GAGCAITGGT GTGCGGTCTG GGGCGGGCGA 120
 CGCTGCGGAG GGCTACCGA ATTTGCTTGT GCGTGTGGTC ACGTGACACT TGGCGCGCTG 180
 55 GCGCGCGCGG GCGCGCTGG CCGGAATGG CTGCCCCGCC CTGGCACGCC GTTCTTGCAA 240

TCACATGATT CATGATTCCG CTTTTGGGGG GGATCACTGC GCAGCCGTTT TTGCTGCTTT 300
 5 TAGCCTCCCT GACACCTCG GCTGGGTCTG GAGCAGGTC CCGGCGGCT GTCCGCTGG 360
 TGGCTGTACG TGTGGGGTGA CGCCATTTTG TGGGACAGCG GCGAOGCATG ACGACGAGCT 420
 10 CCGAGGGTCC GCGGTGACG ACAGCCCCCT AAAGGAGTTT CTTTATTTCG ACGGGGCCCC 480
 TCAAACACTA TATATGAGCA AAGGCAGGAT GGAAGGTAGG CTAAAGCAAG AAAAGACCTC 540
 15 GACCAACGGT ATCGAAGTCT AAAATCTTAG CAGGTACCAG GATGTCCTTC GAAGATTTCG 600
 ACAAGGCGCA ACGGGGAAA GTGAGGAGG CAGTGGACGA AATATGTAAG GATTTOGAGG 660
 20 TGACGGAGGA CAAACTCCG CAGTTGACCG CGTACTTCAT CGAATGTTTG GAACAG 716

(2) INFORMATION FOR SEQ ID NO:943:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 677 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1584RP

40
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

45 GATCCAAAAA GCCTTCGGG CGCGGCACA TTATCACAC CCGTGTGCT TGACGGCCTC 60
 GACAATACAT CCTATGACAT GCGTAATCC TCCTATGTTG TTCGACGCG GCGCAAACGT 120
 50 GCCAGCGTCT CGAAGGCTTC GCGCGGAGC AAGAGTTCTT CCCCCCTGA AGAGGAGGAG 180
 AAGCCATTTA AATGCCAAGA ATGCACCAAG GCCTTCGGC GCAGCGAGCA CTTGAAGCGC 240
 55 CATATACGCT CTGTGCACTC ATCGGATAGG CCGTTTCGGT GCACCTATTG TGATAAGAAG 300

TTCAGCCGCA GCGACAATCT GTCGCAGCAT CTCAAGACAC ATCGCAAGCA TGGCGATATA 360
 5 AAAGACACGC CACCAACCAC CAAGAAAGGC TGACTTTCAC ACATCTATGC GAATACCCGA 420
 TGTTCGATTA AGAGATACAT ACAGCGCATA CAAGCTGACA CAACGTCCCG TACGCCAACA 480
 10 GAGGAGATGA TAAATACTAC ATACTCAATA TATCAATACC TCCTACTTTT GGTAATCATA 540
 TATAACTGTT TTCTTTTCGCA CTGTCTGGT AACGTGTGCA TAGGTTTCCG TGTGCTGCT 600
 15 AGCTGCCAG GATTCCCTTA ATGGATGAGG TCCGGCGGC AACCAGACAA AAGTTGGCA 660
 GCTTAAGATA GTTGGAC 677

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1584UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

GATCCCATTT TGTCCTCTTC GGCTACCGGG ACGGCCAGTA GAGCATCCAG AATAGATGTT 60
 45 CACCAGTAGG CTTGCCCAAGT GCTCATTAGT TCGCGTCACA TGGCTGCCCG TGTACATGAC 120
 AGTGACACAC CATGTTGTAT TCATATCGAA GGTGGAAGGC CCTCGATGC GCCCAACGCT 180
 50 CAATCCAATG GACGGAGTTG CATCGGACTG GGTTTTGGTG TGAAGCTTG GAAAGACTAA 240
 TATTGGGAAC CTGAATCATG GGGACGTGGT GATCTTCCGC TCACCCATGA ACCCCAAGAA 300
 55 AGTATACTGC AAGCGCATCC AGGGTAAGCA GTATGATACG GTGGCAACG GGTATCCTTA 360

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TOCGAAGAGT ACCTGCGAAG TGCCAAAGTC GCACATATGG GTGAGGGGG ACAATGTCAC 420
 5 GCAGTCGGTG GACTCGAATC ACTTCGGGOC GATTTCGACG GGGCTTGTGG TAAGCGAGGT 480
 GACACGGGTC ATATGGCCGC CATCGAGATG GGGGCGAGAC CTGCAAGAGG GCATGGGTGG 540
 10 ACGGCGAGTT GTTGCTTCAT GATTGCGGGA GCGGGGTAG GCGAACTAC CGCTAAGTGT 600
 ACATAGCTGA AAGACTAGAT ATTATATAAT GTGGAACAAC GTGCTGCACT GCGGCAGAAG 660
 15 GATGGCTTAA GAATCGTTGT CCTCTCTCTT GAGGATCTCT GGGAAA 706

(2) INFORMATION FOR SEQ ID NO:945:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 716 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1585RP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

40 GATCCCCGTT GTTGTGCACG TGTGATTCAA TATATACATA CTGCAAGTCT GTACATGTGC 60
 TCTATTATAT ATGGTGCTCA TGTTCGGCTT ACATTCTTTC TTTATACAGT TCATGTCTTT 120
 45 CCGTGTGGC ATACCCAGTG ATGCCCGTCA TACCTGGTAA CCACAGTTTC TATAATCATT 180
 CAGGCTGAAC TGATCAATGG AGCTGCGTTT GCCGAATTTG ACGCAGAGGT TTGTATACAC 240
 50 ATTGATGTCC GCCCTGTAA AGCCCTTGCT AAACGTGCAG AAGCAATTCT TCGTTTGGG 300
 ACACGAAGTG CAAGGCTTGA ATGCTATCAA CTTATCCACA TGCTTCAGCA GCGTCAGTTC 360
 55 CTTTGTGAGC AGCGGCTGCC TCACCTGCTC TGAATCTGG CTAAGCCACT CGTTTGCCAG 420

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CTCAGACACA TTTAACGGTG CGTGAAGCAT CTCGTTGAAC GAGCCTGTGA CCGAGGCGTC 480

5 CTGGAACAGT ATCGTGATCG TGGCGTCACA CTTAATCTTC TTGGAGGGC AGATGTGCA 540

GCTGGGGGCC GTCCGCTGAC GCTTGACTT CGACGCGTG ATAAAGGTTG GCTCCTGTAG 600

10 CAGGAGTTC GGTGGGAAC AGTGGCTGC AGTCCCCCG TTGGAAGGCC GAAGCAGATT 660

CCGACATCAG CCGGACATC GACACGCGC GCGCGGACTC TGGCGAGGC GCGTGT 716

15 (2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 740 base pairs

20 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1585UP

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

35 GATCACTCTA CCGGGGACAG TTGATTGAGT CCAGTGAGT GAATGTCAGA GAGTCACCAT 60

TTTTCAACCT ATGACCTCA TGGGCCAGCA TGAGTCAAC CTTGCAGCCT TTAAATTTT 120

40 CTACATTTG CCGCAGAGTC TCATAGGAAA TAATCAATAC AGGCTTGACT ACATTACGGC 180

CCTGGGCAAT CGCCACTGC CTGACGGACT GTGCAACCGA GCCGTTGAA AGGGAACTTT 240

45 TACGTCCATC GATAGCCAGT GCGAAAGGG CATCGGGTCC CAACCACTTC ACAATCTCAT 300

TAGCCAGTT ATTAACCAGG GACGAAGGC AGACAATGAT GCACTTTTCA ATTGTAGGAC 360

50 GACCTTGGGA GCCCTGCCGT AGTAGGTCC ACATTAAAGC TATACATTGC AGCGTTTAC 420

CTAGACCCAT TTCATCAGC ATAATACACC CATAAGCCCC CCTATTTGAT TCTGAGTCA 480

55

EP 0 866 129 A2

TAGCTGCATT GGCATCCAAG ATCTCAGGCG AAGGGGTCCG CGTCGGGGTA AGAATGGGCG 540
 5 TCGGGGTCTC CTCAAGCACC TCACAACTA TTGGCTCACT ATCTTTACTA CCGGATCCT 600
 TACCAGTGCC ATCGTCTTGC ACCTGCGCGG CTGCCAAGAG AGCCTGTGTA TCACAAAAAT 660
 10 CCTTCATGCG CAGACCACTC ACACAGCGGT ACAGGAATCT TACCCCTTCC ACTTGATGAG 720
 GCGGTAAAT CCGCGCCAGA 740

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1586RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

GATCAGGCGT AAGGGCAGGA TATGAAGTAT GGAGAGTCT ATTTTAACT CAATGGCATA 60
 40 TAAACACCGC ATATTTCTTG TGGTATGAT AACTTCAAT ATCGAATCAG TCGCAGGTA 120
 GAGGGTGGT GAGAGTTTAC CAGGATATCC AGTTGTGCT GGGCCCGCAG CACCAAATAT 180
 45 AACTGAGAAT TTAAGTTTCT CGAAGAGAGT ATGCAACGGG GGCTTGTCCT CTACGATTAA 240
 AAGAGCACCA GCTTTCTCAT GCCTTCAACT ATGTCAATAT AAATATATTG CAAAAGGCTT 300
 50 AAGCTCTGTA TTGAGCCCCG GAAATGTTTC TAGCAATGTA GCTCTCTCAT CTTACATTAA 360
 GGCTGGAAT GTGCTGACCA ACTGCAAAAA CCCAGTCATA TCGTAAATAG TGATGATAGT 420
 55 CAGCGGATA TTTAACCGCG GGTGCAAAAA ATTGATTTCG CCCAGGATCG AACTGGGGAC 480

GTTCTGCGTG TTAAGCAGAT GCCATAACCG ACTAGACCAC GAAACCAACC TTGAAGAAOC 540
 5 CACGCGCGGA AACCGACCAA CACAACCGGT GCAAACCACG TGCGTGAOGA CTCITTTAGGC 600
 GTGTGCTAGG GGGGCGCCCA CTCGTACTTA TTTTATAAAC CTGGATCCA GGTGCGTCCA 660
 10 TATACAGGGC GATCGCGGCC ATCTGCAGCA GCCAGGAACG CA 702

(2) INFORMATION FOR SEQ ID NO:948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1586UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

GATCAACAAA GTCAATCCA AAATGTGCT GGGAGAGAAA AAGATTCGC CATCATTTGG 60
 35 CCTTTTCTAT AGCCATCAAT TCAACAATCG GTTAAGCGAT TTGAAGCCTT CAGCCCTTTA 120
 TGAGGGTGAT CCTGAGAAAC AAGATGGGAC TGCTACCGAT GGAAGCAGCG GTAGTGTCCA 180
 40 TGGGTATGCC ACTGATGATG ATATCATTGT CACAGGCGAG AACACCGTTT ACAGCCTAAG 240
 CCAAGGGATT GCATATCATA TAGATGAGGA AGGAACTAT TATTATGCTG GTATCGATCC 300
 45 GTTTACTGAT GCATTGGAAC AAGAGGCAGA TTGCTTATAT CATGAAAGTG AGGTAGAAAG 360
 CGTAAATGTC AACAACTTGG ACCATCTTTC TTCCGATATC AAGGAAGAAA ACATAGACCT 420
 50 CGATGGTAAC ATAGAATTGT ACGATTCTGA CTTTGACCAC ACTTCCTCG ACCAGGTCCC 480
 GAAGGCTACA GAAACAATCG AAAAATACAA TAATAACCAA TACTACAAGA TGAACACGCT 540
 55

AATCACTGAC TCATCAAATT GCCAGGGCAA CACTGTAGCG CTCTCATCTG ATTATGGAAC 600
AACTTCCGTG CATGTTGAAA ATGTCCTCTAA TGAGAATTCC TTGGGGTCAT CAGGCTACAA 660
GGAGATATTG CTGAAACTA TGATGACTAC CTTTACGAAG GGGACGAAGA TGATTTOGAT 720

(2) INFORMATION FOR SEQ ID NO:949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1587RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

GATCATCGAG AAGGAGCTGG AGGGCGTGGG CATCCGGCTG AACAAAGTGC CTCGGGACAT 60
CATTGTGAAG AAGAAGGAGA AGGGCGGTTT ATCGATCAGG AACACAGTGC CGCTGACACA 120
TTTGACCAC GACGGGATCC GCGCGGTGAT GAGTGAGTAC CGCATCAACA GCGCGGAGAT 180
TGCGTTCCGG TCGACGCGA CAGTTGACGA CCTGATGAC GTCTCGAGG CTCCAGCAG 240
GCGTTACATG CCGGCTATCT ACGTGCTGAA CAAGATGAC TCGCTGTCAG TGAAGAGTT 300
GGAGCTGCTG TACCGGATTC CGAATGCTGT GCCTATATCT AGTGGACGGG AGTGGAACTT 360
AGATGAGCTG CTCGAGGTCA TGTGGGATCG CCTGAACTTG GTGAGAGTTT ACACCAAGCC 420
CAAGGGGACC ATGCCCGACT TCAATGACCC GGTGTGTGTG CGGTCAGACC GTTGACACGT 480
GCGGGATTTC TGTAACCAA TCCACAAGTC TCTGGTTGAG GAGTTCCGGA ATGCTTTTGGT 540
TTACGGTAGC AGTGTGAAAC ACCAGCCTCA GTACGTGGGT CTTGCACACA CTCTAGAGGA 600

TGAAGACGTT GTGACAATTC TGAAGAAGTA ATGTCTTGGC ATTTATGCAT GGTTCATG 660

5 CACACGTTCT CGCGCTGC 678

(2) INFORMATION FOR SEQ ID NO:950:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 702 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1587UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

30 GATCCTAATA AAAGCTTTTC TGCAATGCT CTACCTAGC CTGGAAGTC GCGTAGGGCA 60
 CACGTTTCAA ATAGATGTGC AGGAGATACG ACCTGGGTAT CACCCCCCTT AATTGATTCT 120
 35 TTAGTGCAA CCAGATAGCC ATCAGGTTTC GCACGTTTGA AAGCCAACCG GGCTAGAACT 180
 AAGGACGGTG CGCACCCAC GCTTACCGAA CAGCGGCTG TCGCTCTGC TACTTCTGAT 240
 40 CGGATGCGTA TACACAAGTT TTGACAACTA AGTGTATCGA GGGCATGTC AATAACACAG 300
 ACAGCCTCAT CCACCGAAAT TCGATACACT GGTGGAAG CCTTTAAACC CTCCAATACC 360
 45 TCGTAGAAGG CATTGAAAT CGTTTGTAT TCATCGTAGG TATAGGGGAG GCAAACCACT 420
 TGGGGGCACA AGTCTTGGC TTGGAGACC CACATGCCAT TTTGTATTCC ACATTCCCGA 480
 50 GCAGCATAAT TACAGGAGGC AACGTCGAA GATGAACCC CATGACACAC TGCCAACGGT 540
 ACTTCGGCCT TGCTTGATA GCGCGCTTG ATGCTGAAA TAGTCGCAA AAAGCAATCA 600
 55 AAATCCACGT GGAAGACGTG TGCTGGTGA GCCCGCAAAT CATTTAGGC ACCTTCATTC 660

ATCCGGAGAT GCCTGTCGAG AAACCTCTCGC GTAGAGCCGC CT

702

5 (2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 685 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1588RP

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

25

GATCCTTTAG TTCTCGGAG TTTCAGGCTA GAGGTGCCAG AAAAGTTACC ACAGGGATAA 60

CTGGCTTGTG GCAGTCAAGC GTTCATAGCG ACATTGCTTT TTGATTCTTC GATGTGGGCT 120

30

CTTCCTATCA TACCGAAGCA GAATTCGGTA AGCGTTGGAT TGTTACCCA CTAATAGGGA 180

ACGTGAGCTG GGTTTAGACC GTCTGAGAC AGGTTAGTTT TACCTACTG ATGAATGTTA 240

35

TCGCAATAGT AATTGAACCT AGTACGAGAG GAACAGTTCA TTCGGATAAT TGGTTTTTGC 300

GGCTGTCCGA CCGGGCATTG CCGCGAAGCT ACCATCCGCT GGATTATGGC TGAACGCCCTC 360

40

TAAGTCAGAA TOCATGCTAG AACGCGATGA TTCTTTTCTT CGCACATTAT AGATGGATAC 420

GAATAAGGTG CTTTTAGCAT CGCTGAACCA TAGCAGGCCG GCAACTGGTG TTCAGACGGA 480

45

AAGGTCTGGG CCGGTGCCCG CGGATTGCAA TGTCATACTG CCGGAGAGTA AATCATTTGT 540

ACACGACTTA GATGTACAAC AGGGTATTGT AAGCAGTAGA GTAGCCTTGT TGTTACGATC 600

50

TGCTGAGATT AAGCCTTGGT TGTCGTATTT GTTTTCTATT TGAAGTCTG CAGGAGCAGG 660

CTTTGAAATA GAGTCTTATG TTATT 685

55

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1588UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

GATCCCGTAC	ACGAAGAAAA	TCGGACGGGC	CAACCAAACC	CAAAGTTCAA	CTACGAACTT	60
TTTAACTGCA	ACAACITTA	TATACGCTAT	TGGAGCTGGA	ATTACCGGG	CTGCTGGCAC	120
CAGACTTGCC	CTCCAATTGT	TCCTCGTTAA	GGTATTTACA	TTGTACTCAT	TOCAATTACA	180
AGACCCGTAT	GGGCCCTGTA	TGCTTATTTA	TTGTCACTAC	CTCCCTGAAT	TAGGATTTGG	240
TAATTTGCGC	GCCTGCTGCC	TTCCCTTGGAT	GTGGTAGCCG	TTTCTCAGGC	TCCCTCTCCG	300
GAATCGAACC	CTTATTCCCC	GTTACCCGTT	GAAACCATGG	TAGGCCACTA	TCCTACCATC	360
GAAAGTTGAT	AGGGCAGAAA	TTTGAATGAA	CCATCGCCAG	CACAAGGCA	TGCGATTGCA	420
AAAGTTATTA	TGAATCATCA	AAGAGTCCGA	AGACATTGAT	TTTTTATCTA	ATAAATACAT	480
CTCTTCCAAA	AGGTCGAGAT	TTTAAGCATG	TATTAGCTCT	AGAATTACCA	CAGATATCCA	540
TGTAGTAAAG	GAACTATCAA	ATAAACGATA	ACTGATTTAA	TGAGCCATTC	GCAGTTTCAC	600
TGTATAAATT	GCTTATACTT	AGACATGCAT	GGCTTAATCT	TTGAGACAAC	ATATGACTAC	660
TGGCAGGATC	AACCAGATAC	TATCTTAAAG	AACAACCGAA	AATGCGCAAG	CACACCACGG	720
GTC						723

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1589RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

GATCATTCAA GCATATTTAT TAATTAGATG ACATTAAACT ATTAGACCTT GGTITGGGTT	60
GCTGGACTTA GGGTGTGGT AGTCGGTGGG TTATATATTT TTTGTAGACA GTCACCAACA	120
CACITGATGT ATTCTTTTGA GCTGTGTGGG ATAGGCTCCG ATTGGATGCG GCACTGCTCA	180
TTGGCATCCT GCCCTCAGC AATAACCATA GGGGGCCCG CTAGAAGACC GAAAAAGTAG	240
GTTAGCTTCA TCTGTGATA TTATCTGTG TTTAATTAAA TGGAACTTTA GTGCTCTGGT	300
TCTCTGCCAT AGAGATCAGG ACCTTGGTTA GATATCGGIG CCTTATATA CACTGCTGCC	360
AAGGATCGAT GGACTGTAGC CGAGCACTT CCAACTCAA AGATCCGACA TCAATGTATT	420
ACTGAGAGCC AGTATACTTA CCGCTTATCA CACTAAACC CATAGCCATG GTTACGAAGA	480
TGCTGATCTA TCATCCACA CAGCTCGCCA CTGTAAACGG ACTTGAGGTG GGCGACAGAA	540
GGCACTACA GGATGAGCGT AAATCTCCAA CAGCTAGCAA CACATGCCAT TATTCTATAC	600
GAACAGTAAC GTGCTTGATA TTACAGAATA CCGATTAGGT TTTTCTCTGC CAGACCAAT	660
GCTATTGGTC AAACCTCAAT TTAGTCAGGC TTACATTACC TGCGTACCTC GAAGGTAGCA	720
ATGTTAGGCA CTCTGGCAGT A	741

(2) INFORMATION FOR SEQ ID NO:954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1589UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

25	GATCTTCTTG GCCATTATTG CAGTAGCGGT AGGCGGGCAT ATGAAATGAG ATCGCGGACG	60
	TCCTGCGCTT GAGCACCTGA AAAATGGCAG TAAAAGAAA CGATCCCCGC AACATTTGTT	120
30	CGAGTGACTT TTGAGGCAGA AGTACAGGCT TCAGCCCCGC GCTGCTTTGC TGTGGATTCA	180
	GACCACCGGT GGTGAAGGTG GTGGTACACT GGGTTCAGCT ATGCTCTCAC GCTGCAGTCC	240
35	AGGACAGACA TACCGCCAC TATAGCAGGC CGATCACATA CATAAGTAAG AAAATTAGCC	300
	CCAGTAGATT ATTGTGGGG TCATGCAGTG CTGCACCAAT GGTGATGTG GTGTTGCGCG	360
40	GTAGTCTGCC ACCATGTGA TACCGGAGC CGCCAGATCC AACCGGAGGT ATAAAACTG	420
	GTAATGGGAC AAATCGGGG CCGCCCCGC CGCGCCTCC GCCCCGTAA GAAGGCAACC	480
45	CGGCGCTTTG CGCTCCTCCA TTGAGTCTT TTGGGCTGTT CGGTGGCGGC TGTGCTCCGC	540
	CGTTTGGGCC TTAGGGCTG TACGGGGGCG GCTGTGCGCG CGGTTCGGGT CTTTCGGGCT	600
50	GTACGGAGGC GGTGCGCCTT TCGGATCCTT CGGGCTGTAC GGAGGCGGTG CTCCTTTCCG	660
	ATCCTTCGGG CTGTATGCCG GAAGAACACC CTTCGG	696

(2) INFORMATION FOR SEQ ID NO:955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1590RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

GATCATAATG ATTTGTCCTA ATTCTTTTCT TAATTATTCA TTAAATAATT AATTAATATT 60
 TTATTAATAA AAAATATTKA KAKKKATGTT CGTTTATGAT AAATTCTAAA ACTTIGSARC 120
 ACGAACTGAA GACAACTATG TAACGCTGT AATTAATTAT AAATTATTAT AATTAAATAT 180
 TCAAAAAATG GTAAGATTTA TCGAGGATTA TCGAATTAAA TAACATGTC CACTGCTTAA 240
 GTCTGTAACC GTCTATTGTT TTGATTTTTA TTATTGCTAA CGTAGTCATC AGGCGGAATA 300
 CTTTAATTTT CATTTAATTT ATTCTTTAAT TAATAAAAAA TAAATAGGTA TTCATTGTTT 360
 ACTGCTAAAA CTACTCGGGT ATCGAATCOG ATTTGCTACT TTAGCCTTCG TTCTCAATG 420
 TCAATTAATA TATAATTAA ATTTTCACTT TATAAGTCTT ATTCATATAA TTATTATTTC 480
 ATCTTTACTT GAATAATTCT TAAATTATTT TTATTAATTC TAATTATTAT TTTAAATAAT 540
 CATCTACGA ACCCTTTAAG CCATTACGAT TAACGCTAAC CCCCTTTGTC TTACCGCAGC 600
 TGCTGGCACA AATTTTGGTT GGGATTATTT AATTATATAT 640

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1590UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

GATCTATTAT TAGAGGTAAT ACATTTAAAC TATTATCTAA ATTCTTCTTC TTCTTATTTA	60
TTCTTAACTT TATCTTATTA GGTAAATTAG GTGAATGTCA TGTGAAGTA CCATTATTTT	120
TAATAGGTCA AATTGTACA TTTATTTATT TTGCTTATTT CTTAATCTTA GTACCTATTA	180
TTTCTATAAT TGAAAATATT TTATTTTATT TACTAAATAA AAAATAATAA TTAAATAAAT	240
AATAATAATA TTCATTAAAT ACTTTAATAT TAATATTTAT ATATTATACT TCITTATCAT	300
TTATGAGGGT ACCTCATATT GCTGACTAGC AATAGGGGGG TGAACCTAC GCACCTAAAT	360
GATAAGAGTT TATCATTAAG TTATATACTA TATATTATAA GTAAATTATC AAACCATATA	420
TAAGGTATAT ATATTAAGAA AGTTTGACTG AGTGGTTTAA AGTGTAAATAT TTGAGCTATT	480
ATAAATCTTT ATGATTTTCAT AGGTTCGAAT CCTATAACTT TCGTATTAAA TAATTATTTA	540
AAATAATTAA AATAGTTTAA TAATAATGAG AACATGATGT TGGTTCAGAT TAAGGCTAA	600
CTAAGGACAT TACACATGCG AATCAAACGT TAATATTATT AATTAATAGT ATTAATAAGT	660
GGTGTACTCG TGAGTAAAAA TTAAGAATAA TGAACCTAAA TTAACTAAA TAT	713

(2) INFORMATION FOR SEQ ID NO:957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

EP 0 866 129 A2

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1591RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

GATCATAAGC ATCTTTAGCT CCACTATCCA TGTCGAAAT TTGCAGCTGA TAATAAAGTG	60
GTGTGTGGC CGAGCGGTCT AAGGCGCTG ATTCAAGTGT ATGCTTACAG CTGTTACAGT	120
TGGACACTCA GGTATCGTAA GATGCAGGAG TTGGAATCTC CTGCAACCA ATTATTTTTT	180
TTTTTTGGAG TTCCAATGCA ATATCAATTC TACTGCTGCG AAAAGGTCTC GTCAGCAGAT	240
AAAAGAATAT AGAATATGTA TATTTATATA CAAGAAGCGT TAACTGACTT TTTATTTGTTA	300
TAATGCCATT CGAAGAGATA TCGCTTATTA ACAGCAATAC CCGCTGCAG GTCCCCGCCA	360
ACCGTTGTCC AGTGATGCAA AATATATACC TCGCATGATA AAGAAGGCC TTCAATATCAA	420
ATGGCCCAGG CATTAAATATC ACCGTTGCG CGGCTTCAA CCAAGTAGCC ATCTTTATAT	480
CTGACATATT CCACGGCATT CTCACTATGC TCATCACCGC CGCAAAACCA ATGCTTCTTC	540
TCTTGCCGGT TGTAAACCTT CACTGTACCT TCCTGGTTAG CGCAACTAT CTTATTCAAG	600
TCAAACGCA AACATGTCAC CGGGTGTTC TACGAAAATG TATCAGCCAA TGTACCGGTA	660
CGTAGATCCC AGATCTAATG CTGTTATCCA AGGAACCACT CACAAGGTTT AGAGAATCAA	720

(2) INFORMATION FOR SEQ ID NO:958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1591UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

GATCCCCAAT GATCCCTCTC CGGGCTACAA CATCGAGCAG CTGCTAAAC AGTCAAGAA	60
CAAGGACAGG CTGGTGAAC TGCTTATAC TGTGAAGGG ATGGACCTCT CCATGAGCG	120
TATTCTGGCC CACATCGACT CGCTCGGAA GGACCTATTT CGTCGAAACA CGAAGAACTA	180
CAAGCTCTTC GACCGCGAGA CCGCAAGCA GCTCGTACC GTAGAGGACC TGTGCTACTC	240
CCTACAGGAG CACCTGTTTG CCATGCTCGT GGAGATTACC GAGGTGCCA TGGCACATGT	300
GAATCTAAC CAGGTGTGA TTGTGGGGG TGTGGGCTGC AATGTCCGAC TGCAGCAGAT	360
GATGGCGAGT ATGTGCCAGA GCAGGGCGA CGGCCAAGTT CATGGGACG AGGAGCGCTT	420
CTGTATTGAC AACGGTGCA TGATTGCACA GGCTGGTCTA CTTCAATATC GCATGGGGA	480
TATAGTAAAA GACTTCTCAG AGACCGTGT CACGCAGAG TTCGGACTG ATGAGGTTTA	540
CGTATCGTGG CGGACTAAG TGTGTACCA GTTTAATAGA AGTTTACCG CCTAATATA	600
GCTGTTAACC ATCAGTGGCC TCGATCAGC TGGTCCAGAA CAGTAGTGC CCGTGGCTGT	660
CACCAGCCTA CGGGCCAGC GGCAGGTATC CTGTTG	697

(2) INFORMATION FOR SEQ ID NO:959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 669 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1592RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

GATCAGGAAC	TOGCAGACCT	TGCTCTCTG	GTGCOCTGC	AACTGGATGA	TCTGCOCCAT	60
CTGTGTGTC	TTGAACATGT	TGCGTTGCA	GCCAAAGTCC	TTCGCAAGA	CCTTCAAGA	120
TGCGCTGAG	GTGTACTTC	TGCGGATGC	CCTGCAAGT	GGTCAAGT	TTCTGCGT	180
TTCTCTGCTG	GATACGGATG	TGGATGTAGT	TGGAGGAGGA	GGCTTGTG	TGCGCGTGT	240
CAGCAAAGGG	GTGGAACGAC	TTGAGGTTTT	CGATAGACAT	GGTGGCGGTG	GGGTGTGAGG	300
TACAAGGTAA	GCAGAGAAA	TTTTCAGCTG	TCCTTTTAAA	AGCGCGCACC	TGCGTCTTG	360
GAACGCATTC	GCTTATTTGT	GAACCATATT	CTTATCTGTA	TAGGTGTAA	CCGCAATTC	420
TCTGCAATG	CCGCTCTTC	TTTGGCGT	GGACAACGCT	TCCTTTCAA	CACACTTTC	480
AGGAACCTCT	TTGTTTCTT	GGTAAACT	GTCTCTCT	GCTGTTATC	TCCTGTTAGT	540
AAGGCAGAGG	CTGGGATTAC	AATGAGACTC	GTACACATA	CTTACCTAG	CAGAACACTG	600
CAAATCGCT	GGATTGCTTG	AGCTGTTCT	TCAATACYT	ACATTTGAGT	TGTGGGGAGC	660
GAGGAAAGA						669

(2) INFORMATION FOR SEQ ID NO:960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1592UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

5 GATCCACTTG TTAACGTGG CGCCGCCAAT CCTCATCCCT CCATATGTAA CCACAAGTGG 60
TTTGTATCCC AACAAATTGCA GCTCAATTGC CATCAAGTAC GCGTATCCCC CGOCTAGAGA 120
10 ATGGCCAGTT ATAATTACCT CATAGTCTGG ATGAGCATCA TGTACTGGCT TAAACGGGA 180
ATAGATATCG TTGTACGCCA ACTTAAATG CTCATATACG CCCGAGTGTA CAAAGCAATC 240
15 TCCCGTACAC TTTCCAGGCG CACTAAGTGG CTGGTATGGA ACCCCAGGAA AAATGAAATC 300
CACAATCCAA TCTTGAATTG TTACCGACCC TCTAAATATG ATCGAAATCT GCTTAGCCGT 360
20 GTCATTTATT GCTATCATGC TATAACAGGA AAATGCCCC CGGTCATGT CCGGATCAAA 420
GTCATTTATT GCTATCATGC TATAACAGGA AAATGCCCC CGGTCATGT CCGGATCAAA 420
25 AACTTTAACT ACTTGAGTCC CTGTTGTTC ATGTACCACT TACCGTCATG AAAAGGGTCA 480
GTGAGTATTA AAGTATTCAC GCAGTAAACG CTGTTAGTGA GATATGACAC ATATTTCAAT 540
30 GTATCAAACA TCTCATCAGA GAAAGAATGG ACATGAAGGA AAAAAGGC 588

(2) INFORMATION FOR SEQ ID NO:961:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 718 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1593RP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

55 GATCGAAATA GACAACTCTG CAACGGTGTG CAAATGCCCC AGCAACTTCC AGGAATAAAC 60

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ACAAGTAGAC CATAGCATCC AAGTACCTAT GCTOCTOGCC TTACTATGTC TTTGGAATGC 120

5 AAAGGACCAA ACGTGCTGCA AGACGGAGGG AGAATTCTTC AGAAGAATTA CATTATACAG 180

GCTCGAAGGT GTGACAGOGA ACCTATCATG GTCTCTCTTT GTGGTTCCTG CCAAAGAGA 240

10 AGACCAGACC TCTTCAAGGG TGA CTGCAAT TGGTTGTCTA AGGTGGCCAG TGACAOGAAC 300

AACCGCTTTT CTGGGCAAGT CAGOGAGTTT TATOGTACTA GTAACCGGT TATTTCCAC 360

15 TAGGAGCAAT GCATTCAAAT AAGCAGCCCA CAGTTCCAA TCAAATTCAC TGGCATTCCT 420

ATCTGGAGGA ACATTATATT GGATTAAACAG ACTTTTGTAC ATTTCCAATA TAGTAACGCA 480

20 TGTOCTCAA AATAGGGCAT GTAGTGAAAT CCACTTACGG GAGGGCATGT ATCCATCTTT 540

GGTCAATATT GTTACAGTAT TAACGGCACT TATAATATCT TCCTTGGTAA ACOGGTAAT 600

25 GTTAAATACA GATGTTAAAA TAGGATCATT GGCGCAATCT TCACAACTT GTATAAATGA 660

GCTGCCATGT CCATATATTT CTTCCTACAA TTTGGGCTAA AGTTGCCAAT ATAGTACC 718

30 (2) INFORMATION FOR SEQ ID NO:962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1593UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

50 GATCGATCTG TTGTAATTTG GACACGGGGA GCTGCAAGCA GGGTAACGTA TGAGGGGTGC 60

TGTGGGGCCT GCGATGGCT ATAGATAGGG TCATAACCACA TCATCGGTTT GCGGGGTGG 120

55

TATAGCATTT GGAGGACAGG TTAGCCCGGA GCCACAGCAT AGACAGGTTT ACGAGGCTTG 180
 5 CAGCAGAGGA AAAGATGGGC AAGCGATTTG ACTGGCAGCC GACGGGGAGG CTGGTGCGCG 240
 GCCGGATTAT CCGGGCGTTT TTGCCCTTGA AGCGGCACCC GCAGCAGCTG CTGGACAACC 300
 10 CGAACTACAC GAACCTGTAC CCGGGGGATG AGGTGTACAG CTTTGAGGAG ACGGCGGACG 360
 GGCGATGGTG TCGCGTGTAC CAGGTGGTCC AACCGCTGCC GGAGGACTTT ATCTCGACCA 420
 15 TGAAGCGGTT CTGGACAAG CTGCCGGAGG AGCAGCACCG CGTGGTGGTG TGCCCGAAGG 480
 CGTTTGTGCA CTGGTATGAC GACGAAGTGG TGACCTTTCC GTTCTGGAC CTGCCCGACG 540
 20 AGCGGGAGGT GAAGCGGGAG GTGGCGGAGA CGGACGTGCC GAGCCTGCAC GACCTCTGCG 600
 ATAGGGAAGA CTGGGGGAC CTGGAGCTAT TCCGCAGCT GCGGCGGACG CG 652

(2) INFORMATION FOR SEQ ID NO:963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1594RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

GATCAAGACT GCCGAAGTGC TAGTTTCTTG CTTATGAGG TTTGGAATCT TGTCCAGAT 60
 50 GCGGGCGTTC ACCAGGCGGT TACGCAACTC AAAGTGTCA TTAAAGTGC GAGCAAACCA 120
 GTAGGAGGAT TCTAGAAGAC TGGTAAGCCG GATGCGTTT TTGAAGGGTA TTGCGTTTGC 180
 55 GAAGTTCTCA TCCGCAAAGA GCTCGCTAAG CGACTCTATC ATAAGCAGCT GCAGGACACA 240

TTTTACCACG ATGGTATTCT TAATACTTAC ACGTGCCCA ATCTCCTCGC TGCTTTTGGT 300
 5 GCGCAGAGT CCGCTCATAG GCTTATCCTC TTCAGTACTG GCGTTGCCAA CATCCTCGCC 360
 CTTCCTCTCG CGTTGGGCAC GCTCGACTTC CCGATCAACA TCACTGGCAC ATGATTGGGT 420
 10 TTCAGCAGTA CCGTTGGTGT TGATTGTGGC TACTGATGGC TTTCTTCAC GCTTCAATGG 480
 ATCTGACTCA AAAAGTTCCTG TGGCAGTGGT AAGCTCAAAT AACCGGGCAA ACGAGTTGGT 540
 15 AACCTGCTCC CAATGCGTTG TCCCGAACTT GTTGGTGTTC TGGATAATCA ATTGCTGCAG 600
 ACAAGACCTA CCAATCCTGG CAATGGTGTC ATTTTCCTGA CAGATGCAAG AGACTAACAA 660
 20 AACCAGGAAG CCATCCAACA TTTCGTTTCAG TGAATCAAAG TAATGCGTAA CAGGGC 716

(2) INFORMATION FOR SEQ ID NO:964:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 695 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1594UP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

45 GATCTGAATT TAAACGTGAG ATACCCGTTT TTCTGACAGA GATATATTTT CCTATATCTC 60
 ACATGAAATC TTCTACTCCA CATCAGAAGA GGTATTTTTT GAGTGTATC CAACGACTAT 120
 50 GCAATGACCC GAGAACCTTA ATTGAATTCT ACCTAAATTA TGA CTGGGAC AGTAGTATGC 180
 CTAATATTGT CGAGACTGTT GTGGATTATT TGACGGGACT GGCGTAACA CGTGTGATA 240
 55 TCACCGCATC ACAGCGTGGG TACTATGATG AACAAAGTGAA CAAACCCCTT GCAACGIWTA 300

ACCTATCGCA GTTGCCCTTA TTATCCATAT CTAATGTTAG CAGTATGTCT GTTGCTCCAC 360
 5 AGCAACTCCA ATTCCCGGTG GAATTTGGGC TTAAAATGAC CTGGTTGAAA TGTATGTTGG 420
 CCGTGCTAAG ATCACTAAAT TCTTGGGCGG ACAAGGCGAC GGCTCCAAAT GGCACATTAA 480
 10 ACCACAATAG GGCATCTGTT GGCTCCAGTA CGATTGAAAG GAAGCACTCT TCGGCTTTTA 540
 GCTCTTTTCAG TCACACTATG AACACAACAC CTGTAGGAGA CCAGAATAGT GTCCAACAAT 600
 15 CGGAAGCGAG TGAGGATATT GATGATCCCA CACAGTTTGA AAATTGAG TTAAGGAAAA 660
 CAGAACTGCA AAAATGTATT CGGTATTCA ACTTC 695

(2) INFORMATION FOR SEQ ID NO:965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1595RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

GATCTTGCTG CTATCCAGAA ATGGGAAGTT CTTAGACAAC GGGGAATTAA GGGGCTTTTC 60
 CAATATTTTG AGCGTCGTTT CATAGCTCGG AAGACGCAGC AGAAGCCCCC CCAGTAGTGT 120
 CTGTTTCATGT TCGCTCATGA AAGGTGTCTC TATCAAATCT AGCTCCATCA TCGCAGAGTA 180
 GTTATTATCT TTCTTCCAAG ACAGACGCAC ATGCCGCAAC TTGTCAGGA TTACAGTAAA 240
 ATAATGGTAG AACCGCGGAC TCACAGAAGC GACGACCGCT CGAAATGAAG TCGGCCCCGTA 300
 55 GAAGATCGTG CGGCCCTGCT TCTCTATCAC AAGATGGAAC TGGGAAAGTC TGTTCACGGG 360

GGACACCGTG CCCATAACGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGTCTTCAT 420

5 CCGCGCGAGC TCAGTCTCAA GCTGCTCGAT CCGTGCAGC AGCTCCACAT TGGGCGTGA 480

GCTGAACAGC TCCCGTGAGT TCACGTCGTG CGTAAACTCA GACAGGTACA CACACTGGG 540

10 CAGGCGTTCC CAATACATGT AGAGCACTTC GCGCGCGCT TGTTCACATT GACGCGCGC 600

TTGCGGCAGA ACACGCACGA CTGCTGACC TTCCGCTGG TTTTCACAAT CTGCCATCG 660

15 GACTCTGCCA TCCCGCCAGC TTCAAGCAAA ATGAGTAGGC TATATTATT 709

(2) INFORMATION FOR SEQ ID NO:966:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 731 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1595UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

GATCGCGGAC GTGGAGCACT GGCCGGAGAT GCGCGCGGCC ATCCTGGTGG TTCTGCGGA 60

40 CCGCAAGGGA CACGCCATCG ACGAGCGGTA TGCAGCAGAC GGTGCACAG TGGACCTCT 120

TCAAGGAGCG CGTCGCGAG GTGGTGCCGC GGCGGTACGG AGAGATGGCG GCGGCGATCC 180

45 GCGCGCGCGA CTTCGCGAG TTTGCGCGCC TGAAGATGCA GGACTOGAAC TCGTTTCAG 240

CCACCTGCCT GGACTCATTT CCGCCGATCT TCTACATGAA CGACACTTCG CGCCGGATTG 300

50 TCAAGCTGTG TCATCTGATC AACGAGTTCT ACAACGAGAC CATCGTGGCG TACACGTTTG 360

ACGCGGGTCC GAACGCGGTG CTCTATTACT TGGCGGAGAA CGAGGCGCGG CTCTGCGGCT 420

55

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5 TCCTCTCTGC CGTCTTTGGC GCCAACGACG GCTGGGAGAC CACGTTCTCG ACCGAGCAGC 480
 GCGCCACCTT CGCCGCGCAG TTGACGAGT GGTGCGCGG CAAGCTTGG ACCGACCTGG 540
 ACGACGAATT GCACAGAAGA ATTGCCCCGC TCATCTTCAC GAAGGTGGG CCAGGGCCCA 600
 10 GGACACTAAA TCCTCGCTCA TCGACCGAG ACCGGCCTGC CCGCTGACG CTATTCTCT 660
 GCTATTTTCT GCTCTGTATA CCCTGCCAGA CGCGCTATAT ATATAGAATA TGCATTGCGA 720
 15 CGCTTACGCT T 731

(2) INFORMATION FOR SEQ ID NO:967:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 672 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1596RP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

40 GATCGACAAT CTGAGCGAAA TATTTAGCAC GACATGCTAC ATGGGCTCTA CGGTGATAGT 60
 ATGGGAGTGG AGCAACCGGC TGTCATACT GGAGGCCAGG CGCCAGGCGC AGAGCATTTCT 120
 45 GGGGCGGCGG GTGTATGAGG ACGAGGAGCA GGGGTACAAC TTGCGCGAT ATCGGCTGAA 180
 GATTGAGACC GCATTGACCA GCAAGTCAGA TGAAGGCGAC ACCACATCAG CGACTACCTT 240
 50 TGCTGCACCG AGATCTGGC GCTTCGAAGG GAAAGGCGG CCCCAATCCC CAGTCTATGT 300
 TCAAGAGGGC GAACAGCAGG CCGTCATGGC ATTCAATAAG CGAATGGCA CTOGAGCGTT 360
 55 GGCACATCAT GTGCTGGATA GCATCATATA CTACACAGAC AAGGTGGTGG TGAAGGGCT 420

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TGGAAATTTG TCCGCGAGCT TACCTTCCAA GACCTCTCTG GCGACAAGCG TCAGGGGTGG 480
 5 TGTAAGGAAA CGCATTGGTC TCGAAGGGCG AAATGATGTC TTTGTATACC GCACAAAAGA 540
 CCTGGTATTC GATAGTGATG AAGATATACC CAGAACCTAA CTACTTGIGT CGATATTCTT 600
 10 CACACCGCCT GGTGCGGAAC CGGGGCGATA CATTGTTTTT ACACAAGAGG GGTTGATGCA 660
 TAAAACGGCG TT 672

(2) INFORMATION FOR SEQ ID NO:968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1596UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

GATCTTCGTA TCCATGTGCG AAAGCTCTCT CAAAATCTTT TCGTCTOCAT CATGAGAGGC 60
 40 TGCTACAGCT TTTGAGCCGA TAGAATTGGA AATACCATTG GAGATTGCTA TTAGTAGGAA 120
 GACAATATAA GTACCATCTG TCGATGGGGC AGAGGCTTTA TCAAGAAGGT CCATCAGCTT 180
 45 GTTCTTGGAT ACAGCAGTCT CATTTAATAA TAATGCCTGC TCACCACTGG GCAAAAATTC 240
 AGAAACATTG AGCAGTTCAG AGAGTGAGTT CGACTCAAAG TTTTCGGTCA TTGTCTCTAA 300
 50 CAAGACAAAA ACAACGTCCT TCCTGCTCTC ATGAACATCA TAAGCCTTGA AAACCTOGAG 360
 CAAAATAGTA TTGTCTGGA TCACGTTCAA AAATACCTCT AGAATTAATG CCTTCTCCA 420
 55 CAATAAAGTG TCAGATTTAG GAGACAGAGT GTGGATTAAAT AATGATAAAA TAACTTCCAA 480

TTCCAATTCC AGCAATGTCA AATACTGAAC CTTTATGAGA ATGTAATACA TCTGGGCGTA 540
 5 CGAACCACAA TTGCAAAATT TTTGGATGAG GAAATGTACC TCAATAGCAG CGGCACCGCC 600
 TTTGTTGCA ACAGAAATAA CAGATCTCGG TGTGTCAAAA ATAATAATTC ATAGTTCAAT 660
 10 AAAACCAGTT CTAGGAGCTC TAATOCATAC TCCTCATTTA TGCAATTGCT ATCCAGCAAT 720
 GT 722

(2) INFORMATION FOR SEQ ID NO:969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1597RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

GATCCATCAG CGGGCTACG GAAATCCTGC CCATAGAATG ACTCTCCAAA CCCCTCTGAA 60
 CTATCAGCAA AAGCTCAACA GCATRCACG GTGCGATGCC CAGCAAAAAC AGATCCAGCG 120
 TCAGATAAGC GCTGCCARCG CACTCGATGA CGGAATACC ATCACCGCAA TGGTCCAGCA 180
 TTTGATGCCC AAGAAGAAAG ACCAGCCACC GCAGCAACAG GGACCTATG GCTCTCCGCC 240
 AACTCTGGC AACAGCTCCA CGTACGCCG CAGCCCTGCT GCCACCGGC CGTCTGCATC 300
 CGTAAATGCT CCGCGCGCCG ATGACGCCA AAACGCTGTG CCACAGCGGC ACAGCGCCCC 360
 TGGCTATCC GCTAACGGTA ACACAGCCCC TATGTGGGA AACTCGGTTA GCCTTAGTAA 420
 TGGCTCATCA GCAGGCGCCG GTTTGTACA ACAGTCAAAC TCTCTGGAAT GGAAGCAGAC 480

ACGCCAAGC AGTGGCGGAA GCGTAACCGA AAGAAAGCCA AAGCTGCTC TATTOGCTAA 540
 5 GAAAAAATAA TATCATGCGA CCTATCATTT ACACATATTC TAACGTTCCA CCTGTGTTAG 600
 TGTACTCATT TAATTAATTC ATTAGTGCTG CCACTGCTGC AGACATGTGG CAAGAGGCAA 660
 10 AAATGGTTCC TAGCGGGATC GAACCGCT 688

(2) INFORMATION FOR SEQ ID NO:970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1597UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

GATOGAGGCA GCGGTACCGT CTTTGTGTAC GCATGCGCAG AGTACTGCGG GATACAGGCG 60
 AACATCTTAC GCTGACTACA GTTCCTGGAC ACACCACCTT ACAGCTTTGG GCGTGGGTTA 120
 40 TTGGTGCTCG AAGATATGAT GTTCGGAATT TTCACTCGC CGTCCGGCCT GATGAAACTG 180
 GAAGACAAGA CCTACAGTCA TCTAGCCAAC ATAACGCCCT GTAGTCGGGC TCTOGAAACG 240
 45 AGGTTAGAGC GTAGGAGATG CTCCACGGCG CCGGTGCGT ACAGAGAAGA ACAAGACCGC 300
 CGCATCTCTT TTTATTTACT TGATTAAACT CTGGCCAGT CTGGTTTCCA CTGACAAAGT 360
 50 GCCCACCAGA TGGATCGCGG GCGCGGTGAT CCTGCCCCGG CGATAGCGG CGACCGGAGC 420
 TTGCGTGGGT TTCACCTGCA TCTGCACAAG ATGTTGCTAC GCGGTAGAAG CAGCGCGTGG 480
 55 GAGGCGCAGC GCGCGCAAAC AGGAGGTCAG TCTGACGGC TACTTCGCCC GCGCTGCTGC 540

ACCGGCTGAA TTGGGCTCCC GGCAAGTCTT GATTGCTACG TTGAGTCATA GTCTCAGTAA 600
5 TTATCGCATG GTGTACTG CGTTGCACTG GACCACACTG TGGGCTCCTT TTGGCCCAACA 660
GATGAACCTG CCATCAGCTC TCGCCAGGA CGGTCACAAC AGGCAGCAGT AC 712

10 (2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 740 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: PAG1598RP

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

GATCCTCATA ATCATAGTAC AATATCATTT CCAATAAATG GAATAGCACT AAATAAATTA 60
35 GTAATAACAG TAGCACTCA ATGTGACATT TGTCATATA CTAAACAATA ACCTAAGAAA 120
GCTGCTGCTA TAGTTAAAT AAAGATAATA ACACCAACTG TTCATACAAT AACTCTAGGT 180
40 GATTTATAAG AACCATAATA TAAACCTTTA CCAATATGAA TATACATACA AATAAAGAAG 240
AATGAAGCAC CATTAGATG CATATATCTA ATTAATCAAC CTAGTTGTAC ATCTCTCATA 300
45 ATATGTTCTA CTGATGAGAA AGCTAATTCA ATATTAGATG AATAATGCAT AGCTAAAAAA 360
ATACCAGTAA GAATTTGAAT AACTAAACAT AAACCTAATA AAGAACCTAA ATTTTCATCA 420
50 TAATTAATTG ATGATGGTTG AGGTGAATCA ATAACATAAC TATTAACTAA ATTTAAATAT 480
AAATTTGATT TTCTATATGC CATATATTTT ATTATTAAAA TATTATTAAA TTATTATTTA 540
55 ATAAATATTA GATTATAATA TAATTCCTTA TAATAAATTA TATTATTTAA TTAATATATT 600

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AATTTATTAT TTATTATTTA TTAATATTTA TATAATCTTT ATAGGGAATT GAACCTAATA 660
 5 AACCATTAAAG ATTTAATTAT TTAATTATTT AATTATTTTA ATTATTTAAT TTATAAATTA 720
 TTAATTAGAG AGATAAGGGT 740

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1598UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

GATCTTATCG TCTAATGGTT ACGACATCAT CTCTTCATGT TGAAAATATC GGTTCATTC 60
 CGATTAAGAT TATTAATATA TTTTAATAAT TATTATAATT AACAAATATTA ATTAGAGGGG 120
 TACCAACATA TTGCTAACTA GCAATAGGGG TGTGTACCTT ATCTCTCTAA TTAATAATTT 180
 ATAAATTAAA TAATTAAATA AATTAAATAA TTAAATAATT AAATCTTAAT GGTTTATTAG 240
 GTTCAATTCC TATAAAGATT ATATAAATAT TAATAAATAA TAAATAATAA ATTAAATATAT 300
 TAATTAAATA ATATAATTTA TTATAAAGAA TTATATTATA ATCTAATATT TATTAAATAA 360
 TAATTTAATA ATATTTTAAAT AATAAAATAT ATGGCATATA GAAAATCAAA TTTATATTTA 420
 AATTTAGTTA ATAGTTATGT TATTGATTCA CCTCAACCAT CATCAATTAA TTATTGATGA 480
 AATTTAGGTT CTTTATTAGG TTTATGTTTA GTTATTCAAA TTCTTACTGG TATTTTMTTA 540
 GCTATGCATT ATTCATCTAA TATTGAATTA GCTTTCTCAT CAGTAGAACA TATTATGAGA 600

EP 0 866 129 A2

GATGTTCAAC TAGGTTGATT AATTAGATAT ATGCATCTTA ATGGTGCTTC ATTCTTCTTT 660

5 ATTTGTATGT ATATTCAATAT TGGGTAAA 688

(2) INFORMATION FOR SEQ ID NO:973:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 625 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1600RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

30 GATCTAAAAG AATCCATGTA TGTACACATA TTACGGAGGG TTAAGGTGAC GAACGGTAGC 60
 TACAGGCTTA TAAATCTGGG TTCTTTTGCA AAAGTTCATG CAACTCATCT GGGACGTTGC 120
 35 GCCAGTCTTC GGCAATCCAT TTCTTTATCC TATCTTCATC GGCTGTGCT AGTATATCTA 180
 CTTCAGAGA GCTCTGGCA CATGTAAAT TGCCAGCGG AGAGAGGAGA GGCGAAGATT 240
 40 CTTGAGTGGG GTAAGAACT TGTTTGTATG GTATGCTGCT AGCCATCTTC TTCCGTCTGT 300
 GTTCTTACC GTTGTTTAAT GATACTCCGA TATAATGTTT TATTAACCTC TCIGCGTATG 360
 45 GGGCAAGTT TTTGGGCTG TAGTGGCCA CATATTTGCA CTTCCAGTAT ACAGACCAAT 420
 GTAGTTCACC ATATGCCGGG ATGTTCTTAT GTCTACCAAG GTTAGGCACA TAAACGTTTT 480
 50 TCCATTGGCA ATTTTATCT TCAATCTTA TGCCGATGAA CATCATTTCC ACTATCCACC 540
 AGGCAATGAA CTGAAATATA CTCTTTGTTT CATGTCCATC GTTCTTTGCT GGCCGGATTA 600
 55 TACATCTCCG GAAGGAAGGC CTGGG 625

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1600UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

25	GATCAAGCAG CTACTGCTCA OCTGGAAGAA GCAGGGCCAC AAGGCCCTGC TCTTCAOCCA	60
	GTCCAGGCAG ATGCTCGACA TCCTGGAGGC CTACATCTCG CACAAAGATC CCGAGCTGGC	120
30	AGGCCTACAG TACCTCCGGA TGGACGGAAC CACAAACATC GCACACGGGC AGGCCCTCGT	180
	GGACCGTTTC AACAAACGGC CGTACCACCT CTTTCTTCTG ACCACCCGCG TGGGGGGCCT	240
35	CGCGGTCAAC CTCACGGGCG CGAACAGAAT CATCATCTTC GACCCCGACT GGAACCCCTC	300
	CACGGAOCTG CAGGCCCGCG AGCGCGCCTG GCGCATAGGC CAGAAGCGCG ACGTGACTAT	360
40	CTACCTGCTC ATGGTCGCG GCTCCATCGA GGAGAAGATA TACCACCGCC AGATCTTCAA	420
	GCAGTTTCTC ACCAACAAGG TCCTCAGCGA CCCCAAGCAG AAGCGCTTCT TCAAGATGAA	480
45	CGAGCTGCAC GACCTCTTCT CCTTCGGCCC GGGCGCCGCG AGCGACTCCT TTGCTCTGA	540
	GATCGAGCAG CAGACCGCCT CCTTCGCGCG CCAGCCGGGC GCCCAGGCA CCGACGACTA	600
50	CGACTCCGTC CAGCGTTTCG AGGGCGTCTC CAAGCTGGAG GGCTTCTTCA AGGCCA	656

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

EP 0 866 129 A2

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1601RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

20	GATCTTTTTC CCCGCAAAC CGCACACTC GTTCCAGGGG TACTTGGGCA AAAAAAGGC	60
	GACGGAGAGC AAGGTTCTAC GCGATGTTTT CAGGAAGGGA GATGCATGGT ACCGGTCAGG	120
25	CGATCTCTTG AAATCCGACA AGTACGGGCA ATGGTACTTC GTGGACCGGA TGGGTGATAC	180
	GTACCGGTGG AAATCCGAAA ATGTCTCGAC TACCGAGGTG GAGAATCAGT TGCTCTCGTT	240
30	CAACAAGGAC CTCCTTGACT GTTGGTGTGT AGTGGGCTG AAGATTCAA GCTACGAGGG	300
	TAGAGCCGGG TTGCTGTGTA TCCAAC TGAA TCCAGCGGC CGGGACTGG ACCATGCCAG	360
35	TTTGTTAGAC GACCTTGTCG AGTATTTGAA ACATGCTCTT CCTGGTACG CCTTGCCGCT	420
	GTTCATCAAG TTCACAAAC AGCTGGAAAC AACCGATAAC TATAAGTTTG CCAAGAAACA	480
40	GTACAAAAC CAGCAGTTGC CTCATGGTGC GGATGGGGAC GAGACAATTT ACTGGTTAAA	540
	AGACTACTCC CAGTACAAAG TCTTGACCGA CGAGGACTGG GAGCAGATAT CAACCGGAAA	600
45	GGCAAAGCTT TAGACCAGAC AATGCCGGGA TTGACACCGG TAGGGAGTTC AAAATAAAAA	660
	AAATACCTGG GAAGCCATCC ATAAAAGCCA TTATCAACTA TAGAAATAGA AAAGT	715

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1601UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

GATGGCCCTG TCCCGGGACG GAGAGCGGGC GCTGGGCTAG CATAAAAGCA CGCAGGTCAC	60
TGTGCATGAA ACTCGAATCG AACGCCGTAC TCGATGGTAG AACTAAACGG GCTCCGCTTC	120
GAAGTACGCA CAGTTGAGTG AAATGTCAGT GTGGGCGCAA CGGCCCCAAG AGCAGAATAG	180
CATGGACATC GAACAGAGGT CATGCGAGCC GAGTGAAGC AACAGCCATG CAGGATCGCC	240
GGGTACGAA AAAGTGCAGC CGCTGTATGC CGCAGAGAAC GGTTCCACGG AGACTGCCCC	300
GACAGCCACC GGGCTGTTTG ATAGCTCGCA CGTTGTACCG GTGTGCAAC GCGGGGACT	360
GCTGAGTAGG CTGGGCTTG TCGCCGAATT CCGGAGCGCA CGTCTCTATC CCCCAGGGT	420
CAAAAAGCTG ATCTGGTCA TGTGCGCTT TGCATGTATT CTGGGTCCCA TGGGGACCAA	480
CATCATCTAT CCTGCGATCG GGACTATCAT GCAGGATTTT GGCACCTGCG GGTTTCTGGT	540
CAGTGTGICT GTAGGCACT AACTGCTGC GCTGGGCATC TTCCCCATCT GGTGGTGTG	600
GCTGGCGGAC AAAAACGGCC GCGAACAGT GTACGTGCTG TCGTTGCGC TGCTGGTGGT	660
GTTCAGCGTT GGGCAGGCT TCTCGCGCAA CATCGAGAC	699

(2) INFORMATION FOR SEQ ID NO:977:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1602RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

15	GATCCAAGCG CCGCACAAAC CAGCGATGTT TGCAACATAT TGGCTAGTA TTCTCGTTC	60
	GACTTTACCC CTGCGTAGCG TTGGCGTCAG ACTGCTGAGC CAGGAACTC GGGGGGCCAT	120
20	TGAGGGCGCC ATTTCTCTCG CCCAGTGGT TCTGTTCTATG AAGGGCACCC CAGAGTTCCC	180
	TCAATGTGGC TTTTGAAGG CGCCATGA GATCTGGGC AGACAGGGCG TGGATCTGC	240
25	GAAGTTTGGC GCGTTCAACG TGCTGGAGGA TTCTGAGCTG CCGAGCGGGA TAAAGGAATA	300
	TTCCGAGTGG CCTACAATTC CACAGCTCTA CGTCAACAAG GAATTTGTGTG GGGGGTGGCA	360
30	CATCTCACC AACATGGGCG AATCGGCGA GCTAACTACT ATGCTGAGG AGGCATCCGT	420
	TCTGTGCGG GATACTGAGT GATGCGCGT ACGGCTCCCG ACTATATTTA TAGGAATACA	480
35	GCTTGTAATT TAAGACTTGT ATTCTCATGC CTTTAGACTT GTAAATCATG GTTGTTTAAT	540
	TCACAACTC CGTCTTTTCA GTTGAAAGAA GTGAGAACAG CTTGCTTTCC GTCATGTGTG	600
40	AAAGAGGCTT CTGATGGAGG AGGCGTGAC ACGCAGCAG AGAAAGTCTC TCAAAAATG	660
	ACGTTCTAGT GGAAGGGCGG ACGCAATCAC CCTTGAATGC GCGA	704

(2) INFORMATION FOR SEQ ID NO:978:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1602UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

GATCGTGCCC	GGGCTTGTC	TTGTGCCAG	AGTTGTCTT	GTGCCAGC	TTTGTCTGC	60
TGCTTCGTC	GCTGCCCGG	GGTAGTACA	CGCCGAAGT	CTTCAGCCG	AGCGGGCCG	120
GGAAGTGCAC	CGTCAGCTC	TGTTCCAGG	GAGAGAGCT	GCCGAGAAC	TCCAATTTTC	180
TCTGCTTACA	CTTCAGCTC	TTCTGTCCA	TGCTGGTAC	GTCCAGGTAC	GTGCCGCTGT	240
AGCCACATT	GGCATAACG	ATATTTTCTG	CCTTCGAGCA	GTAATAATC	CCTCCGATGA	300
AATCACAATC	GCCAGCAC	TGCTGGCAG	CGAGCAGGC	ACCTGCAAG	ACTGTGACA	360
GCTTCATAAT	TTGTAAACG	TTGTAAAGA	ATGACTAGTA	GTTAGAACAG	ATAAAAGAGT	420
GCTTGTCTGT	GTGCGCTGC	GCCGTCCAC	GCCTCCGAG	CTCACCAGC	TTCTTA	476

(2) INFORMATION FOR SEQ ID NO:979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1603RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

GATCCGGCAA	GATCGTCGT	CAGTTGACG	GCAGATTGAA	CAAGTGCGT	GTCATCTCTC	60
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CAAGATTCAA CGTCAAGATC AACGACGTCG AGAAGTGGAC TGCCAAACCTA TTGCCAGCCA 120
5 GACAGTTCGG CTACGTCATC TTGACCACT CCGCCGGCAT TATGGACCAC GAGGAGGCCC 180
ACAGAAAGCA CGTTGCTGGT AAGATTTTGG GTTTTGTCTA CTAAGGGCT GCTATATAGC 240
10 GTATCTAGCT CTAATGTACG ATACTCAGTG TCTATTACGA CCGCCGGAG CTCCACGGC 300
CACATAAGAG GCCAGCCGGC GACGCCAAGC GCGAATTCAG ATGGTTAAT TAGCAGTAGA 360
15 TTAGTAGTAT ATATGTACAA ACAGCATACA CATGAAACGC GTGCGGATC ATAATCTTCT 420
AOCCTTTCTA CCACCTTCT TTCTGGTAGA GTGGATGGG ATAGGAGTGA CGTCTCGAT 480
20 ACGCCGATT CTCAAGCCG ATCTGGCCAA AGCTCTCAA GCAGCTGAC CACCTGGACC 540
TGGGTCTTG GTCTGGTAC CACCGTAGC TCTGATCTG ACGTCACAG CAGTATGCC 600
25 GACCTCTTIA CACTTGGCAG CGACGTCTG AGCAGCCAAC ATGCCAGGT ATGGAGAGGA 660
CTGCTCTG TCGGCTTGA ACTTCATACC ACGGTAACT CTGGCAATAG TTCTCTGCCA 720
30 GACA 724

(2) INFORMATION FOR SEQ ID NO:980:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 721 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1603UP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

55 GATCTATTG TGCCGTCGC CATTAGCAA GCGCAAGCA TGATCCAAA TCATGAGAGT 60

EP 0 866 129 A2

	ACCTCGGGC TTTCACITTC CAAGCCTTTA TCAACAAATC TGGTACACGA TACATCCATC	120
5	GCGACAGCAC ATATACCAGA ACGGAAAGC OGACAAGATG GCACTAGACT CTGGTAGGTA	180
	ATCTGAGTTC GACCATATOC ACTTCGTTAA TGGTGATAGT TGATAAAAAG AAACGATACT	240
10	GAAAATTTTA ATGGTTACCA ATCTCATCTC ATCGCCATAC TGAAAGAATA TTGTAGGTCT	300
	CGCAGTGGAA CAAGGATCAA GCCCAGCCTA AGACAATAAT GGTTCAGCG GAGGCAGTAC	360
15	AGGAACTACC CCCAGATGAA GAAGAACTGG CCTTGGCTAA GCTAGTGTIT GGCGACACAG	420
	CAGACTTCCA TGAAGCGCTG CGAAATGCAG ACCTTAATTA TGTTCCTTCA GATGAAGAOG	480
20	TATATGGCCA GGAGTGTTC AGTGATGACG AAGAGGGGAC TGAAATTGGT CACCTGAATG	540
	ATGACCAATT GTTTTTTGTG GACGAGGGTG CAGATACCGA GCGAGGAGCA GATCGAGAAC	600
25	GGAGGCCATG GAGGTGGAOC AGGTATGCGA GGAAAGCGAC TCCGAGAGG AAACGGGTAG	660
	CAGCGCTGCA TGGTCAGATT CGGATGACGA ACACTTAAAC GTTACAATAG GGCAAACCAA	720
30	T	721

(2) INFORMATION FOR SEQ ID NO:981:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 638 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
40	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1604RP

50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:
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	GATCCCTATT AGAAGAGGTT ACTGGGGCTC CAACCTTGGT CAGCCACACT CTCTAGCCAC	60
55		

GAAGACCTCT GTTAAGTCTG GTTCGGTCAC TGTGGGTTTG ATCCCTGCCC CAAGTGGTTC 120
 5 CGGTATCGTC GCGTCTOCAG CTGTCAAGAA GCTTCTACAG CTTGCTGGTG TCGAGGATGT 180
 GTACACTTCC TCCACCGGTT CTACCCGTAC CCTAGAGAAC ACCTTGAAGG CTGCGTTCGT 240
 10 TGCCATTGGT AACACCTACG GTTTCCTGAC CCCAGACTTG TGGCCAGAGA ACCAGTTGCC 300
 AGCTTCTCCT CTAGACGTCT ACGCCGACGA GCGCGTTGCC CAGAAGAAGA GATTCTAAGT 360
 15 AGTGTGTGTA CATACCAACA GTTGTGTTCT TTGCAAGTGA ACCGCCCGCC TAAGCCTTTA 420
 GCGCGATGCC ACACAGACTG CCGTTGGGCA GGAGATGGT TGTCTTCGA CGCTGGTACA 480
 20 GGGCTGGAT GCGGTCTGC GGCTGGGGT GCATATCGGA GATATGGGC CGTGGCCGTA 540
 CGGCAAAGAA TCAGCAAGAC ACTAGCGTCT GGCATCTTTT TTCAATGCAT TATTTAGCTT 600
 25 TTTTTTTTTT TTTTTTTTGA GTATAGACAC ATATAAGT 638

(2) INFORMATION FOR SEQ ID NO:982:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 710 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1604UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

GATCAGAGCA TCCGATGAGG TGGCACCGGC CGGTCCGCT GTGTCTTTCT TCGCGGTATC 60
 GGCITCCGAA ATACTTAGCT TCTCAATACT TGGGACTGCC TTATCTTCAG AGGAAGCGGT 120
 55 AGCATCTCA CTCTTAGGAG CGCCCTCTGC GCTGCTCTTA GGCTCTCTT TTGTTGGCTC 180

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CTCCGCCCTTA GCCTCTTCTT TCTTCGGGAC AGGTTTCTTA GCACCAACTA GCTTGATAACC 240
5 GGAGCTGGAA GCCAACTTGA GGGTCTTCTT TGGTTTGGGA GCAGTGGCAT TGGGCACAGT 300
TCCCTTCTCA AAGTTGTTCA GGTTCACCGG AGGGGTGGCT GACTGGCCCT GTCCGTAACC 360
10 ATAGCTCTGG TTCCCCCTAC GGTCCCCCTG TGGCTGTGAG TTGTACTGCT TGTAGCTCTG 420
ATACCCACCT TGCGCATTGT ATTGCTGGTA ACCTTGGTAG CCAGCTTGTTG CTGGGTTGTA 480
15 CTGCTGGTAT CCCTGATAAC CCTGGTAACC GCGGGCTTGC TGGTTGTATT GCGCATAGCC 540
TTGGTACCCA CCTGCCTGTT GGCCATACGC CTGGTAACCT CCCTGAGGCA CATACCCCTG 600
20 GTAATTCTGG AAGTTACTTG GGTGTGAGTA TTGGCCGAAA TTGCTGCCC CTGACCTTGA 660
TTTTGACCTT GATCCTTGGC TTGGGACTGG CCTTGGTGGT TGCCTTGCGA 710

25 (2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 688 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1605RP
40

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

GATCTTCTCA AAAGTAGCAT TTACAATCTG CGTTAGCGTT GCTTGTGCAA TTCCCTGGTT 60
50 GGACGAGCTT AGTGACAGGA TGAAAATATT ATAGATTTGT CTGACGGCCT TTAATAGTGA 120
TGACCGTGA CAATTGCAAT AAGGCTCATC TGTCAATATA CAGCTTGCGA GGGCGGGAC 180
55 TACCTGCAAC TCGACCTTCC CATCAGTGGC TTCTCCATCA AAACAGTCGG TTATGGTATC 240

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AAAGGCAGCA TCTATCAGCC GCATTCTTGG AGGTGGTGTA ACACCAGAGT CTGGCAACGT 300
5 CGTGCCTTGG TCGTTTGATG CTGCGGAATT TGGAGGGTTG ACTAAAACAT TCTCGTCTAA 360
CGCCTTAAAG GCAAACAAC TTAGATAGACA ATCAAGAGCG CTAACTGTA TTTCTGGAAC 420
10 ATTAGTCTTA CAGCAAGCAC GTAGTGCTC AAAGACCAAC AGAGAATOCA AAAACTTTGG 480
ATCGTTTTC GATTGCAGGA GTTGTCTGGT CAAGTTTTC ACAGTTTCT CAACCACTTT 540
15 TTCATTATTA GGATGTTTGT GCATGGATTT TGCTTGTAAT ATACCTCTTA ACCTTAGTTT 600
CACAAGATGC ACTGCGGATT TCATGTGTA TGGACTACCA GAGACATTGG AATATGCCCT 660
20 TGTGTGAGCG TTGAGATTAT CCTGCGAC 688

(2) INFORMATION FOR SEQ ID NO:984:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 725 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1605UP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

GATCAGAGCA TCCGATGAGG TGGACCGGC CGGTCCGCT GTGTCTTCT TCGCGGTATC 60
45 GGCTTCCGAA ATACTTAGCT TCTCAATACT TGGACTGOC TTATCTTCAG AGGAAGCGGT 120
AGCATCTCA CTCTTAGGAG CGCCCTCTGC GCTGCTCTTA GGCTCTCTCT TTGTGGCTC 180
50 CTCCGCCCTA GCTCTTCTT TCTTCGGAC AGGTTTCTTA GCACCAACTA GCTTGATAC 240
GGAGCTGGAA GCCAACTGA GGGTCTCTT TGGTTTGGG CAGTCCCAT TCGGCACAGT 300
55

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TCCCTTCTCA AAGTTGTTCA GGTTCACCGG AGCGGTGGCT GACTGGCCCT GTCCGTAACC 360
 5 ATAGCTCTGG TTCCOCTTAC GGTTCOCCCTG TGGCTGTGAG TTGTAAGTCTG 420
 ATACCCACCT TGCGCATTGT ATTGCTGGTA ACCTTGGTAG CCAGCTTGTG CTGGGTTGTA 480
 10 CTGCTGGTAT CCTGATAAC OCTGGTACCC GCGGCTTGC TGGTGTATT GGCATAGCC 540
 TTGGTACCA CCTGCTGTT GCCCATAGC CTGGTAACCT CCTGAGGCA CATACCCCTG 600
 15 GTAATCTGG AAGTACTTG GGTGTAGTA TTGGCCGAA TTTTCTGOC CCTGACTTG 660
 ATTTGAACT TGATCCTGG CTGGGACTG GCTTGGTCG TTGCTTGGC ATTGAATTG 720
 20 ATCTT 725

(2) INFORMATION FOR SEQ ID NO:985:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 678 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1606RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

GATCAAGCAT ATCAAATTTC CGGCAATCTG CGGGTCATT TTTTGGACA ACAGGOGTCT 60
 45 CCACAGGGTC CATCTCCATC AGCGGAGCTA TACGTTGGA CAGTGGCTC AGCTTGGTAC 120
 TCTGGAGAG AATTGAGACG CCTTGGAGC TGGCTGTATG GTAAGTGTG TCCGTGCGT 180
 50 AGGTGGTCAA AGACAGGAC TCTGAATACT GGCATTTCG ATCCCGGTTG CGCGTACGT 240
 ATCCGTGCGC CGTGGACTTG ATGGCAGTGG TGTCCGAGCA CGAAGACAGC GAAGGTAGTC 300
 55

TCAGTGGCCG CGTCGGCGAT ACGTGTACT CGAGCACAGA CTCGTTGTGT CCCCTCCCG 360
 5 TCATGTTCIT CGGCTCAGTT CGCGACAACG CTCGCGACCA TGCGTGCCCC CTCGCTTCT 420
 TTCTGTGGAA GCGCCCAAAC ATTAAATCTA GCTGCTTCTT CCTGGTACTC TGTTCGCTCT 480
 10 GTTCTGCCC GCGAGCCCC TGGATTCAA TCTCTGTACA GCGTTATGC CGCACTTGCT 540
 CGTCTAATT GGCTGCCACA CTCCTGCTGC TCGAACCTAA GCGTCTGTA CGAACGCTT 600
 15 TCGTTGACTT GACCGTTGG GCGTAATCTA TTATTGGAAC CTGTAAAAG CGGCTTCTG 660
 TACGCTATTA GTTAGCCC 678

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1606UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

GATCCGCTTG AGTACTGAGA TATTAACTCA ATACCAGGAT AAGCTTTCAA AGCACCGTAA 60
 45 TCCTACTGTG CAATGGTGGG GACCTACTGA TTTCTCGCAC TACGTCTAG CGCTGAAAT 120
 TTTATCATAC GTGTCCCGAG ACGAACTGGG CCTTGCAGAT ATCGATGAGG CTGGACTTA 180
 50 CATGGAAAGT ACCACGGAAT ACGGGTTAAA TGTGGCGGAC GAAGAGCCTC TAGATATTTG 240
 GGAATTAGAA TACGAAGAGA AAAAGCTGCA ACGGTTAGGA TTAGGACCCA AGTACAGCAG 300
 55 CATGACTTAC AGAAAGCATC CTGCCAGGGC GTGGCTGTA TTAGATACAT CCAAAAATGG 360

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TTCTAAAGAG CATAAGCGTA AAGGAAAGCA ACACAAATTA AAAAAAGGAC AGCAGTCTAC 420
5 AAAGATAAGG GTATCAAAAA AAAGGOGACG CGTACAACCA CACAGCATAT GOGATTAATA 480
ATCTTACAAT CGTACTAAGT AATACATACC GOGCTTATAG AATCTGCTGC TGCACGGAAA 540
10 GTTGCATATG CGAAAACATG CTATGCAGTG GATGATCGCG TACCACITTT TAATCOGATA 600
AAAGTGGACT AGCGATAAAT AGTAATTTC AATAGGAATG TGAATTTGAA TTGAGAATTG 660
15 GGATAATGCT GTGGATTTCCT GTGATTATAA TACCATAAAT ATA 703

(2) INFORMATION FOR SEQ ID NO:987:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 622 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1607RP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

40 GATCACACGA CAGTGCCAGT CGGGGCAGCC GGTACCCGTT GGCOCATCG TGAAGCTGAC 60
TCCGAAGAAC CCTTCTACA AAGTCCCCGA GACGGAAGAC CTGTGAAGG TCATGGGCAT 120
45 CCTTGGCTCC GCGTGCACC GTGTGCCAT TGTGGACTCC AACTCTTCAT CTATCOGTGG 180
CATTCTGTG CAGGACGTC TGATGAAGTA CCTGTGGGAC AACGCCCCC AGTTCAGCAA 240
50 CCTGGAGGTG CTGCTCAACT CGTGCCTGCA AAAGTTGGGC ATGGTGTGC TGGATCCACA 300
TACCCCTCCT ACTTGGGGC AGTGGGTGT TATTTCATT CTGACACAG AGCGCTGCT 360
55 CGTTGCCCTG CACAAGATGC ATACAGAACG GATATCCTCC ATGCGAGTGA TCGACCAACA 420

GGGCATGCTG CTGGGAACA TCTCTGTGAC AGACGTCAAG CAGGTTACGC GCACCTGCA 480
 5 GTATCGTTG CTGCACAACA CCTGCCGCCA TTTCATCAGC GTGATCCTCA ACAACCGGG 540
 CCTGGAGATG GGCAAGGACT CCTTCCCCAT CTTCACGTT TACCCACCT CGTCCCTGGC 600
 10 CCGCACGGTC GCGAAGCTGG TC 622

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1607UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

GATCGGTGCC CGCACCCTCG CCGATTCTTT CGCAGCTCG TTOGCAATGT TGGTATOGA 60
 35 CTCTGCTTC TTATCCCAT CCACCTCCGT CCGCGCGCTG TCAAAGCTC GCTTGGCTGC 120
 GCGGCCACTC GTACCTGCCT GCGTTCTTC ATCTCAATA ACTATCACTT GCATCCCGTT 180
 40 AGTAGCTGCA CGGTGCAGAG GCGTGTAAC CTCCCTCAG CCTTCAAAA CGCCCCACCA 240
 CATACTTCT CGTCTGGAA TCATGATTGC CCTGGTAAT CTTACGCTA GACTAATTT 300
 45 GGTCATAAC TCGCTCTTG CGACTGGAA TTGGTGGTC AGATGGTGAA GTCTCATGTC 360
 GTCCATTTCT GCGATGTTA AAATATGGT TTOGAAAAA GCGTCTTG CCTTGACTG 420
 50 ATGCTGACT CACAGAGGAC TCACCAGAGC TTGAACGCA GCCAGGAAGC ATTCTGTCA 480
 TACCAGAAAG GGCCACGGC GAGAATCAGA ATGATGTTG CATAGTCGGG CAGCAAGAGT 540
 55

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GCTCCAGCGC TCGGGGTCOG CAAGCGCAGA TGCAACAACCT CCGTGACAG CATCACAAGC 600
 5 GGTATAGCAT GCCTTCCCA ACGATTTCOG AGGTGCGGA CTCAGCAAG TATTCCCGAC 660
 CTGGCCGGTT ACAG 674

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1608RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

GATCAAAACC ATCAACAGT TTATTCATGA AGTGTCOGAC GATTTCAGG TCATCATAAT 60
 35 CGACGCAATT CGTACTTTGT CCTAAAGTT CCCAGATGAG TGGAAGAATA TTCTATCCTT 120
 TTAAATTGAC ACTTTGAAAA GTGCAGAGGG TGGGTATACA TTCAAAAATA ATATCGTAGA 180
 40 TGCGCTGTTT GACCTGATCC AACATGTACC TCAGTCAAGG GAACAGGCTC TGGAACACTT 240
 GTGTGACTTT ATTGAGGACT GCGAGTTCAA TGAAATCTCA GTCAGGATCA TTTACTTATT 300
 45 GGGTAAGGAG GGCCCTCGA CAGAAAAGCC TTCGCTTTAC GTTAGACACC ATTACAACAG 360
 AGTTGTCTTG GAAAATTCAA TCATCAGATC TGCTGCTGTT AGCGCATTTG CCAAGTTTTC 420
 50 CTCTCCGAAG AAAGATCCGT CGTTAGCTTA TTCCATCGAA AAATTGCTAA AGGGTATCCA 480
 AACCGATGAG GATGACGAAG TGAGAGACAG GGCAACCAAT CTAGTAAAGC TCCTTGAGGA 540
 55 GAACAAGGAA AAGCCTGGTG TTGCCGATGA ATTTATCCAG CCAAAGCATA GTTACGATCT 600

ACTTGGCCCTG GAAAAGTAAA TTAACGAACT ATCTCCACCA TAATGAAGAT GGCTTTGCCA 660
 5 CACCATTTGA CGCGTGGAGC ATTCCAAAGT TACACAGAAG AGGAGCTCAA GGCTATTAAAT 720
 TTGAAGCAGA AAC 733

10 (2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: PAG1608UP

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

GATCTGGCCA AGGATAAAGG TGTTCATCAA GTCATTGTGA ATGAAGCCCG CAGCCTGTGG 60
 35 CGCCTTAGTG CCATTTCCTGA TGGTCCATTC TCTGACTTCG TCGGGCCCGC AGGTGAAGAA 120
 CGAGATCAGA TCCAGCTTCT GTCTCATGGT GGTGATGATC TTTGGGAAGG CGGACTGGAC 180
 40 GCGGATCTTC TCGCACTCCT CGACAGCCTC CTCGGGCGTC ATGTGGGACA GTCTCTCCTC 240
 CAGGCACACC GAGAAGGGTA TAATTAGATC GCCAGGGGAG TACTTGTGCA TCCACTCCTT 300
 45 GATCTTCAAG AGGTGCTTGT TCTTCTTTCT AATGTAGTCC CGCTCCGATA GGTGATCAG 360
 GTAGATGGAT GGCTTGGCGG TTAGCAGGAA CATCGAGTTG ATGACCTCCA CCTCCTTGGT 420
 50 GCTCCAGGAC TGGTTTGGCA CTCTCTGACC CGACTTCAAA AGCTCGATAA TCGGCTTCAC 480
 CAGCTGGGCC TCCTCCTTCT TCTGTTTCAC CTCAGGGAC TGGCCGCTC TCTTGGTGAT 540
 55 CTTCTCCACG GGCTCCAGGT GCTTCTCCGC GAACTCAATG TCCTTCAAAC GCAATTCCGT 600

GTTAATGATG TCCAGGTC TCAGCGGGTC GACGTCACCC TCAATGTGGA TGATCTGGC 660
 5 GTGGTGAAG CAACGCACGA CCTGGTAGAT CGAGTCCACA GATCTGATGT GCGATAAGAA 720
 GGC 723

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1609RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

GATCAGACGG TAATGGGGG CATGCTGGG CAGGTGGAGC ACGTATCTAG CGTCCATCGT 60
 CTCTTGCTGT GGTGGGGGG GCGGGGCAAG GGCTGCTG CGGAGAAAT ACASTAGGGA 120
 TCTGTGGGC CCGGCAACCA GGGCAGGGG GGCGCGAAC AGCGCGTTT GCGCCTTAAT 180
 CCGGACAAAC GCATATAAGT AGAGGCTTAG GCGCTGCTG AGGGACGGCA GAACACACAC 240
 AAGGACCAAT GAACACGATT ATCAACTTCC AGGAAGGCAG CGCGCAGGCT CTCAGCGAGC 300
 ACAGCATCTT CCAGATGTG CTGGTGCCA CTGCTGAAA CGGTCCATCA GGACACCTTG 360
 TAGTGGAGTA CCGGGGCGAG TCTACAGCG TGAGCTGGG GAACGTTATG CCTGTGGAGG 420
 CTACGCAGAC GGTGCCCAAC CTGATGTTAA TCACGACCGA GCGGGGAATC GTCAGGGAGG 480
 GGGACCTATT CACGCTGGG ATGACAGACC CAGATGCTCC CTGGGGTTC GACCACAAGT 540
 GGTGGGAATA CTGCCACTTT CTGGAACGA ACATAACGCT GGGCTGGGAT GACGGGGTGT 600

CCACGTGGT GCTAAAGGC ACCCGCAGG TGGAGCAT GGGCCCTGG CCGCCGGGC 660

5 GGCACAGGGG CTCACCGTA CGTGTGTTG TT 692

(2) INFORMATION FOR SEQ ID NO:992:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1609UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

30 GATCGAGAAG ATTTGGAGAA GGAAAGCGTC TTGGTGCTAG CCTCGTGACC CCTCCCGGG 60
CTGGAAGTGC GCGATATACT ACATAAAATA CGTTATCCCT GGAATTTGTA GCATTAAAGG 120
35 ACTTATGGAC TATTCTGTAT AACTGGCTT CCGCTGCCA CCGTAGCAA TGCCAAACTC 180
ACTCGAGGC CTGCTGCTG GCGCAACAAT CGGACTCAG CCGACCGAG CCGCGAGTC 240
40 ACGTCCCCC CGCATTCGG CCCACATCAC TCGCTTGGC TCGCTTGGC ACCCGCCAC 300
GGGACTCCG GCGCGCAGC CCGCGTGAT TCTAGTTGCA TAGGAACTA GGCTAAAATC 360
45 ACGTGAAGTA ATGCGCGGC CACATCATA CATGGGACG GACCGGACT ACCCCCCCCC 420
CCCCGGGGG CCGCTGCAC AGCAGCGTA TACGGCGCAG GCGCAGTCG GTGCGGGCC 480
50 TCTGAGAGG CGCATGGCG CCGATGCTG ATGGCTGCT CCGTGTGGC GAAGATGTGG 540
AGGCACGTAC GCGGCAGCT CAGTTACCG AAGTTACCC TTCTTCTGAT TAAATTTGGA 600
55 CTGAAACTTA AAAGCGTCA GCAGTGCAA ATCCACGTG AGAATAATTA CAGGAAACAG 660

CGGTGGACCA GCTGCGGAAC TAGACGACGG GTTGGTGTGG CACGCATAGA AGGTATGTTT 720

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(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 731 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: PAG1610RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

GATCAATTTC CTTTGGTATA GTTGGCGTCC CAGGCTCCGA GATAGCCCCA CATGATAAAT 60

30

TGCTATGCA CATGATGTCC TGGTGTGTCAT TGTGTGTCAA ATTGCTCAA TCAAAAATGA 120

AACTACCATC ATCTGGTTTC ACTTTCAGTA AACTATCGTT TTTCTCTGTT GCAGGCTCGA 180

35

AATCCATATC ATCCCGTAGA TATTCTATGT ACAGCAGAAA CGGAACCTTC TCTGCTGAGT 240

TCAACACCTG AGCTTCGTGA GCAGCAATAT TTACAATTGG ATGCAGCTTG CCTTCTTAT 300

40

TAGGCGGCAA CAGTGTAGGG ATATCTAAGT CAGCTGGCAA GTCCCTATTC ATGATAGAAA 360

GCTCAGCTCT CAATGAAGTT AGGCGAGCTT CAGTGGGAAC TTGGGCAAC TTCTTGATA 420

45

TGTTTTCTAG AGCAATCACA AACTGCATCT CGCAGCGGAA GTAATTGGC TTCAAGATTT 480

TGATTTTATG TGTGGCTGAT AACTGGAGG GCTCCAGGTT ATAGATGTTT GCTCCATGCC 540

50

GAGATGTCTT CGTTTGTGG CTCTTCTTTA AATCATTTGA CGGAGACTGC GTGATGCTAC 600

CATTCCATG CTGCTCAAT GATTGCTGAT CCTTATACGA GTGGAGTGAC GTGCTGGATC 660

55

GAGAATTGAG ATGCAAAATTA GGCATAGAGT TTGTGTATTC CTCTAGCTTA GCACCATCGT 720

TATCTTTGGG C

731

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1610UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

GATGATCTG TACAGAGCGG TTACAACAGG CACTTGTAAA AAGCAATATC GTTACTTTTTT 60
TGCAITGTCAG TTTTTCCTC GAGCCTCGTC AGCGCGAGGA ATGAGTAATG GATACTTTGA 120
CGACAGAAAA AGTGAAAAC TTTAGCGGAC ATCGCAACCT GCTCGTTAGT AGCACTTAAG 180
CGCAGGTTAG CACAATGGCG CCAAAGGATA CGGCGGTGTC GGAGACCTCT ACGCGGTCTC 240
GCTATATCAA AAAGGGCAAG ACTTTAGAGA ATGACATTGA GCTACAGTCG GTGACGCCAG 300
CCACCGGGGA GTTCCCGGAG GACCACAGG AAGAGGGCGA CTACCAGGAG ACGGAGGTCA 360
AGAGGGGGCT GAAGCGCGG CACATCTCGA TGATCGCGCT GGGCGGACG ATAGGCACAG 420
GCCTGTTCAT TTGATTGCA TCCCGCTGC GGACAGCGG GCGAGTGGG TCGCTGTTGG 480
CGTACATCTT CATCGGTACG GTGGTGTACT CGATCACCA GTGCTGGGG GAGATGGGA 540
CGTTCATTCC TTGACTCCT CGGTGACGG ATTTTCAAAG CGGTTTCTGT CGCCTGGGTT 600
TGGCGTGGCA AACGGGTATA TGTACTGGTT CAACTGGCG ATCAAGTTTG CTGTGAGCT 660
TTCTGTGGTT GGCCAGATCA TACAGTACTG GACGGACGC GTGCCAATCG CGGCGTGGAT 720

TGTGATTTC

729

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1611RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

GATCATCGT GGTGTCGTTT ATTACCTGTA ATTCCATTGA TATCCTGGCT ATGCAGTGCT	60
GGAAACGCTC CTCCAGCGCC TCTATTTTGT TATTCAGCTC CAAGTACTOC GCGAGCTTAA	120
AGGTCAACGA GAGCGACCCCT GGATTGCACC TGAOCCGCGAT CTCAAGGACC TTCTCGTGCT	180
CGTTCTCGTC CACAAACATG GCGTAGTTGT ACCATATCTC CGGCGCAAAG CACATGTGCT	240
GCACAGCCTG GCGGTGCACG TATTCCAGC GCTGGCGCAG CACGACTTGG GGCAGGTGGA	300
GCTTGTTGTC CAGCTCCAC TGGATCCACT TCGTCCAGAT CTGCAGCTGG TACTCATCGT	360
ACTGACCGGG CGCAGGCAGG TTCTGCTGTG TCGCCTGGTT TAGCTTCGTG GGCAGCGAGC	420
GCGCAGGCC CTTCGTCAGG TTGACCACT CCTGGTACAG CGAGCGCGCA TTCATGTAGC	480
TGCGCGAGAG CTCTCCGATG AACTTCCGCG CCGTCAACTG GTTGAACTCC TGCTCCCACT	540
GCGTGTATTT CTCCAGTAC CGCTCCAGCG ACTCCACTGG CAGGCACAGC AGGCGCTTGT	600
ACAGCTTGCG CAGAATCTCG ACCCGGCTCT GCTCCTCCCA CTTGCTCACC GCCTTCCACT	660
GCTCCA	666

(2) INFORMATION FOR SEQ ID NO:996:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1611UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

GATCTAAGGG ATGGGTGACT GCTGCCGGTG CTCACAGCAG TGGCAAGTAG CTAGTAATGG 60
 TGGGAAATCG ATCAAAGAGG GTGGTCTGG CGGTACAGGC AGAAAGCAAG CCGGCCGATA 120
 CAAGTTCAG TTCTACAAGC ACCTGCAGTT CCAGGGTACG AGGTACCAGG TGGTGACTTC 180
 GCGGCCGTAT CTGATAGAGC GGTACGGGGA GCGCAAGGCG GCGACGATCA GGTGTTTGT 240
 CAAGTGCATC CATCGGAAAA TCAACGACGA TGTGACACCG ATCAGCGACG AGCGGGTGAC 300
 GCACGGGGTG TCGAAGTGGG AGAAGTCGAA GCTGTTCTTG CTGCTGGTGA CGCTGTGCA 360
 GCGGGGCGGG CCGGAGTACT GGCTGGACAA GACGAACGGG TGCCAGAGCC GCGCGGGCGG 420
 AGACGGCGCG CGGAAGAGCG ACCAGGTGGA GGAGGGCGGG AGCGGGCGGG GCCAGAGGCT 480
 CGTCTGCACA CTGGTGGAGC AGATCATGCG CGAGAACATC ACGGAGGACT ACGACGAGAG 540
 CGTGCAAGAC GAGAACTACG TGTTCCTGTC GATATGGGCG AACTTCATGG AGGGGTTGAT 600
 AAACCACTAC CTAGAGAAGG TCT 623

(2) INFORMATION FOR SEQ ID NO:997:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1612RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

GATCCATGCG ATAAATCTCC TAGTGGTGTG GTTTCACACG AAGCAGCTTC CGTGGTTCTC	60
GTGGTTTTC CTGCAGCTCT GTTCAGCTT GATTMTGGTG TTTTGGGGA CGTGGACCAC	120
GAGGTGGCGC GAGCTTCGGC ACACGTTTTT TGAGGGTCTC ATAGATCAGG AACCTATTAC	180
GGGTGGGGCT GAGTCTCCCT ATCATGGCAG TTCTCAGAAC AGACAGCAGT TTGAGATGAA	240
GGACTTGGAG GCACAGAAAT AGCCTACATT ATAAATAAGC TTGAGATCAT TCTAGOGCCA	300
CGGTGAGACT GATCATTCGT AAATAGCAIT TTAATAACGT AATATATCAT ACGCTGGTTA	360
TTTGGATGC AGGACTCCGA AATAGTCTGA CAATTATGTA CTGTTAAGTT ATTTATTTTC	420
AGACGGGGTA TCTGCTTGA AACCTGTTCC AGTGACAGC AGATCCAGCA GCTCGAATAC	480
TGATTTTTC GTATTGTTAC CTGGTCGACA GATCTCCAAG CCACCTCCA ATCGCTGCGG	540
CAGCTGCAGC ATTGCTACCG TAGACTCCAG CCTAGTGACA AGATGATCCA ACAAGGATAT	600
CCAATCGTAT TCGTGTCTT GGCTCAGCGC TTTATCAACC TTTTATCAC GATCATATG	660
TGTGGGTAGT TGTAGGACAC TATTGTGAT TTCGATCAGA CCGCGGTT	708

(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 732 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1613UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

GATCAAATAG ATGTGCGCTG CCACATAGGA CGGAGTCGGG GCTAAGCTGT GTGTTTACC	60
TGGAGGCAAC TGTGTGACTC CTGTGTCAGC AATCGCGGCC CGAAGTCGGG AACAAAGGAC	120
TATATAACAA GCGAGGAAAC CACCTTGTGA TAAGCAAGGG GACCAACGAC ACAGCAACGA	180
CACAGCAACG ATGGGGGACC TGGGGGCTCT TATTGACTTG ACGGGGATAT CGGAGACGGG	240
GTATGAATCG ACGAACCATC ATAGGATGAT ACACGGCGGC AAGGGGCTCT ACGGGGGTCT	300
GCTAGTGGCA CAGGGGATAC TGGGGTGGTT CTACTTTGTC CCCAGGGACT TTATTCCGCT	360
CTGGTGCAC TGCTGTGTCA TGGTCGGGGG AGACAATGCT ATCAAGACGC AGTAAGAGGT	420
TGAACGGCTG CGGAAGGGGA GCAACTTGGC GCACCTGTTG GTGGGGGGGT ACCAGAAGGA	480
CAAGGAGCTG TTCACAATGC AGATCATCTA CCGGGGGGAC CTCGGCAAGC AGCGGACAC	540
GCTGCACCGC AAGGACAACC TGGGCCCTGT GGACGGGTCC CACCTGGAGG ACGCTGGCAC	600
GCTATGCAGG CCGGATCTAC TGTCCAACCG TGAGAACTG CAGGGGGTGA GCGGTCTTC	660
GAGACGGATA AGGGGCTTAA TAACATTCTG GAGGGGTTCG ACAACACGTC GTCCGAGTAC	720
AGGCTGCTG GC	732

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

10

(A) ORGANISM: PAG1614RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

20

GATCGGGGG ATGGACCGT GCTTGGACG CCTTCTGGG CACGGGGGG CGTCTTCCG	60
CGCGTGTCAG GAGCAGGTG AGCGGGACTA CGGGGGATG GAACAGTTC ACAAGTTCC	120
CGACACGATC CGTGTCACA AGTTGGTCAC GTATATATG CGGTGTTCG AGCGGTCTG	180
CGTGTAACCG CCGAACCAGC AGCGCTGCCA TCTGAAGAC ATCATGCTCT TGGTGTGTA	240
CTGGGGGAG GCGGGGGGC ACGGCTCTT GTCATGGG ATGTTTCAG CGTGCGGGC	300
ACGCTACGGG GTGCAGAAGC TCTCTGGA GCAGGTATG ATCATCATG ACGCAAGTT	360
GCGGGGGGA CAGTCATACT TGATGATCC GCTGGAGG AACGCAAGC CGGCATCTT	420
CACGGGGGG CGCTTGCTG ACACTATCG GCACACAATA CCAACATG CGGACCGCG	480
GAGCCTGGG CTCGCGCGT TCTCACTCC GTCACGAAG CGGGGGGTG CTGAGAAAT	540
CTTCAAAGAC TGGTCCATCT ACTGCGACAA ATCCATATG CGGACGATC CTGATCACTC	600
GCCCAATGGC ATTCTGGCT ACGTCCGCA CTCTGCAAG CGATGGAGC AATCCATCTT	660
TGAGTATTTT ATGCTCTATT GGAAAACGC AACAGCAAC CACTCCAGC ACAACATTTT	720
CCACACC	727

50

(2) INFORMATION FOR SEQ ID NO:1000:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

55

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1614UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

GATCCTTTTC ACCAACAGCT GTCTGGGCCA GCTGGGGCCT GGGATGAGCT ACAACGAGGC	60
AGTGAAAGCG CTGACGAACC TGGGCTGGA CAGCTTTACA CTGCGGGGA CGGTGGGGTT	120
TCCGCTGAAC AACGTGTA CTGTGCGGT AGAGGAGGT GCTCAGATGG AGCTGCTGAA	180
GGGTACCTG CAGCAGTTC GGCAGGAGCT GGCCAGCGG CTGCTGGACC GTGTGTATGG	240
GGGGAGAAG GCACAGCCCT CGAAGTTCTG GCTGGCCTTC ACAAGGCGCA AGTTTATGAA	300
CAAGGCGCTG TAAGGCGAAA TAGGTACGTA GCTGGGCGCG CCAGGAAGTA TTTACAAAGT	360
TGGCTGTATC GCTACGAGT TTTGGTGGCG TGTGCTTGT TGGAGCGAC GAGGAGTTCA	420
ACGGCGGAG CTGGAGCTG TTCGGCTCT TTCAAGATCG CGTTCAAGTC AATGCTGAGG	480
TGGTGTTTT TGGGCGGAA GCGTTGGATC CGGCGCTGCA GGTCTGTGAG CGCTGGAGG	540
ACACGCTCAT AGTCTGCATC TTCTTTCACG CGCTCTTTGT ATGTTTGGAA GCACTGAGCG	600
ATGTCTTGA TACCGGGCTC GACTCTGCTG ATCATCTGGA TGGCTGGCG CAACAGCTGA	660
TGGCGGTGCG TGTGGGGTT CGGCTGCTA ATCATCTGCT GGATTTGCTC ATCGGTCAAG	720
CCCGAT	726

(2) INFORMATION FOR SEQ ID NO:1001:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1615RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

GATCATTGAG	CTGGAGGTCA	GCCGACTACT	GTGGACCCC	ATATTCAAGG	TCCCGAGGT	60
GCAGAAGGAC	ATGGTGGAGA	TTCTGGGCGA	GTATATGCTG	GAGTCGGGGC	GGCGGTACAA	120
GCAGGGTTTC	CATGAGCTAT	GCGGCATGTT	CTACATGCAG	CTTTACCGCA	ACGGCTACCG	180
GGACGGCATC	CAGCACACCA	CGCTACATAT	GTTCAGGAG	TTCATCGCAG	AGGTAGCTGT	240
GACCTTCTAC	GACGAGGGAA	ACCTCATOGA	GTGGACGAAG	AACAGGTTTG	AACCGATACT	300
TGACACCGG	TTGCCAGGCT	TGTACGAGCA	GCTTCTAATG	CACCATGAGC	TGGACAACTC	360
GATATGGCTC	ATCCGCTGGA	GCAGGCTGCT	CTTCTCGGA	GAGTTGAGC	TGGAGTACAC	420
GCTTTGCTTG	TGGGATCACC	TGCTGACATT	TAGATACCCA	GTATCCAGC	TGTTAGCAGC	480
CATTATCGTT	GTCTGTCTGA	CACTCATTTG	ACAAGAACTG	CATTCTCTTG	AAGACCAAGG	540
CGACCTGATG	TCTATCTTAC	TGCACTACCC	TCTCGAAGC	TGCTGAGGC	CCCCAGATGA	600
TCCGCTCCGC	CCGGAGGCTT	CCTGATCTGT	GGCTCGCGGA	ACAATATGAA	GACATGCAAC	660
TCATCTGCGA	TTCACTAATT	AAGTCGACA	ACGGCGCCTG	GTTC		704

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 706 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1615UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

GATCTCGTTA TTCTGGACAA CATTCGGTAT AGGGACTGCT CCTGCTTTGT GTGAGGAGAC	60
GTGTGCTGAC TTAAATAAG TACGATGAAA CGGTCAGCCT ACGGTGGGGC CCCGTTTTTC	120
AGTTTCCAC GGAGAGGTA TCAAAGGAGG TCGAACACAG CTACGTTATT GGTTCGTATA	180
GCATGCTTTT GAAGCCCTTA GCTTCACGAG CGCTCCGACC ATCCAGCCA CCGGCCCCCT	240
ACGCCAAGG CCAGCTCCCG CAATACGCCA GCGCGTGGG CCCCTTTTCG TAAGTATATA	300
TGGCGTGGCC GCGCCCGCGG GCGAGGTGG CGCGGTGAC AATGGCTTCT GACTTGACA	360
AGCTCCCGGA GCGGTTCAGT CGCTGCAGA GCTCAGCCA TAGACAGCTG CTCGTCCTGG	420
CGCAGGGGCT GTGCATCCCT GCGCTGTCCC CGTCCCTGCA CAAGGGCCAG AGTGGACGGG	480
TGTGCGTCTG TGGGGGGTGG CTGGAGTACA CGGCGCGCC GTACTTCAGC GCGCATGCCG	540
CGCGCTCAT GCGCTCGAC CTGTGCAAG TGCTGTGCGA GTGGAACGCT GCAACGCCA	600
TCAAGGCTTA CTGCGCGAC CTGATGGTGC ACCCGCACCT GCGGACAGT AGCTCCCTGG	660
CGCGCGGCT GGAGCCCGCC ACAGAAGCCG TGCGCGGCT CGTGA	706

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 687 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1616RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

GATCTGCTTC AAGAGCTOCT TCTGGTAGGA CGAGCCCAGG ATGAAAATCT TGGAGACGGT 60
GACAGGGTCC AGGAACGGCT TGAACAGGCG GAATCGGGCG GAGAAGCCGA ATGGCGCGTT 120
GATCATGTAG AACTTGCCCA TGGCTCGGG GTAGTAGTTC TGGCCGATGT TCGAGGCTC 180
GGCACGTAG CTGAGCACT GCGCGCTGC GGAGATGGAG ATGCCCTTGA GGTCTAGGAT 240
GGTGCAGGAC GTCTGACGA GGCAGTGGC CTGTCTGGAG CTGGCCGGCA AGGGTACCG 300
CGAGAAGGAC TGTACTCCC ATATCAAGTT CTTCAGCATG CGCTCCTGG TCGIGATCTT 360
GTACATCTCC GTCAGGTCA CCGCGCCAG CTCTCGATG TACACGGCC TCCGTCCTT 420
GTCGTCTTG TGGTAGTACT GCGGGTAGAA CTGGCCACC AACGGCTTTT CCTCGTAGTG 480
GAAGTCTCG AAGATCGTGT CCAAGCGGT TTCTTACGC CACTTCTGC AGTTCTCAA 540
CATTGCCCGC GCAGCGCCC ACGTTOGAAC TTGCGGCCC GCAGAAACCG CAAAAGCGTC 600
GAGTGTCCA GACGCTTGGT GAATCCGCC TGCTTCAGCA CCTTGCGCAG CTCTCCAGC 660
GCGGCTCG TGCTCGCTC CGTCAGG 687

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1616UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

5			
10	GATCACCTTT TGGCAGGAAC GCCACAGAAA ATCCATTACG CGATTCTGCC CGTTCATTTC	60	
	TGTACGAATG GGGAAATGAC TGTGCGCCAT GGCACAGGTG ACTATCGCAT TTGTTTTCGG	120	
15	GGCGTGATG CCCAGATTTT CTTCAGAAA GCGGCCACCC TGCGGGATAG GGCCTTACCT	180	
	CACATGAGGC GCAAAGCGAC AATAATCGCA GAGCTGCTTC TTACTTCATT CTCTACCOCA	240	
20	CTAACGTAAT CGATCGGACA GGCACAGTCC TACGGTAATC CTCTGAGATA CCAGATTGGG	300	
	TTGCATAATG ATCTCGCCTA CAGGGCGGTG TTTGTTTCAG CCCATATCTC ATGCAAGATC	360	
25	GCGATGCCCC TGACGATCCA CCTTCACCAT TTACTCGTTT CTTTTTCATG TTTTCAAAAA	420	
	GAAACGAAAA GGTGAGATAA AAAGCAAACA TTACTACCGA CATTTAAAT AGGTGATGTC	480	
30	CAGGACTGTA CCTCATTTGT GCGCTAACA GCACAGCAA TGCTGTGTG ACCCCTTGTG	540	
	CTGTTTGAAT TTTCAACAGA CAATCGAAC AACTGCCCC GGAATACGA CCTTGCAGTG	600	
35	GCCGAATCT GTGTGCTGG CCACGGGGC AGTGGCAAGT CATCACTCGT TGCTCGATG	660	
	GCTACACGGA CTGGAGAGTG GCGT	685	
40			

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1617RP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

5	GATCTTGACA CCAATOGACT TCCGGAAGC CTGAGTCAAG GCGTGGTCT TGGATAGCTC	60
	CAACGAGAAT ATCTCTGACC CTGCCATGCG TGTGAAGGC ACATCTGCGC CCACTGACTG	120
10	CGACAAGCCC ATGCCAGCG CGTTTTCGCC GGTGACGGC GGACCAGCAA CCAACACGGC	180
	CGCCCCGCA ATCGTACCGT TCTGCACCAT TTTGAGAATC ACGCTGCGG CCTCCGCGC	240
15	CTGTAACCTGG CCCACCAATC CCTGGGAGCT CGGCTTAGGC TGTAGGTTCT CGTCCAGTCC	300
	CAGGCCAACA ATGTGGAAT GTGTGCAAT TAGCGACAAG GACTTCAGAG ACATGTCATG	360
20	CGCTCTCTGT GTTGAATCG ACATATTATA GATCTTTGAA ACTTTGAAAC CGTCAAGAGA	420
	GTCCAATGGC CTTGTGCGAT GACCGTCTAA CTGTTCAAAC GGTGTGCAA CATAACCAAT	480
25	TTTGCCCGAG CCGGAGGACT AAAACGCATG TTATACGAAG TCAAGAAGAA GCATCGTTTG	540
	AGCTGCTAGC AGTTCCTTGA CTCTCAACTT GGTCCGAGCG TGCGGTGTGA TGCTTCGCAT	600
30	GGGAGAGTAC ATATGTGGTT GCAAGCCACT TTGGAACCTG TGGGCTAAG ATGTACGCAT	660
	CACCGTGAAT GGAAGCGGT ACTTGGTGAC TGGGCTCTC AGT	703
35		

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1617UP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

5	GATCAGTTTG TCGAAGAATT CATGTCATGC AGAGAAATGG GAAGCAATTT ATGCTCAGCT	60
	CCCTCCCCCT GTTCTCTTTC TACCGCCAGG CCATGCAGGC ATGTCAGGCG CTCAACACAC	120
10	CTAGTGACAA ACTCGCCGTT GTCTTGACAG CCTATGCGTT CGTAAATGTT AAGGCCATCC	180
	GATGTTTGAA GAGGTGACAG AAATTCCCGC TGTAAATTCT CAAAGAACT GTCCAAGGGC	240
15	GTATCCTTCA CAAAGTCGGG GCGCCGCTGC AGCACATCTT CCAGCTTCCT CTGTTCCCCC	300
	GAGGCGTTGC TCATGCTCGT GGCGAATGCA CTGCTCAGC TCGGCTCTG CAAGTACGTA	360
20	ATTTTAGCTA TCGAAAATTT TCCCTCTGG CGATGAGTC ACGAAGTCTA CATACCGATT	420
	GACTAAGACA CTTGCCACCC GTTTGGCGCT CATGCCACTA CACCAAGGAC CTCTGGACAT	480
25	CGAGGATCAA CTTGCCATCA TTGCGGACGC CGGCATAGGC GATCTTGACA GCTCAAGCA	540
	AATCTTTTCC GAGCTCATG ATCCAAAGCT CCTGCCATG TGCAGCGACC CAGACAGCT	600
30	CTGCAAGCGG CTGCACATGG CTGCGGCCAA CGGACAAGCC GACGTGGGCC GCTAACTGCT	660
	CTGCTGCTC GAGCCCCCGG CGGGACGCGA CTGGGG	696

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1618RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

EP 0 866 129 A2

GATCCGGCGT CCGGAAGAGC AGCTTATGCT GAAGGGCTAC CTAAGGGACA CAATCCCCC 60
 CCCCCCAAA AAAAAAGCA TGAGACTCTG TATCAGTAGG AAGTCTATCG CATCTTCTTA 120
 TTTAGCCTGT ATATGTCTTT TCCGGGTGTA GACAKTGCGT TGGACGAGTA TGCTCGATGC 180
 GGAATATAAC GTACTTTTTT GAAGAGTAAT ATGGACTTTC GACCTGCAAA GTACCGTCTG 240
 CCGTTCGGT GTCAGACACT CATCGGAACG CAATTGTGTC GCGATCAGG TATGCTTCTG 300
 TTGTATGCTA TGGTAGCTAT AGGGTCTGGA CCGCTATCCA GAGAGATATT ATCCCATTA 360

(2) INFORMATION FOR SEQ ID NO:1008:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 637 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1619RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

GATCAACAAT GTGCGCGGC TGCTCTGTT CCGCCCGGC GGTGATCTGG ATAGCTACGA 60
 GCTCTCGG ATTCGTCGC ATACAGGCG CGCAGGGTG CCGGCGATCA TCGACACCT 120
 CAAGAGTTAC ACCGGCATCG AAGACTTCGA GTACCACGAA CCAGTGAAC TGGGCCAGTA 180
 TGCCCTATC CTCATGATG CCGTCCCCGT AGTAATCATG CTGCGCACT ACTGGTCGGT 240
 TGTGGTGTC ATCGCCCTTT TCCGGCTCT GTGGGGTTC TCCTGGTGT CGATGTCAT 300
 CGCACTTGT AGCGGCGCA TGITCAMCAA GATTAAGGAC ACTCCCTACG TGGCTCGTC 360
 CCGTGATGC AATTACGTC AGTACTTCG AATCAGGCAG CAACAGGTT AGTTGGGGT 420

GGAAACTCAA ATCATCTCCG TCATATATGG CACCCTCAGC GCAGGAGTGG TACTACTTGC 480
 5 CATTGGCACC AAAAGCATCA GAGCTTACTA CATCAAGTAC AACTATAGCA TGCACGGGGT 540
 GGTCACCTTG TTGTTGTCCC TCGCCGCAAT ACTGCTTATC TATATCTCCT TCGCCGCGCT 600
 10 GCTCGCAGTC TTCAAAGTGA AGAACTTTGA GTATTCA 637

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1619UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

GATCGCTTGC TGGAGACCAC AGATTTTCTA GCGTTGTGG TAAGGGGAG ATGGGGTGA 60
 CAACCAAGGA GGAAAAGCTC ATGAAGCTGA ATCCAACAGC TACAGATGG AACAATTACA 120
 40 TTAATACTGA TACCACTGG AGCAAGCCG CTCACCTTC GTCAACAGAG GCTGGACAGG 180
 CAATTGAACG AGAAAAAAA CTAGACCGGA GGCAGACTGA GAAGGACAGT GTAGAGAGCA 240
 45 GCAAGGTTGA GCGCCCGGTA GTAGATGCAT CGTAAGTAGG GTGAAGCAA ATCGCCGGGT 300
 GGAAGAGCG CGACCGACTC ACCGAAGATG ACCTGCACTG GGAGCTTGAC AGAGAAACCT 360
 50 TTTTAAGCA TGTGCTGCT GCTGCTGGT ATGGGACTG GTATCACTCC GTGGGGATAT 420
 TCTTCTCGG CGGATTTTGA TCGTTTGGT TGGGCTACTT CAAGTTCAGT TTATCACTG 480
 55 TATCTTCTGT AATGGTTTTG ACGGCTTTGC TATACCGTAC ATCGATTTGG AAGTACAGAG 540

GGTCGATAAG GGAAGTGGTG CAGAAGGAGC TCACAGTGCA GAAAGTAGAG GATGACTAAG 600
 5 AGAGCATGGA CTGGCTCAAT AACTTCTTGG ATAAATTCTG GACCAGAATA GAGCCCAACA 660
 TTTCGGTGAT GGTGTGGAT CAGGTGAACC ATGAATTGGC TAAGAACCGT CTGTGCCGGG 720

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1620RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

GATCAAACCTA TTTCTTGTTT TGTTGGTGGG AGCATACCTT CGTCAGTACT AACTTCTTGG 60
 35 CTCCACTCCA TAAATTGGTA TTCCCTATTG GGATTAAATT CCGGACCCAA GGTAACGACC 120
 AAAACATTA GAGCAATAGA TCCCCACACA AAATAGGCCA TAACTCTACC ATAATCATAAC 180
 40 AATTCTTTAT TGCCATTATC GAGTGGAAAA TTTCTTGCAA GGCTGCTTTC AAGCAACGAT 240
 GAGGGGCTAG ATGCCAAGTT TCCCAATTGA TATGCCAAGC CCACGAAAAA GGTTTTCGTG 300
 45 TCTGAGTTTG GAGCTAAGCA GGTAAATGA TGTGGGACAA GGCCCCATGC TCCTTGAACA 360
 AAAAAGTGA GGAAGAACAC GGACACTATA ATACTTCTAT CATGTACAAA TCCCCAAGGA 420
 50 TAAACAAGAC AGGCAGCCAA CAAAATACAC ACGAGGATAA CAACTCTTCT AGAGCTTATG 480
 CTGGAAAAAC GTGAAATGAA AAGTCCACCT ATTATAGCAC CAACGTTGGC TGCACAATTT 540

GTGACGGCTG ACTGATTGGG AGAATAACCA AGTTGTTTAA TGAGCATGGT TGGAAAGAGA 600
 5 TCTTGAGACG CATGAGAAAA GTAATTATAA CCGTCATAA GCAATATCAT GTAGATGACA 660
 ATGT 664

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1620UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

GATCAAATAA AAATAGAAAT TAGCTTAATG GTAGAGCATT CGTTTTACAC ACGAATAATT 60
 35 TGAGTTCGAT TCTCAAATTT CTAAATAATA ATTAACAATA ATTTAAATTT GGGTAAAAAT 120
 TAATAAATAT TAACGTATAT AATAATTATA TACTTTATAA AATTACTCAA TGTTATTAAT 180
 40 AAATTTATTT CTTATCATTATA ATAATGATGT ACCTACTCCA TATAATATAT ATTTTCAAGA 240
 TTCACTACTA CCTCATCAAG AAGGTATTTT AGAATTACAT GATAATATTA TATCTATAT 300
 45 GTTACTTGTT TTAGGTTTAG TTTCTTGAAT AATAATTATT ATTATTAAAG ATTATAAAAA 360
 TAATCCTATT CTTTATAAAT ATATTAAACA TGGTCAAATA ATTGAAATTA TTGAACTAT 420
 50 TTTACCAGCT ATTATTTTAT TAATAATTGC ATTTCCATCA TTTATTTTAT TATATTTATG 480
 TGATGAAGTT ATTTCAACCAG CTATAACTAT TAAAGTTATT GGTTTACAAT GATATTGAAA 540
 55 ATATGAATAC TCAGATTTTA TTAATGATAA TGGTGAACT ATTGAATATG AATCTTATAT 600

EP 0 866 129 A2

AATTCCTGAA GAATTATTAG AAGAAGGGTC AATTAAGAAT GTTAGATACT GATACTAGTA 660
 5 TTGTTATTCC TGTTGATACT CATGTAAGAT TTATTGTTAC AGCTOCTAGA TGTTATTCAT 720
 GAATTTT 727

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1621RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

GATCCACCCA COGGTACCTC CTACTTGGCC GTATCTGGGT CTCGGTGGCG CTTCGCGCTG 60
 35 AGATGCTGTG GGGCCGAAAT GTACTCTCAA ATGGGCTTGT TCAGTGGCCC ATACAGCTCA 120
 TTAAGCTCAG TGGCCCCGAT GCTTAGTAGT AGCTGCGCGC CTCTTCATAC TGCTGTCTTG 180
 40 TATTATTCAT CTTCCTGTAT TTCTCTCTG TGTCCGCTCA CGCTGCAGG GGGGACTGCC 240
 TGGCGCGCGC CGCTGTCTCT GCTTTCTCGT CTGCTGTGAA AATGACAAA CTCCAAAAAA 300
 45 TCGAATTGTTG CGCGCCCGAC AGTTGATTAA GCTCGGGCAT CTCTATTCTC TATAAATTGT 360
 TAAATTAACC ACACTGTGAA GCCCTGCAAT CCGCACGCGC CGCACGTCA ACTCTTGGTC 420
 50 ACAACCTAGC CCGGGGAGTG CAGTCTCACA AATACAAGGC CTGGGATATC ATGTACTGAG 480
 GCCTCCTGAA CGTTTTGCGT TTTTCTTAAA ATCGCTGTTC ACAGTCTTAG CGCAAAAAAA 540
 55 ATAATTTAAA AAAAAAATGT AAAGTCTTAG TGAAATGAAA AAATAAATA AAATAGACCG 600

CCAGCTGCAG AACACCTCTT CAAAGCATAT AACTAGCATA CGCATAAACA TATGCTTGTA 660

5 TACTC 665

(2) INFORMATION FOR SEQ ID NO:1013:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 666 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1621UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

30 GATCTCTTGG TTCTGCGATC GATGAAGAAC GCAGCGAATT GCGATAAGTA TTGIGAATTG 60
CAGATTTTGG TGAATCATCG AATCTTTGAA CGCACATTGC GTCTCTGGT ATTCCAGGGG 120
GCATGCGTGT TTGAGCGTCA TTCTCTTCTC AAACCTCGG GTTTGGTAAT GAGTGATACT 180
CGGTGTAAG ACAAGGTTAA CTTGAAAATG CTGGCCATGG GCGGAAGTTC CGGGAGCTGC 240
GGTCTGAGCT AGTTTCTACA CTGGGTATTA GGTTTGACC AGATGTTGA GTGGAGCTGG 300
CGCTTGAAGA ACGTACGACA AACAGGCCT TCCAGGCGAA TAGTATTCCC AAAGTTTGAC 360
CTCAAATCAG GTAGGATTAC CCGCTGAAGT TAAGCATATC AATAAGCGGA GGAAAAGAAA 420
CCAACGGGA TTGCTTAGT AACGGCGAGT GAAGCGGCAA AAGCTCAAAT TTGAAATCTG 480
50 GCGCTTCGG CGTCCGAGTT GTAATTTGAA GAAAGTACCT TGGTTGCTAG TCCCTGTCTA 540
TGTTCTTGG AACAGGACGT CATAGAGGGT GAGAATCCCG TCTGGCGGGG GTGCTAGTGC 600
55 CATCTAAGGT TCTTTGACG AGTCGAGTTG TTTGGGAATG CAGCTCTAAG TGGGTGGTAA 660

ATTCCA

666

5 (2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 676 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: PAG1622RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

GATCCGIGTA TTTTITATTT ACATTATTTA ATTAAAAATA ATGATTTTAA TAAATATTTT	60
TTATAAAAAA TAATTAGTGC ATTGTTACAT GTTCATTAAA GAATGATTAT TATCAAAACC	120
ATCAACTAAT TGTTATATAT TTATTAAATA TTAATTTTAC TTAATTAGA ATTAGGAAC	180
TTATCTATTA GTCTGGGCTG TTTCCTTTT GATTATTAA CTTATCGCTA ATAATCTGAA	240
ATATTTAATT TTAGATTAAT AATATATCT GAGATTTAAT ATTTTAAATA AAATAAATAA	300
TTATTCCTTA AATAATATTA ATAACTATAC CATATATATC TAATATTTAA ATAATCATAC	360
TAACATATGT TCGTAGAAA ACCAGCTATT TGCAAATCAG ATTGACTTT CTCTACTTAC	420
CATTATTCAT CAGATAATAT TGCTACATTA ACCTGTTCAA TCGTTTTTAT ATTTTATTAT	480
ATTTTAAATA TAATAAATAT ATATTTTAAT CATTGATAA TAGTAAGATC ATCTGCTTTC	540
GGGTTAATTA ATATTAACTA AATTTAATTT ATTTTAATTA ATTTTAACAT TGTTAAATAT	600
TTATATTATT TTTAATATCA TTTTITATTT TAATATTATG CTAATATTAA TTAATTGCTG	660
ACCATTTATA CAAAAG	676

(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1622UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

GATCCAGTTA CTTAGTAGAA TGATAAAATT AATAAATATT ATTTATTAAT ATTGGGTAA 60
CAATAAAATT CAATAATTTA TTAAATAAT GATTAAATAA TCICAATATA AAATTATTAA 120
TATAATGAGA TATATATTTT TAAAAGAAT ATATAATTAA ATAATCCCAA CCAAATTG 180
TGCCAGCAGC TGCGTAAGA CAAAGGGGGT TAGCGTTAAT CGTAATGGCT TAAAGGGTTC 240
GTAGAATGAT TATTTAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA 300
GTAAAGATGA AATAATAATT ATATGAATAA GACTTATAAA GTGAAAATTT AAATTATATA 360
TTAATTGACA TTGAGGAACG AAGGCTAAAG TAGCAAATCG GATTCGATAC CCGAGTAGTT 420
TTAGCAGTAA ACAATGAATA CCTATTTATT TTTTATTAAT TAAAGAATAA ATTAAATGAA 480
AATTAAAGTA TTCCGCCTGA TGACTACGTT AGCAATAATA AAAATCAAAA CAATAGACGG 540
TTACAGACTT AAGCAGTGGG ACATGTTATT TAATTGATA ATCTCGATA AATCTTACCA 600
TTTTTTGAAT ATTTAATTAT AATAATTAT AATTAATTAC AGCGTTACA TAGTTGTCTT 660
CAGTTCTGTC TGCAAAGTTT TAGAATTAT CATAAACGAA CATAACTCTA AATATTTT 718

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1623RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

GATCACAATC GCATGGTATG ATCGTTTTAG AATCAACGAA ATATGACAAA ATGAAGGAAC 60
ATATTGCCAT AAGGACTTCA GGTATTACAG TOGCAGATAT TCTATCGAAG TCCACTGAGT 120
ATGGTTTAGT ACCTATACCA AAAGAACAAT TTGAACAGAT TAAATGGAA TTAGAGCATC 180
CAAAGTTTAC TAGAGAGATG ATGTGTGAAC ACGCTGGTGA CTTCGACTTA ATTGCAGTGG 240
AATTAAAGGA ATACAATGCG CTCAAAAGC AATGCGAGTT CTCCTTTGGT GACATTTTCG 300
ATAGCATTAA CACTGACGAG GAAAGTGAAG CATCTGATTT TGAATATCAT GATGACGAGA 360
TAAAGCAGCT TAACAAGACA GCCAAACGCT TTGGGTTAAT ATGTATTCCA GAAGCTGCGT 420
TTATCGCTAC TTCCGTGCGT AGCAAGCGCTG ATGTGATAA TGTCGTGCTG CTACCAATAA 480
GCTACTATAA TAAGTTGATT GCGAATGAAG CAAAGAGCCT CGAAAAGCTG ACTGACTGGG 540
ATCTTCAGTC AGAAGCTAAA AAACGTGGCT ATCATATAAA TTTCAGCTTC CAGAAGGAGG 600
ACGCCCCACC GCGCCTTCA ACCCTATGTC CTCACGGAT GCGAAGTTT TCCCCAAAAC 660
CGTTCGACTT TGTCACTAGA CTCAAAACCT ACTAGAAGGG CGTTTAATGA GGCTGCTACT 720
GTGCGCGCAC AGAGCGAATT TGAACAG 747

(2) INFORMATION FOR SEQ ID NO:1017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 758 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1623UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

GATCAGCGCA AAACACATCT GTATTCCAG CAGCATGTCC TCCTCCACTT GCGCATGGC 60
CTGGCTTGCA AAGCCGTCCA CCTCGCGTC AAATGAAATG CTGTCCGAA TATTCTCAG 120
TTTGCAACC ACAGGGTTC CGTGCTGTC GTACTCTGT TCCTCATCTT CCTCACTGC 180
CTCGTCTCG CCGCGCAGT CCACGGGCT AATGCTCAGC TCGGAGGCT CCTGGGATA 240
CCGCTCCGC AGCGTAATGT CCACCACAA GTGCTGCTC TTGCTGATG CAGCCGCGT 300
GAATGAAGAG CTTGCCAGG GGATCAGATC CAGTTTAGG TCACTTCAA ACTGGATTTT 360
CGGGTACTCC CCGCACCA CCGTCAAGT ATCGGCATAG ATGGACTCAA GCACTTCCAG 420
CTCTGCTTT TGCTCTCTT GATAGTCCAT ACCTATCCG TCGACCACT ATGAGGCCAC 480
GCGCAGCTTA GGGCTAGACC GTTACAGCTG CAGGTGACG TCCGGGGAC GATGCGCTAT 540
CGCTGGCGAA ATTTTTCGCC TATACCACCA CTATGTTAC CCGTCTATA GTGCTGCTCT 600
CCGACTCAC TGATGGTCT GTCCCGCGG GACTGCTCC TGTGCGGC AAATCCAC 660
CGTCTGAAC GCTCGTTCCA TCTGCTCAC GGGTTGACG AACGGGAATT GCGCGCGCG 720
AGAAATCTTG GCGAACCATG CTGCACTAG CCTACTG 758

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1624RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

GATCGCAGT CATTTTACCT ACAGGCTGGG CTTTGAAGA AGACGCTGC ATGGTACAAT	60
GTCGTAGCCA GGATCCCAAC TGTGACCAAG TTOGCCAGAG AACCGAAGCT GCATGACCCA	120
GTTAGCGGCA AGTACAAGGG CGAGCTGGAT ATAATGACGG ATAGATTAAA CAGAAACACA	180
GAGACGTACA AGACACGGGC TGGGAGTTCC GACCGGCAGA CGGCGCGGT GCACAAGCCT	240
TCTAAGCTGC GGTTTATCGA GGACAAGCTG CGGTGCTGT TTTTCAGCA GCATCCTGG	300
GAGCTGTGCG GGCGAAGGT GCTGGTGGAG AACATGGGAA ATGAGCAGTA CCACTGGTGG	360
CGGATGTTGC AGCTAGGCAA GCGCTTGAC GGTGAGTCTG TGGTGCAGCG GACGCTGTAT	420
CTGCTGAAGT CCGGCGGCA CCGGAGATG CTGGGGCAT ACGACCAGGC GCGTTTGAG	480
TTCTATCGTC TGAGGATGCA GCAGGAGCTG GAGGAGCAAA TAGCGTACGA GGAGGOCAG	540
ATGGTTGGCG CTGTGTTCAA GACAACCGCT GTGGAGCAGG GTCTGCAGCA AGAGCAGAAG	600
GTCTCGACA AGTGAAGGA GGACGTGGTT GCGGGGTGTC AGCTGATGTC TCGAAGAAG	660
AACTCTACAA AGCAGTCGTG GCGCGAAGCC	690

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs

EP 0 866 129 A2

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1624UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

GATCATATAT CTTCCTGTGG TAAGGTCTGT GGAAGCAGC TCTCTGCGG GAATCACACT	60
TGTCOCATGA CCGCCACGA TGGTAACTGC ATGGATCCAT GCGCTGTTAT AACTGAGCAG	120
AAGTGTGCAT GCGAACAGAG GCGTTTCCTT GTTCCTTGCC AGTTCCCCCA TTCCCCAAGT	180
TGCACTGCAA AATGTGAATC ATTGATGTCT TGTGCTGCC ATCGGTGGC TGAAAGATGC	240
TGTTCCGGTA GACCGCATTC TGTCAAGCGG AACTCTAGC GCGCGGTGA GAGTCCAGAT	300
GATGAATCTG AAGTTGAGGC CCAGCAAGTG TGCTTAAAG ATTGTAATCG GGTGCTGCTT	360
TGTGGTATCC ACATGTGCAA TTACAAATGC CATGCAGCA AATGTCTCC CTGCTTAGAA	420
TCAGATTCCA ATGACCTTAT CTGTCCCTGT GGTAAACAA TGTACCAGC CCGTGTCCGT	480
TGTGGAACAA AGCTCCCTCG CTGCACTCAT CCATGTGAA ACTGCTGCT GGATACTTGG	540
CCCTGCGGAC ACAGTCCACC TTGCATAAT TGTATCCCT TAGATGAAC TTGCCCCCA	600
TGTACCATCA CAGTCAAGAA AACTGTGCGC TGCGGTAAAA ACGAGATCAG GACATTCTGC	660
TACAATGATG ATGTGTCTGT TTGAGACCG TGTTAGAAGC CATTGTCTTA TTGCAATCAC	720
TTCTGCCAAG TTCCCTGTCA TT	742

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 725 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1625RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

GATCAACTAC GAGGACTTGA CGACCGCAAG ACGGGAGCTC GCGGCGGCGC TGGCCACTTT	60
GGAGAATATG TAGCGCACAA CATCAGCAAT GTTACAGTAC AGAGTCTAT CCGTGGGGTA	120
CGGCTATGAT GAATAGAAAT ATATACACAG CTGCTGCAG GCAGCTTAGA AGCGCAGAGG	180
CTTGGGCTTC TCCACGAGT ACTCCTGGTT AGTGAAGTGC CCGTAGAGG CCGTAGGTAG	240
GTAGATGGGC TTGGCGAGGT CGAGCTCTTT GACAAGAACA CCTGGTCTGA GGTGGAAGTT	300
GTGCGGATG ATCTCGATCA GCTGCTGTC GGACTTGGTG CTGGTACCGT AAGTCTGAC	360
GTGGATGGAC AGCGGCTCGG CAATACCAAT GCGTAGGCA AACTCAACCT GCACACGCTT	420
GCACAGGCGG GCGGCCAACA GCGACTTGGC GACCCAGCGC GCAGCGTAGG CAGCGGAACG	480
GTCGACCTTC GAATAGTCTT TTCCGGAGAA CGCACCGCCA CCGACCGCGG CCGCACCGCC	540
GTACGGGTCA ACAATGATCT TTCTACCGGT CAGACCTGCG TCACCTTGTG GGCACCGATC	600
ACGAAGCGGC CGAAGGCTGC AAGTAATACT TGGTGTTTTC GTCTAGCATG TCGGCAGGGA	660
TGACCTTGCC TACGATGCGA TCGCGCAACG CGGAACGCAG GTCTCGGTG GAGATGTCTG	720
CCGCG	725

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1025UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

GATCTGGCTC TGGGCCATCC CAAACAACCT GGGTGTGAC AAGAAGTACT ATGATGAGCA	60
CAAGAAGGAA TGGGCCATGT ACCAGGAGAT GATGAAGCAC TATGCCAAG AGGACCTTGT	120
CGACACCAAC ATGCAGGGCG GGTTTATCGT CGGCGCGCCA CTCCACGAAA TAGAGCTGGA	180
CAACTTCAG CTGGCGTCT ACAAGGAGCT CGTAACTAGC ATGTTCCCT GACTTCATGG	240
AGTCCAGCAT CGCCATGTT TTATGCCAA TACTTTTGAG ACTATACTTA TATTATATAC	300
TGATAACAA TTTCGCGCGC TCTCTACGC CCACTACTTG TTCTCGCGT AGAAGAAGTT	360
CACGGCATC AACTCGAGGT TCTTCTGCC CGCAAACTG CCACACCCA CAGGGGGCGG	420
CTTCTCGGTG TAGCCCCAGT TCAOGGACT CTGCAGGGG GTGAOCTCT CCTGCTCAG	480
TTCTAGCGC CGGGCTGCC GAAACAACAA CCACACGTAC CGGTGAGCC CTGTGCGGC	540
CGGCGCGCA GGGCCATGT GCTCCACTG CGGGGTGCC TTAGCACCA CGTGGACAC	600
CCCGTCATC GAGCCAGCG TTATGTCGT TTCCAGAAAG TGGCAGTATT CCGACCACTT	660
GTGGTCCGAC CGGAGGGAG CATCTGGTC TGTCATCCC AGCGTGAATA GGTCCCTCC	720
CTGACG	726

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 643 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1626RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

GATCGTGGG GACCATGGGC AGATGGGGCC CTTAATATAA GCCCCTCCTC GCAGGCATGA	60
CGTCTGCCAA CTCGACCAT TCTAAATGGC CAGCTGCTGC TTGATGGTA GGTCCGGCG	120
CTGGCGCAGA AGTAAATATA GCCATTAAAT CCCCTTCTAA ATATACATTA CATAACAGCG	180
CTCCAGAGGC GCTCCCGAGG CGCTCCGAG GGGCCCCAGG TCTCGCGCA GCGAGCGCG	240
TGCGAGCTGG CCTCTGGCC ACGCAGACAT GGGGCGGAC GGGCCAGT TATATACAGC	300
CTGGCCTGTC TCATATGCAG ATGGGTCTGA GCGAAAGAAG TTCTCGCTC TCGAGAAGC	360
AGTCGTGTG ACCCTGGGC TCGGGGCCA ACGGCGAGC AGAGAATCTT CCAGCGCTTC	420
CCGCGACCC GCACTGGGG TACCCGTGCA GGTAAGGATA CTTGCGGCG GCGCGGCAC	480
CACCGCCCTC AGCCTGACTT GCGCAACGGC CATAACGAGA GGACCCGCT GCTTCGGCG	540
TTTCGTGCCT GTGCACTGA TCTACCGCC TGCTCAGCC GGCCTGTCA ACGATGGCA	600
CCAGACCCCT CAGAGGTGC CTTGTGCC CAGTCGAGC CCA	643

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1626UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

GATCCATGCA TATTTCGAA CTTACGAAA AAGGCGTGAA GAGGCGGAAC GTAATCTAGG	60
TTTGAAGAA TTAATGAATG ACAACATAGA CCTTGTACA GGAGAAAATA ATGAAGAAGC	120
CCAGCTGAAA CAAAAGAAGT TGTTAGAGGA GCAGTTGGCA AAGTTGGAGA AATCAAAGGA	180
AAGACGACAA GCACGCAAGG CCGCGAAGGA GAAGAGCAA GATGGCAAAG TCGTGAAAGT	240
AAAAAACACC ACGCGACGCT GCGCAACATG CCGTGGGATC GGGCATATCA GAACTAATAA	300
ATCCTGCCCC ATGTACAATG GTGGCGTTGC AGCAAACGCA AACGCAAACG CGAATGGGTC	360
GAGTGCAGCA GCTGCAGGTT CTTCAGGGAT GGCTTCAAAT AATAGCGCTA CCAGCAAGTC	420
TATACTCCT AATGCCAGTA TTCCGCCGAC TTCATTGAC TAGCTGGCAG TATAATATAT	480
ATCTAATATG TACCAATTGT ACTTCTTTG ACTGCTATAG AACTTTCTCC TCTTCTTGCA	540
TCACATGTGC AGCACTGCAG CACCGTGGC CTGCAATAC TTATGGACCG CGGCAAGGTC	600
GGCTCGTAT CCAGCGTACG CTATGTATCC TCGGGGACCC TTATTGGTGC GCGACAGGG	660
ATAGTCACA GACTCCACAG AAGTGTCTC TACAATGCAG AAGA	704

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1627RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

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GATCTTCCTT GAATTTACTT AGCAGCTCGT TAATTTCTCTG CTCTTCTGTC TCTCTAAGCT 60
GGAATCTGTA AAAGTCTGTC TTGGCCTTCT TGTCACCAT GCTGGGAGGC TTCTCTTCC 120
GTGTATGCTT AAGAAGTGA TTGCGGTCA GAATCTACG CCTTATGGAG TTTAACGATT 180
TTGTGTCTT COCTACTACA AGTGTGAACC CGTCTCGTC CACAATACTC GATTGAACCT 240
CATCTGCGC AAGTTGTTC CGTGTCTCA ATAACAACAT ATGCTGTGA ATGTGCTGC 300
GCAAGTACTC AAGGTGAGT GGCTTATAGA AGCTCTGGAA GGTCGTATC GAAGGAGCT 360
GGAACGCCA CTCCACCAAT TCCTTTTGT TTGTGCGTA TTGTGCGAGA GCAGCCAGC 420
AGTTCTCCAG AGATGCTGG TCACAACT TCAACAGAGC ACTGTTCTC GGTGTATAC 480
TTCTGTCTC CGCATCCCG GTGTCTCTGA AATCGGAGT CAGGCGACC AAATCCACT 540
CGTGCAATCC GAACTGTG TGATGTAGCA GCTCTGCCAC ATGCGCCACA GTCTGTACT 600
GCGCGCAAT CCTGCCAAG CTCTCTTGA TAGAGTGCAC CTGTGTCAAC AGAGGTAAAT 660
TGACAATAAA CAGGCAATTA GCTCCGATT CCACCTTCGT CTGATGCTC CTC 713

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- 45
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- (A) LENGTH: 736 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1627UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

5	GATCTTTGAG ACGCGGCGCTG GAGAGTTTGT AGCAGATTGT TGACCAACGC ATAGCAGATG	60
	CTAGACCTGA GTCATACACC CTCGTCCTTG TTGGAGACAC GGAATTGCTA AATTCAAAAA	120
10	TAAAGGAGGA GGCAGATGAA GTGATTGAGG CTATAACGCC AGCTGAACTA CAATGGGAAG	180
	TTGGGGAATT GCTGTATTTT CTCATGGTTA AAATGAGGAG CAATAATGTG ACTTTAAAGG	240
15	AGGTGGAAGC CAACCTAAAC ATGAAGCACA TGAAGATTAC GAGACGGGCT GGAAACGGCA	300
	AACCAAAGTA CCTACCCGCG CAGGAGTGGC AGAAGAACA GGAACTCCT GTAGATATTG	360
20	CACCATCTGC CATTACTTGT AACGTGTAT CCTCAGATGA TGAGGCGCA TTGAAACAG	420
	CAATTACAAG GCCAATTCAG AAACTACTG ATATATTAGG TCTTGTTGAG CCTATAATAA	480
25	AAAAAGTGAT AGAGGAGGCG GACAATGGT TGACTGAAT AACAGCGAGG TTTGATGGAG	540
	TAAAGATAGA AACACCAGTA CTAGAGGCTC CTTTGGCGA CGAGTATTTA AAAGGATTAA	600
30	CGGAAGAGCT CCGTACGGCC ATAGATATTT CGATGGAGAA TGTCGGTAAA TTTCAATGCG	660
	CACAGCTGAG AGACGATATT CTCAAGGTG AAACGCAACC GGGGGTGGTA TGTAAGAGAT	720
35	CCCGAGGCCA TAGAGA	736

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1628RP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

5	GATCTGCCCC TTTAAGCAAC CACATATTAA GCGCTGACA CACAGACTGT CAGCGCTTAG	60
	AAATACTTCG GTGAGTGTC AGAAGCCCGA GCGCTGGAG TTATTCATGA TCACGTGATG	120
10	GGTATTGACC TTGCGATCCA CAGACAGGCG GAAATATGCA TATATGTAAG CCAAGATGCC	180
	GGCAACCAAT TGGTCTAACT GTAATGCATA ACACTGTATT CCGCGAAGCG GCTCTGAGCA	240
15	TGTATGGTAT TCGGCGCTAG ATTGTCAGCC CACGTATATT TCCAAGTGAC GCGCTGATGC	300
	TATTTACAAC ATAATCACTA TTGACGAGCA AGGATAGTGG TCGCACGTTA CGAAAAAGAA	360
20	ACGTTGAAAA ATTGGATGG TGGTGATGAG GTAGAGATAT TAACGTTAAT GGGGAGCAC	420
	GAATTTGGTC GAAGTTCTAT ACTGCCAAGC ACGTTCCGAG ATTGCTGAGT TGATGGGTTT	480
25	CAAAAGTATT AAAAAGGCGG TAGTCCCTAA ATTATCGGAA AAAGCCAAGG AGGAAGAGTT	540
	GAGCACTTCG GCGTCTCTG ATTCTACTTT AGAATCAAGT TCATCTTCCT CGTCGGAGGG	600
30	CAGCTCCAGC AGCAGCTCTA GTTCTCCCGG ACAGTGAATC GAGCTCGTGG GACAGCGGCT	660
	CCAGCTCTTC TAGCAGCAGC TCGAGCTCCT CCGGGAATC GGGCTCC	707

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1629RP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

5	GATCTCCAC ACTAGGCTGG GTCTTACTGT CCATGAATAG CATTGAAGA ATGGAGGAAT	60
	CGGTCTTCAA GTCAGCGGG AAATTTTCAG GGCAATATAA TGGTTCOCOA GTATTAGAA	120
10	CTTCTOGACT GTCGTCAGTA CTGGGCOOCT TTAAATOGGC TGTTCOOCTT GAAGATATAC	180
	ACCATTCATT CCAGTGTATC GTACCCGAAA AATTAGCAGT AATGGCACTT GGAACATCAT	240
15	COGGAATCGT GTAAGCACTT GCAATAACTG AAAGCTTTGT AAGAGAGGTA AAAATCGGTG	300
	CGCGCGTTCC AAAATTGTCC AATTGTGAGA TTGTGTGATC TTCATTAGGC CTACTGGCCA	360
20	GTTCACCTAG TGATCTAAG GGGCTTATTT CAGTGGTTAG AAATTTATCC TTCTCAGTTT	420
	TGACTTACA AGCAAACTCA GTGAACAAAG GGGGTATCG ACGAGCAGCT CTGTGTGTAAG	480
25	CTGCTGAGGT TTTCOCTTGT GAAATAACAT GTTCTTTAGT TTCATGTAGG GCTCCAATCC	540
	ATGCCGTTAA CTCITTATAA CTGGTTGCTT GGAAAATTAA AGTACCAGAG TTATTAGAAT	600
30	ATTCTTCTTG AGGTGAAGAA GTTAATGGAG AAGAGATAGT CATTGGAAG CAGTATTTAC	660
	GTGCTCTTTC TGGATGGTGC ATGGCACTGA GTAATAATAC TCCAAATCTG TCCGTTTCTT	720
35	CGACTGCACT TTT	733

(2) INFORMATION FOR SEQ ID NO:1028:

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|----|-----------------------------------|
| 40 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 742 base pairs |
| | (B) TYPE: nucleic acid |
| 45 | (C) STRANDEDNESS: single |
| | (D) TOPOLOGY: linear |
| 50 | (ii) MOLECULE TYPE: DNA (genomic) |
| | (vi) ORIGINAL SOURCE: |
| | (A) ORGANISM: PAG1629UP |

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

5	GATCTGGGCT CGCTGCTGGC GCTCGAGCCC TACTGGGCAG AGCGCTACCC AATAAACAAC	60
	GCCCTAATCG GCGGTGCAGA TAAATTGCAC AAGCTCTACT CAACCGATT TTGGGCCCATC	120
10	GTCGCCGCCA GGACTTTTGG CTTGAACCTC GTGACAAGC TTGGACCGCT GAAAGACCTC	180
	ATAATGGCAA AGGTCAGCGG CCCAAATTAA TAGTCACGTG TACATAAAGG TTTTCTTAAT	240
15	AGCTATACAG CTTGCCCGCG TCCTCAGCTT GCAGCGGCA ACCGGGTGC AGCCATGAGC	300
	GTCTACTTGG AAATACCAT TGGGACCTT GTAGTAGACC TGACTACAA GACATGCAGC	360
20	GCCGAGAGCT ACAACTTCCT CAAACTCTGC AAAACTCGCT TCTAGACTG TCAGTGCATC	420
	TACGACCTCC ATCTGAAGG CTCAGCAGC CTGGGCGATC CACAGGTGG CTTTGCATT	480
25	CGCAGGATT TGCTGTACA CAATACCTCG ATCGAAGCC TGCGGACAC ACCGGGGTTC	540
	ACCCCGAAGC TCATTGAAGC CTCGGTGGC GCTCAACCG CAGAGCGCTT CGGACAGGTC	600
30	GCCTTTGTGC TCAAGCCCG CACTCGCTTG CTGGGATCCA ACATACTGCT CGCGCTTAAT	660
	CCCGAACTCG GCGGCACATC AACACAGTGC GCTTGGGCA GGTATCGAC GAGTGGCTGG	720
35	CAGTTCTGCA GCAGCTCAGC GA	742

(2) INFORMATION FOR SEQ ID NO:1029:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 692 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50	(vi) ORIGINAL SOURCE:
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(A) ORGANISM: PAG1630RP

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EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

5	GATCGACTTT CAAACATTAT TATACAGATG GAGGGCATCT CACATCTTGC ACAGCAAGAC	60
	GGCAATCCAA CAGGTTCTGT AATGCAGCCT AAGAGGCGAA GGGTTGAAGA TGGAGCGTCT	120
10	AGTGATGGAG AAGTACGAGG AGAGATAAAG CGCAAGTATG GTATTGGGCG GCAGTTGATG	180
	GCCAAGATGG GATATAAGGA GGCAGCGGT CTAGGGAAAG AAGGTACGGG ACGCACGACG	240
15	CCGATATTGG TATAGCAGCG GCCGCAGGGC ATGGGGCTTG GAGCCAACGT CTCATTITCC	300
	TCTGACTCAG AGCAGAGTGA GGTGGAGCTT GTGACTCGCG AGGCAGTGAA GTTTGAATCG	360
20	AAAGGTGTGG AGACTGACAC AAGCAGAATA GCAGACAAGA TAGCAAAGCT GGAGATCGCA	420
	GGAGTGCAAG TCCCGCAGA AGTGATGAGT TTGCGTCTG GCACAAAGAC GCTGGGTTAC	480
25	CAACGGGCTG CAGCGATGGA AAGGGTGCTC TCGGAAGTGC TGCAGGTGGG TGAGCAACTT	540
	GCGACCTTAC AACTACGCGA AGATCAGCTG CAGCAAGGGC TAGATGCGGC CATTGAGAGT	600
30	AGTGACCTGT TGAACAAGTT CTCAACGGCG TGCAACAGCC GACTGCGCTG CCGGAGCGGG	660
	TAGCGGCATA TTGGCCTTGG AGGACCCAGA AA	692

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1630UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

EP 0 866 129 A2

GATCGTCGCC TCATCGGTGA GCTGCGCCCC ACCGGCGAAC CTGGCAGCCT GCGCGGCGAC 60
 5 CCGCGCGCGG TGGGCGACCC GGTCCAGTC GGCGAGCCCC GTGGTCCCCG GACCATGGTT 120
 ACCGTATCGT CCCCAGACAA TGGCGAGGGG TAGATGATGC CCTCCTCCGC CTCGCGCGTA 180
 10 CCGCGCGCCT CCGCGTGTG CGCTCCTCT GTCCGGCCTG GCGCGTCCC GTCCCCAGAC 240
 AAACGGTGCC CCGCGGCAC CCCAACGCG AGGCTTTCCG CCGCGGTGG CCGCGGCGC 300
 15 CGCTCCGG CTCCGCCAAG GCGTTGCC TGACCCAGTC CTGTAGGTG CTCGTGGTCA 360
 TCGAAGGGCG TCCAAGCAAT TGTGTACGA TGATCTATGC CAGCCGAGC CTTCGTCACC 420
 20 AGCGCGGCA GCTGCGGCAG CTGGGTTTG GTCTGTCCA TATCGTGGTC TGGTCTCTG 480
 TAGGCATCAT ACATCTCCG CTATCTTCT CTTCGGCCTG CACCGGTACC GTGCATTGGA 540
 25 AACGCTGCTC CTGCCCAGG GCAGTTCTAT AACGTTGCCA GTGAAAATG TGCAGTACCG 600
 AACAGTAGCT CATCGGCAC CAGGCGAACA CATAGGCAAC AGCTTCGGTG TAGCGGGCTG 660
 30 CCGCCCCGAC CACGATACTC ATGTTACATA GACTCACATG ATCAGGCAGC AC 712

(2) INFORMATION FOR SEQ ID NO:1031:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 729 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1631RP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

55 GATCTAATTT ATTACATTA ATTAATAATT AATAATATTT AATAATATTC AATAATTTAT 60

EP 0 866 129 A2

	ATATTTTATT ATATTTAATA ATTATATAAA TACTTTAATT ACATAAATAC TTTAATTAGA	120
5	GAGTTAGGGT TCACCCCCCT AATGCTTATC AGCATTATGA GGTACCACTC TAATTAAAGG	180
	TAAATATATA TATTTAATAA TAAAAGGATA TAGITTAATT GGTAAACTA TTGACTTCAA	240
10	ATCAATCATT AAGAGTTCAA ATCTTTTAT CCTTGTATA TTTAATAAT ATAAATTAAT	300
	AAATAATAAA TATGATAAAT CATAATATTA AAGATATTGA TTAATATTTT TAATTAATTA	360
15	AATAATATGC AATTAGTATT AGCAGCTAAA TATATTGGTG CAGGTATTTC AACAAATGGT	420
	TTATTAGGAG CAGGTATTGG TATTGCTATT GTATTTGCAG CTTTAATTCA AGGTGTATCA	480
20	AGAAATCCAT CAATGAAAGA TACTTTATT CAAATTGCTA TTTTAGGTTT GCTATTAGTG	540
	AAGCTACAGG TTTATTCGT TTAATGATTT CTTTCTTATT ATTATATGGT GTTTAATTTT	600
25	ATTAAATTAT ATAATAATTA ATATTCAAAA TAAGTTATAT TAGCTTAATT GGTAGAGCAT	660
	CCGTTTGTGTA ATCGAAAAGG TTAGGAGTTC AAATCTCTTA TGTAACAATT TAATTAAATT	720
30	AAATAAAGA	729

(2) INFORMATION FOR SEQ ID NO:1032:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 716 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1631UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

55	GATCTTAAAA TAAGATAGAA TGGTAATAAA TATCATTCAG GTACAATAGA TGCTGGTGTT	60
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ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCTTA AAGTATTAGG TGAAAAGAAT 120

5 ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGTTA CTAAATCTTT AAAAATAAAA 180

TAACCATGCA TTGGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA 240

10 TGTACATGTA ATAGCATTAA ATGCATAATT ACTATTGCTG CAATAATAAA TGGTACTAAA 300

TAATGAAATA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TCCTCATAAT 360

15 CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA 420

GCACCTCAAT GTGACATTTG TCCATATACT AAACAATAAC CTAAGAAAGC TGCTGCTATA 480

20 GTTAAAATAA AGATAATAAC ACCAACTGTT CATACAATAA CTCTAGGTGA TTTATAAGAA 540

CCATAATATA AACCTTTACC AATATGAATA TACATACAAA TAAAGAAGAA TGAAGCACCA 600

25 TTAAGATGCA TATATCTAAT TAATCAACCT AGTTGTACAT CTCTCATAAT ATGTTCTACT 660

GATGAGAAAG CTAATTCAAT ATTAGATGAA TAATGCATAG CTAAAAAAT ACCAGT 716

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1632RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

GATCTTCGGC CGTTGCGGC CCAAAACCCG CAGCTCCCAT ATACCCGTGT TCAGGTTGAA 60

55 GCTGATGCTA GCGTGCTGCC GCGACACCAC TTTCGCAGGC CCCAGGTGCA TGTGTACTGA 120

CCGGTCTGTC GGAGACGTGT TCCGCCCGAT ACTCGTCATC ATGTCCCTTCA CGTAGTACGT 180
 5 CCAGTCTGCT CCGGATATCT TGGCGTACGC CTGTACTTCC GTTGCCGTGT TCTTGTGCTT 240
 CGAATATACT TCGGACACTG TCGTGGCTC CTTCGGGCA TCCAGCACCG AAATCACCGC 300
 10 ATTGATCAGC TCTGTCTCC GTTAGTACTC GGTCTCGTGC CGCCCGTCTC GCTCCTACAT 360
 AACTGCTGGT GCTGCTGAGA CGCAATGGG TAATTCATCT CGTGGCTCA ATTTGCTCC 420
 15 TCCACTGGCT GCGCCAGGT AACGTGGAC TTCGGTTGCT GTGGAAGGGG TGGTGGCTCA 480
 GCGTAGCTCG GTACAGCTGA TCTGGTCTT AGTATCAACA AAGCAAAAAT AAAAATAATA 540
 20 ACAATAAGCT TTTCAGTGTG TGGAACGTC CCAGAACTG ATTCCAACGC TCCAACACCG 600
 CACTTCTTGA AGCAACCTCA CGCACCTTC TGAATGACAG ATCACCTCA CTAAACGG 658

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1632UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

GATCGAGACT GTGATATAGC TGTATAAGAA GGTTTGAAA CCTAGTAAA TACCCAACTT 60
 50 TTTTAATTCG AACCTTGTAC AGGTTTATA CTCAATTGTA GCCTTGAGTT GCAAATACCC 120
 GAGGCATAAA ATCAAAGCGT ACTTAAAAAC AATCACTACA TACAGTCTC CACACCTGTC 180
 55 CAGAGTGGAA TAACATGAAG AATAAATATT AAGGACAGTA ATGCTATAAA TACATGTGCT 240

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TCAAATAAAT ATATGCTTGC TAAGGGTTTT CAAATTGGT TTGGGGCAA GAGTACGCAA 300

5 TAAGTGGATC TTGGGAAAGT GATGGGGGCA GATAACGACC AAACAAGTGA GTTTCCACGT 360

TACCTATATC TTCCTCTGGG ACAAACCTGC CACTGTTGAC CATGTTGTG CTAGGTGTTT 420

10 GATGTATGGA TGGAGTATCA GCACGTCCGG TAGAGGAAGT GGGAAATTAGT GAAACTAACG 480

TCCCGGAGAA ACTGGATGCC ACAAGATTGT TTGGTAGTGT GGGGGGCGTG TTAGGATTTT 540

15 TAATGTTGGT TACTGGGGTG CCTGATGGCA ACGATGGGC AGAAAAGTAT ACTTGCTCCT 600

GTGCTTTCAA AGATGGGTCA ACAGCCCAAT TGTGAAAGAA ACTGGCATTG CTAGTCTCAG 660

20 GGATGCTAAT AAGCTCTTGG ACAGAGTTGT 690

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1633RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

45 GATCAATTAA TAAATGGTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA 60

CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT 120

50 ATTGAGTTTA TATTAAATTC ACCACCTCTT ATTCATTTCAT TTAATACTCC TCTAATTCAA 180

TCTTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAAATTG 240

55 GTAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAA ACTGAATATC TACATATTAT 300

ATCATTAAATA TAATAACTCT TTAATTAGAG TGGTACCACA AGAATGCTGA AAGCATTAGG 360
 5 GGIGTGTACC TTAGCTCTCT AATTAAAGTT ATAAAATTAT CTTAACTAAT AAAAATAATT 420
 AATTAAATAA ATAAATAATT AATTAAATTT AAAATGTTTA AAAAAAGAAA TAAATAATAT 480
 10 GTTATATTTA AATAGATCAA AATTTCACA ATTTCCATTT CATTTAGTAC TACCATCACC 540
 ATGACCAATT GTTACATCAT TTAGTTTATT AGGTTTACTA TTAACTTTAG CTTTACTAT 600
 15 ACATGGTATT ATTGGTAATA TTTATCCTTT ATTATTATCT TTATTAGTAG TTTTATTACT 660
 AATAACTTTA TGATTTAGAG ATATGGTAGC TGAACCTACT TATTTAGGTG ATCATACTTT 720
 20 AGCTGTAAGA AAAGGTATAA CTTAAGGTT 749

(2) INFORMATION FOR SEQ ID NO:1036:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 732 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1633UP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

45 GATCTTAATT TAAATTTTAA ATTAACATTT TATAATTTAG AAATATATAA TCTAGAGATA 60
 TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120
 50 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTIG TGGCATCTTA 180
 ATTTTATTTA TTAAATGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240
 55 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTTAAATAT 300

AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTA TTAATATTAA GTGATATATA 360
 5 ATTTAATTTA TATAAATTAT TTAATTACT TCATTGATAT ATATAATTAT TAAATGTACC 420
 TTTCATAATA TTTATTTTFA TTAGTCTAGT AATATTTCTA TTTAATAGTC TACCCTTTAA 480
 10 TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC 540
 TAATAATTTA TTATCTAAG TATATAAATT AATTAAATCT TTTTATTAT TATTTAAATT 600
 15 ATTATTAATT AGTAAATTAT ATTTATTTAT TTTATTAACA TAATTTTTTG ATAATAATAT 660
 ATCATTATTA AATGGTTAAT TTATTAATAA TTATCTTTAA TGATTTTAAT GATAAACCAT 720
 20 TATTATTATA GA 732

(2) INFORMATION FOR SEQ ID NO:1037:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 702 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1634RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

45 GATCCATCTG CGGTTTGTC GACGTCTGT GAAACTCTAC CAGGCGAATA GAACTCTGAT 60
 AGACGACTGG CAGGTGCTG TTGAGTGGCA ATAAOCCGAT TTGCATCATC TATATGGGCA 120
 50 TTCTGCTAG TATCTATCCT TAGACTCGAT AGGGACCCAT GCTTTACAAG TTCAGGTTTC 180
 GCTTGCGGAG CCACGACATC CTTTCTCGA TTTAGGAATG ACAAATTGA GGAGTTCTC 240
 55 CTATGCTTGT GTTCAAATC ACCAGCAATG CTGGCTCGTT TATTGGTACT CGCAGATACA 300

TTCCTTGAAT GTCCATAGAT ACTCGAAGAC GGCTTCCAG TGGGAGCTGG AACGGCCAGA 360
 5 CIGTCTTGIG CACCTAGCCC TTCTAATCG TTTGGAGAGG AAAGCATGGA AATTCGATTG 420
 AACAACTCCA CAAACGAGCC ACCCGATTTT GTCTTCTTAT GTCTGGCTCT TATACTCTCT 480
 10 TCCGGAATGG CCTTTTCAAA AGTACGCTGC ATCGGAGATA TGCCAGGATT ACTGTAAGGA 540
 TTTCAGGT CTGGGCCATC AGGCTGTTG TCCACAGCAG GCTGCATAAA TACTGTGGGA 600
 15 TAGATTGCTT TCTCGAGGAA GTGTAAGAAG CTGGTGAGTT TAGGGTTTGT GGGCCGTGTT 660
 CGTAAATGGT AATGTGCTGA TTCTGGCTT GATTCTGCAA AA 702

(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1634UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

GATCAGAGG TGGCCAAGCC CAGCATTGTG TCTAAGTTAC ATGTAGAGGT CGAACAGCAC 60
 45 GAGGGAATGC TTTCGCTAC GGCGAATTC GAGACCTTCA GACTGACACC GCAGATTTTC 120
 TGTGGGCTC ACCGACCTT AAATAGCTAC AGCAACACAG CTGGCCGGT GTACACTGAT 180
 50 AGCAAAGATG AACCGGTCTA TCATTGCTC GGTGACTGCG ATGGCTCGG ACGACGCCAG 240
 CAGTCTTCGG CATGAGCGT CGAGTACTC GCGGAGTCA GAGGAAAGC TGTCAACTC 300
 55 GTATGGGCC TACAGCACCA CGGGAATCGT GATGACATCT GTGATGATGA ACAAGGCCCA 360

GCGCAAGGGC GAAGTGTCCG AGCAGTGGAT GCGGCTCTTC CTGGACAGCA CGCCTGTGGA 420
 5 GGACGTGGCG GTGCTGCAGC GCGGATGTC GGTGACGGG CGCTGCTGG ACACGTTGCA 480
 GCGCATCTTG CAAAGCATGC ACGGATACCG CCAGATCGTC CCGGGCTGG CGATGTTCAA 540
 10 AGAGGCATGG AACCTGCAGT GCTACCACGG CAACGAGGCG GACTTTCCGC TGCTCGAGT 600
 GCGATCAAG GTCAACAGCC TGACCACACT GGCCAGCCTG CTGGTGGAGC ACGCGTGTG 660
 15 CGGTTACAGC ACGCGATCG AGCAACTCAC CACGGTGCTT CAGTACCTCA ACAAGCTGCT 720
 GCAGGGGTGG CGGTC 736

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: 1635RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

GATCTAGGG TGGTTCATGG CACTGAGCGG GACCGTGTC TTGGACGGT CGAACCGCAG 60
 45 CAAGAGTCTG AAGTCGCTGA ACGGTGCTT GGAGCGGCTG AAGCGCAATC GCGAGGGGC
 GTGGATTTTC CCAGAGGGCA CGCGGTGTA CACAACGGAG ATGCAGCTGC TGCCATTCAA 180
 50 GAAGGGGGCG TTCCACCTGG CGCAACAGGC GCAGATTCCG GTGATTCCG TTGTGATGTG 240
 CAACACGAGC ACGGTGTTCA ACCCGCGCT GGCATCTTT AACCGGGCA CGATCACGC 300
 55 GAAAGTGCTG GAGCCGATCG ACACGGCTAA CATGACCAAG GATGACGTGG ACAAGCTTGT 360

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GAGCGACGTG CAGGCCAAAA TGCAGGCGGA GTTCGAGGCG CTTGGCTACG CGCCTGGGAT 420
 5 CGTGGACACG AGCCTACCCG AGGAGGCGCT GCGGCGGAG TTTGTGGACT GCAAGGAAGA 480
 CATCAGGAG GTAACGGCC TCCTGAAGTA ACCTTGGTTG GTATCATATA AACGTTGCGA 540
 10 CGAGTTATGT ACATATAGCG CTGCTAAGTA GGCATTCACT CCCACGAAGT CATACTGGC 600
 TGAGCTCTAC GCCCCGCCGA TGTGGGCCAG ATACTTGTCT ACCTGGCCAG CGGACCGAG 660
 15 CCAGATGAG GACTTGTCTT GGATGTGCTC GGGAGTAAGT TCCAGAAATG CGCTCGCCGC 720
 GGTCGTTTAC GGCCTTG 737

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1635UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

GATCGGACTG ACGGTGAATA GCCACCGTA GCATGCGCG CTGAGCGCG TGGCGAGCGA 60
 45 TAGCAGCGGT CGTCCGAGG CTCTGGTGGC CAGGACAACG ATCCACTGGC CCACCAAGGC 120
 CAGTAGGAGG ACTGCCCCACT GGAATGACAT CGTCGACACA CCGTTGTGGA TGCAGAGGTC 180
 50 AATTATCAAG CCCGACAGGA AGCGCGAGCA CGTCGAGGCA ATCGCAAATT CTGGCAGCAC 240
 CGACGCCTGG CCCAACAGGC TCGACAGCGA GGCATGTTG GTGAGGAACA TCTCCATCGG 300
 55 GCCCAGCGAC AATAGCAACA CAAGGGCCAT GAAGTACGCC GCTGGGTCTT GGAAGAAGTT 360

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GCGCAGCCGG CGGCGGATGT CCTGCGGCAG CAGCGGCTCG GTGGGGCTCT GCATGCCGGC 420
 5 GAAGGTCAGT GTTGGGGCCT TGACCTTGAG CATAGTGACG ATGCTGTGTC CAAACCACAT 480
 GCAGAAGCTG ATCAGCGTAT ATGCGACAGC AAGAGTCCTG AATACACGAG AAAGGTCAAG 540
 10 GTACGGCAGG CCATTTCGAA ACCATGGTAT CTTGAGCAGC TCGACCCCTA GCACAGAAGC 600
 CATCCCGTAA AACGTGGCGG GCAGACTTAT CGAGCACAAC TTGCTCGCGG GGTACAGTTT 660
 15 TGATGCGGTG AACAGCGCAC TGAAGT 686

(2) INFORMATION FOR SEQ ID NO:1041:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 720 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1636RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

40 GATCTTCTTC TGCTCGATGG ACGAGCCAGT TGTATCTTGG ACTCTACGGA TAACCCACAC 60
 CTTTTCCTTC AGCGACAGGA ACTTGGCATC GGTGGGTGA TTGGGTATA GATATAGGC 120
 45 TAAGANCGCT ACCACAAACG TTAGGCTGCC GATTATAATT GACAGAATTT TOCAATGTGA 180
 GATAGCTGGG TTCTTTATCA GCAGGATCAA GTAGGAAAGG ACGCCCATTG GTATGGATAC 240
 50 ACTGACCGTC GCGATAACAA AAATCGGGGC GGTGCTGCC TTTTCATTCT CTGTTAAGAA 300
 CATCAGCATT GTGTGTTCA ATGCAGGAAT GATAATAGCC TCCGTGAAAC CTAAGCAGAG 360
 55 ACGAAGAACA TATACACCTT TGTAATCGT CATTGCACAT TGTACCATCA TAATGATGCA 420

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CCATATCGTC AGGAGGACGA TAACAACGTT CTTCAAAGGA AACTTCTGGA TAAACAGCAA 480
 5 GTTGATCTGT CCGTAATAT AGCCAACGTA GAATAAGGTA TTCACATTGT TGTAACGATT 540
 CAAGGACATG TTTACATCTT CAAAAAATCC TAACAGAGTG CTGTAGGACA ATTGCGCCTT 600
 10 GTCTATGTAG GTGATGAAAT TAATGCTCGC CGTCAGTCCC ACGATGTACC ACATAACCTT 660
 TCGTGCAAGC TTCTTTTCTT CGGCTTCTGT GATAGGAGGG ACATCCTTGT CTTGCTTCAA 720

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1636UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

GATCCGCAAG ATGACCGAGG GTAAGGGCCA CCTGCTTTCG CACCACCGCT TAGTTTCCTT 60
 40 TGGAGGTGCA GGTGGTCAAC ATGCAGTTGC AGTGGCACAC TCATTGGGCA TAGAAACGT 120
 CCTCATGCAC AGGTACTCAG CAATTTTATC TCGGTATGGA ATGCTTTTGG CGGATGCGGT 180
 45 AAAAGAGGAG CAAGTGCCAT GCTCCATTTT CTTGCAAGAT ACATCTTCTA AAGACCAGCT 240
 AAATGAAATA TTCCACCAAT TGATTACCAG TACCTCAATT AGCCTTCTTA AGCAGGGATT 300
 50 GCGCGACGAT CGGCTTGAAT TCGAGAGATA CCTGAACTTA CGTTATGAGG GTAAGTAAAC 360
 AAGTCTTATG GTTCTACAAG AAGGAGACTC GTGGGATTTT GTAGAAAGGT TCACAAAAC 420
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CCACAAGCGT GAGTTTGGCT TTGTTTTCGC CGAGAAGAGG ATTTTAGTGG ATGATGTCCG 480
 5 TGTCGGTGCT CTAAGTAAGT CTATGGTGCG GAACAGGAGC CTGTTGATCA GCAGTTATCC 540
 CAGGTCACCTC GTTCTACAGC TGACCCCTTCT AAGGATGCAA AGTTCCTTAA GGACGTGTAT 600
 10 TTCGTGATG GGTTTATTAA GACCACCTAT TTACAGGTTA GATAGTTTAC CGGTAGGTAC 660
 CTGTATTGAA GGACCTG 677

(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1637RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

GATCTGCTCA TACTGAGCGG CCAACTGGTC GTACTCCGTA TGCAAAACAT CTGTGGTTTC 60
 40 CTGGAAGTGC GCCACCTTGA GOGATATCTC ATTAAACTTG GTAACCAGCT CTOCCAACCTG 120
 ATGATTGACT GCACTGGTTT CGGTCAGCAG GTCCCTCCAGT TGGCCAGTTC TGGTGTCCAC 180
 45 TTCCGCCAAG TATCCGCTGT ACAATGTATA CTCGTGGTTC GCAGACCCCA GAGCAGAAGC 240
 TCGCCGCCAC TCTGGCGCCA GCAGCTCAAT TACCTGAGGT TCAATCTCTG TTTCAACCGT 300
 50 TGCCAACAGA GTGTCTACTT TTTGGGGTAA CGAACTATCC CCAAAAAGCG GAGGCAGCTC 360
 ATCGTGAGAG GAGGCACCGG GATTTGCCGC TACATCCTGT ATGACTGAGT TCTTCCGGCT 420
 55 CCTAGGCATG GTGCAGTTGC TGCCCTCAACG GCTTTCCTCC TGGTGCAGGT CTGCAGTGGT 480

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TCGTGCTTAT GCGCAAGCAG AATACCATGT TGAGCCGGCG AAATCTCATC ACGTGATCAT
 CATCTTGCAA CGGCTCGGAG GACGCTGATG CACTGTTCCTA TAGGCTTAGG GCGCAATTAT
 ACGCTAGCTA GTTATATTGA TAATATGTAC ATGATGCCCTT CGGCACGACA GCGCACTCAG
 TGCTGGGCGG CCGCGCCGGG CTCCGGCAAG CTCTGTCTC AACTTGGGCC TTCTCGGCT
 CCACGT

540
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720
726

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1637UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

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GATCTTGCGG TCCTTCTTGT CCAGCTGTAG GTCCGGATGA GGGTACGCTT CGCTCAGGTA
 CTCAGCCCGC AGCTCGCCGC TCTCCATGGA CGCTCCAGG ATCGAAGGCG CCGGCACAGC
 CTGGAGGGG AGGGGGGGCT GCAGGAGGGG CATCTCCTGT CGCTCCTGGT GCATCTGCAG
 CGCCGCAGCG CTGGGCTCCA GCGCCGGGTC GAAGTACTTC ACATTCGTCA GGGCCGACTT
 GTACAGATTC AGGATGCAGC CCTTGAGCTG CGCACGGTGC AACCGGTACG CAGTCGGGAC
 ATACTGGTAC CCGCTCGTCC CCCCTCCCGT GAAGTGGGCG CGCTCCGATC CGATCGAAGA
 CAGTGACGCT GTTGGCTGGT GGCTGTATCG CCCCTCGGCG GCGGGGCTG CGCCCTGGCG
 CTGTTCACCC CACCCGAGCC GAAACACAGT CCGTGTGTAC GTCTCCCGGT TCAGCCCGCC

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TCCACGTGCG ACCGGGCGAGC CCGCCCGGCTG CGAGCAGGGC GACACCTGCT CCTCGCAGCG 540
 5 CGCACCCGGC TTCATGTCTT CACATGTTCAG CGTCGGCTTG TGCGCTTGCC CCGTCGGCAC 600
 CTGTAACTGC ATCGGGGTCT GTGGCTGCTG CTGCTGCTGC TGGGTGTGCT GTTGGCGTTT 660
 10 GCCTGTTGGC CTTGTTGTGT GTA 683

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1638RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

GATCCTGTGCG CTGGAATGT CGCGGACGAG AACAGACAAC CGTGGGGGC GGGCGGATCT 60
 35 GCCGGAAGCT GTCCGAAGGA GACCAAGAAG GAAATTGTAA AGCTGCAGCC AGCGCCGATT 120
 CCACAGAACT CTCGTTGGA ACCGGTGCAG ATGGGGACGG GGGCCGGACG GGCCACCGAG 180
 40 GACGGCGGCT GGCTTTCTGC GCACGAGGTT GCGACAAAGC TTGCTGACGA CGGCAGGGG 240
 CGGGGGGCGT CGCAACCGAT GGTGACGACC GCGAAGGAGA AGTGGGTGCC AATGAAGCCG 300
 45 GCCATGCTTG TGCCCGGGCA GGGCTTGCGC AAGATGCAAC GCAAGAAGAA AAACGGGCAG 360
 GCGGTCAACG GCGGTGCGC GAAGCGCAAG ACCCGAAACA AGGCACCCCT CAGCCAGCAA 420
 AAGAGAGCTC CAGACTCCCA CAGGAAGGCG CATGACGAGG CGAGCGCGC GAGCGCCACG 480
 55 CCATCTGCAC CGGAGGAGCA CGTGAACAG CGCGAGCTCG GCGAGCAGCA GCAGGTCCCC 540

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GAGGCGCAG AACAGGGTGC GGAACACCG ACACAGCATA TGGGCGAGAT GCAGCCCCAG 600
 5 CCCAGAAGAC GCTTCTACGG CGGCAGGCAG CAGCACTCCG CTGACGGACA CAAGCCAGTT 660
 TGIGT 665

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1638UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

GATCTGAGAA CTA CTGTGTG TGGCTAGCG CAACTTATC AGAATTCCAT CAACTCACCG 60
 35 AACCATAGCA CATCTAGTC ACCTCCCCCT ACCGCTACAG ATACCGGGAA TGATCAATTT 120
 TTGGGIGTTC ATGCTGTAAC CATATCGCAT GATGACAAGT ACCTAATATG CATGAGCAAT 180
 40 GACACGTACA TTGATGTCTA CGACATGTCA GAATTATCGC CTGATTGTGA ACGCTGCGAC 240
 GAAATTAGGA CTCCTAGACT ATCTAGACTT AATATTGGGA AGCAGATGAT GTCCATGAGC 300
 45 GGGCCAGTTG GACCCGATGA TTCGCTTTTA CTAATCAGTG TACAGCCACA CGAGCTTCAG 360
 CTATGGGATT TCAAAAGGCA GATTATGGTC CAAAGATATG TAGGACAGCG GCAGGTGGCA 420
 50 TACATCATCC GTTCGTGCTT TGGGTATGGG GACAACCTAG TTGCTGGAGG TTGGAAGAC 480
 GGAAGATAT ACATTGGGA TAGATATTAT GGTAATATTA TTGGCGTTCT ATCTGGGCAT 540
 55 AACATGGAGA GACCCGACGA CTCCAGAAAT AAAAAGTTCC CAATGACCAA AGTTTGCAAT 600

ACTGTAGCAT GGAATCCCGT CAATTCAAGA CTATTTGCOCT CTGGAGGAGA TGAOGGTCTG 660

5 GTGAAGATAT GGAAGGTIGA CCTAATTGA TGAATCCTAT AGCATGAOCT TATTGTCTA 720

TAGAACTTCG AGAAATCCTG CCGATCTGTT GTTTCCTAAA TTGTA 765

10 (2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 658 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: PAG1639RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

30 GATCCATCTG ACTATTGTTT CACGOGATTC GGGGACCAAC TGTGCAGTCA GGCCAGGAA 60

35 CCGGGAGAAA TAAGCCTTGA ACGAGCGCTG GTGATATTA CAGTTGTGCG CACCTTGACA 120

TOCTGCTCG TACAGGGTGT CGTTGCTGAG GAAGATTCTG GCGCTGTCCA AGAAAGCAG 180

40 TGTTCGCTGG TGCCACAGCT CGTCCTGGGT ATGGTTGTAG ATGAAGGCAC AGCTGCCAT 240

GATCAGCCCA TGGTTGTAAG TCCACTGCAG CTTATTTAAG TTGGTACAGT TGTCGTTGAT 300

45 GTCTGTACCG TGTAGACGA CGTGCCAGTT TGGCTGCACA ATCGAGATCA GCGCAAGGCC 360

ATACATCCAG TCGTAAACCC GTTCGCCCCA CTCTAAGTAT GTGGCATTCC CCGTGTAAAG 420

50 CGTTAATCGT GCGCCATGT GGAACAGCGC ACCGTTGGAA ACGGAGTTTT TGTAGTGGTA 480

CCCGTCGTTT CAGCGGAAAA TCTGCCATCT GAGCCCGCCG TTGCAGTCT CCATATCCCA 540

55 GCGCAGGCC ATGGTATTAA ACACCGCCTG CGCCAGGCC AGCCATTGCG GCTGGTCCGC 600

GGGCGGGTTC GGAAGTTC GCTCCGGGC AGCATCACC GCCATCCCC AGAAAAA

658

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 730 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1639UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

GATCGAGCGG GTGAGGGACA CGGTGCACAT AACGACTGG GACGGTGCT GCTATGTTTC	60
CAAGTGGCGG ATTGTGACCG TGGCGAAAG CGTGCTGGAG CTGTCTCTGA AACGAGAGCG	120
GGTGCCCGGG CGCATTGAGT TTGCCCCCCT CCAACGAC AACATCAAGT CTGGGTTTGA	180
GCGAGCTCAC TACGCTGCG TGGCAAGAT CTCTTTGAG TTTGACAAGT GCACCTGGGA	240
CACGCGAGCG CCGCGGGTTC CTATCGCAGC CAAAGTTCCC GACGACTTTA GTGGCAGGT	300
CCGTAAGGCC CAAGATTTC AGGAGCTGCT GCGATCGCC AGTGCTCAGA CTGAGGTGAA	360
GCTGGGACAA GACTGCTTTG ACTTTCCACA AGAGTTTCAG AACATGGTTG CGCTGGCAGG	420
GATACCGACA CTTATTGGT TCACGCGAC AACTCTTACT GAGCACTCG AGCGCTTATC	480
AAAGCAAGAG ATTGTGGACT ACTTCAAACC CGCAATTGTT GTTGCCTAC GTGCACTGGG	540
GTCCAAGGAG GAGTGCTCT TGGACCTGG AAACACGCA CCGCAAGAG ATAGTCATCC	600
AGGCCCAATC CTAAGAAGG TGATCTTCAA TCCGTGGTCA CAGGATACGT ATTCTCGTGG	660
CTCATACACC GGTAGTCAAG TGGACGACGA CCAGCTGCCC TTGAACGTGG CCTCAACAA	720

CGGCCAAGAT

730

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1640RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

GATCAAGCCG AGCACGCTGA CCTTGGCTCC CCGACGCAAC ATCGGGTTGA CGGGCTCCCC	60
CGCGGTGGGC TCCTCGAGGC CATCGCCAG CTGGGCACTG GCGGGTGGC GCGCGCGGC	120
GAGGCGCGCC ATGTCCATGA AGACGGGAT GTACGAGCC TCGTGATGG TGTATATAGT	180
GTTACAGCAG AGCATCAAGC AGTACAGCAC CGACATCAA ATGAGCGCGC CGTAGGTCTT	240
GCTACCCCTGG CTGACAAACG GCGTGGCAAG TCGCGCGTAC ATTACAATCG ACAGCGTCAT	300
GAGCCACTTG CGGTAGTTTG AAAAGTCCG CAAACCCATG AGCACAATCG CAATGAGGCC	360
CTCGATGGAC GTGTACAACG CCGCATATA AAGCACATAT GCGTGAACT GCACGTCCCT	420
TCCGCCACG TAGATGTAGC AGTCATGGC GCGGGGGGG CAGTGGGGG CGGGGTGGC	480
CTTGGGGTGC CCGAGCTCGT GTGGATGGT CTGTAAAGAC GCAGGCACAA AAGAACGCAT	540
CATCAGTAG GTGGGCGCG TCGAAAAGCA CACAAGGAGC CATGCAGGAA ATACCCACCG	600
GCCCCGCCAC CGGCGCAGCA CTCCTGTGG GCGCGCTGCC CGCCACTAG CGGCTGCTGC	660
TGTTCCAGCG TCACTGACAC CTGCATGTCA GCGCCCTTGC TT	702

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(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1640UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

GATCAACGAG CTGGCGCAGC TGCAGCTGGA CGATGCGGAG GAAGGCTTGG AAGAGGCGGG	60
TGGTGGCGCAG GAGGGGCGGG CGCTGTGGGC GCAATTGGAC GGTGACGACG ACCTGAAGGA	120
GTACGACTTG GAGCACTACG ACGAGGAGGA TGGGGGCGGG GGTGCAGAGG TGAAGATGTT	180
CCCGGGGCTC TCGGGCGAGG CCGCTTCCA CGAGGGTGAG GAGGGGCGAG ACGGTACCT	240
GAGCTTGCCA ACGTAGAGG AGGAGCAGGA GGAGCGGGG GAGCTGCAGG TGTACCGAC	300
AGACAACTTG GTGCTGGCAA CCGGACCGA AGACGACATT TGTACCTGG ACGTGTACGT	360
GTACGACGAC GCGGCGGGGT TCCACGACGA GCGGTGCGG CAGGAGGCGG GGGACGCGCA	420
GGACCCCGAC GTGGGCGCGG GGCTGATAAG GGACGCTCG TTGTACGTGC ACCACGACCT	480
GATGTTGCGG GCAATTCCCGC TGTGCGTGA GTGGGTGAAC TACCGGCGCG GGTGGAATC	540
TGACGCGCGG GCAAACTTTG CCGGGTGGG CACCTTCGAC CCCACGATG AGCTGTGGAA	600
CCTGGACTGT GTGGACCGG CGTCCCGAC ATGATCCTCG GCGAGCGCGG GGAATCTGCG	660
ACCGCGTCCA AGAAGTCGAA GAAGAAGAAG AAGGCG	696

(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1641RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

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GATCCCTTAG CGACTCTCTC CACCGCTCGA CGAGGOCATT GAGCTCTTAC GAACTGCACA      60
AACTACTCG AACTCTGTTT CCAGACTTCT TTCTGTTTGT CTCAACTGC TTTCGCATGA      120
AGTACCCCCC AGGCTATTTT TCTTACCCGC CTGGTGTGTTG TCTATATACC CGTGTGTAAT      180
TTTGATAAAA AACTCAGCTC TTCTCTACG GCAGAAATAT ATATCCAGTC CTTAGCGCCA      240
TGCGAAAATC TGCTTTTFTA CGCTGTGTTT TCCAGTCTT AGCACTGGCA GAAAAAAGAT      300
GTATGGCGTA TAGGCGCTGG CCGCGGGAA AAAAAAAAAA AATAGAAAAA TAGAAAAATA      360
AAAAGACGTG GGCCGCCCCG CGGCGAGACG AAGAAAAAAT AGGCGCCAC CCTTCCAAGC      420
AGACGACAGG CGAGACATAA TAAATCCCA CACCAAGGA AGAAAGTCTT GTGCACGCTC      480
CCGGCTCAT ACGCTGCCAT TCTGTTCAT CCGGCTTGA AACCCAGTAG TGGCATGTCA      540
AAGCATGTCT CCGACGCTCC GCTGCCTTGC AGTCGACATC CTCTTCTTAA CCCCAGCCAG      600
ACTTCCATA CTTTGCACTT CACATAGCAT ATCACTTTTC AGATCACTAC GTGACATTOG      660
GTACGGAATG GCACTCCAAT GCCGACAACC TCTTCTTACC CGTGACTTAC CCGATGTGCC      720
AACTA                                          725

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(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1641UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

GATCGGGTAG TGAGGGCCCTT GGTGAGACGC GGCAAGTGTG CTGTGGTCT GTCTCGGGG	60
GCTTGCTCTT GGGGACGGAC TGCTTGCGTG CTCTGTCTA GACGGCCCTG GTAGACCATC	120
TCTGGTGGTC GCTTGCTACA ATTAACGATC AACTTAGAAC TGGTACGGAC AAGGGGAATC	180
TGACTGTCTA ATTAAACAT AGCATTCGA TGGTCAGAAA GTGATGTGA CGCAATGTGA	240
TTTCTGCCCA GTGCTCTGAA TGTCAAAGTG AAGAAATCA ACCAAGCGCG GGTAAACGGC	300
GGGAGTAACT ATGACTCTCT TAAGGTAGCC AAATGCTCG TCATCTAAT AGTGAAGCGC	360
ATGAATGGAT TAACGAGATT CCCACTGTCC CTATCTACTA TCTAGCGAAA CCACAGCCAA	420
GGGAACGGGC TTGGCAGAAT CAGCGGGGAA AGAAGACCT GTTGAGCTTG ACTCTAGTTT	480
GACATGTGA AGAGACATAG AGGTGTAGA ATAAGTGGGA GCTTGGCGC CAGTGAATA	540
CCACTACCTT TATAGTTTCT TTAATTATC AATTAAGCG AGCTGGAATT CATTTTCCAC	600
CTCTAACAT TTAAAGTCT ATACGGGCTG ATCGGGTTG AAGACATTGT CAGGTGGGGA	660
GTTTGGCTGG GGCGGCACAT CTGTTAAACG ATAACGCAGA TGTC	704

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1642RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

GATCGCGGTT TOGGAACGGC TTGCTTOGCA CAAAACACAG GGTTGGAAGT TACATACTCT	60
TCAAGAAATT GACGAGGCGT TGAAAGCGCT GGAGCTACGC GGGTCAGGGA NIGATGGTAA	120
TGCGTCATAT AAGTGCAACT GCCAGGCCAC TATGCATCCT CTTTTTGAGC TAGCCCCAAA	180
TTGCGTGAAC TGTGGCAAAA TTATATGTTG CCGAGAAGGT CTTTCATATGG ATTCTGCAG	240
TTATTGTGGG ACGCTGCTGA TACCGAAGCA GCAGCAGCGG GATATAGAGA AGGTGTTGCA	300
GCGCGAACGC GAATTGGTAA AAGCCAAGAG ACAAGAGACC GGCTCGACTG GCAAGAAGAA	360
GGAAAAGGTC TTTAAGATTT CGAACGCAAA GGGGAGAAAT ATGTTGAGTG AGCAAGAGAG	420
GCTATTTCGAC AAAGTTGACA GGCAGCGGGA CGTGAAATGA AAGCAACCA GGTACTTGGG	480
GCAGAGGACT GTCTCAGGAG GAGGACTCGA TTCTGAAGGC TGAGGAAGTC GATCGGGAAC	540
TAAGGGCGGC CAGGCGCGCT TGGAGAATCT ATTGCACTTT CAAGACACTA GCGAAGAGAG	600
GACTAAAATA ATAGATACTG CCAGTGACTA CAGTATGTCA AACGACGCAG GAATTTGGGG	660
GTCGGCATAT GAGAAGGC	678

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 703 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1642UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

GATCTCGTAC CCGGTACGGT GCGGAGCTT GCGGCGGCA GCGGCGGCT GCGCTGCTTC	60
TCCGCGGACA GCGGCGCAA TACCGTGTTC TACAAGCTGC ATGGATCGCT GCCACAGGCC	120
GTGCGTGTTC CGACGCTGG GCACCTCTCC TCAGACGCTG CGGCAACCG GGGGAAGCAC	180
CTGGTCTGT TTTGTACGA CGTCGCTCG CGTGGCTTGG ACCTGCGCG TGTCAGCACT	240
GTCATCGAGA TGGACCGCC CTTCGGGTC GAGGACCATC TGCATCGTAT CCGGCGGACC	300
GCGCGTGCG GTGTGGCTGG CGAGTGTTC CTCTCTCTGC TGCGCGGGA GGAAGAGGGC	360
TACATGGAAC ACATCGTGC CCACCACTT CGTGGCTGG AGCTGCTTCG CTACGATCGA	420
GACCTACTGG CGCGGGCTT CGCGGCGCT GTGCGCGCT CGACCGTCC GACCAACGCA	480
ACGGACGCG OCTGGACAG CAACGCGACA ACTTGGCACC TCAACGTCCA GCGCGTGTTC	540
GCTCGAAGAC CCTCGCGAA GGATCTTGC ATCAAGGCT ACACAGCCA TATCGCGCA	600
TACGCAACCC ACATCTCTCA GGAAAAAGCG CTCTCTCAAC GTTCGCTGTC TGCATCTTGG	660
CCACCTGGCG AAAGCCTTTG GACTTCGGA GCGCCCCAAA GCA	703

(2) INFORMATION FOR SEQ ID NO:1055:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 616 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1643RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

GATCGGAACA AGGAGCAGCA GTCCATCCAG CTGTGCGAGC AGCAGCAGGG CACACTGCAG	60
GACAGGAAGC CGACATACCA AGTCATGTCT CTCCAGAGCG ACACGACGGT GACCAAGTTC	120
AAGGTCGAGC ACTCCATCAG CAAGCGTTTC GAGTTCATGA ACAAGCCGAA GGCCAAGCGC	180
GCGACCGCGC CGCGGCAGGC GCGGACCAGC AGCCCTGCAA TGGCCTGGG CGCCGGCAAG	240
CGCGTGCA CA AGCCCAAGGT GCAGCAGGGC CGCGCGCGCG CCGGCAGGC CGATTGGCG	300
AAGCAGAGTA ATACGCCAG GGGACTTGG TGGCTCGGA GAAGACCAAT CGCTGCAGGA	360
ATTCTGTG CAGTCCGAGA TTAAGAGCGA TCTGTTGAA CTGGAGGAGC AGAACGACGA	420
GAGCGCAAGC TCCAACAAGG AGAAGCTACC CCGAGCTCC TCGTGGTGT TCCAGCAGCA	480
GCTTCTGCCC ACAGATATGG ACGACTTTT CAACCTCGAC CTGACCATA TGAAGAACAC	540
CGATGATGAG TGGTCCAGG GCTGTGTCG CACTCTCGG GACGCGACCA CCTGCAACAC	600
CATGCCCATC GAGGAC	616

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1643UP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

5	GATCGTTGCA AAGAAGCTAT TACGGTGTCT ACACGTTGCA GAACAGCGCC CGATGCCATA	60
	TCCACACCG CCGCTGTCAA ACGGTCTCTT GGCACGAGC GCTGACGGG GGAGCGCGC	120
10	AGGGCTGGCG CAGCAGGCG CCGAAAATC GTACTACCG CTGGTGCGG ACGGCGACA	180
	GCTCAGCGG CCACTGCTGC CCGTGTCCAC GCGCGCGAT GACGCGGCG TCTACCGCTA	240
15	CCACAAGCAG ATCAGCAAGT CGTTCAGGA CGACCTGATC TACTGCGCG GCGGCTGCT	300
	GAGCAAAGTC GAGCTGAGC AGTGCTACCA GCTGGACATG CTGCTGCTGA TGGAGCAGCA	360
20	GCAGCAGGCC CAGCCGAGTG TCAAGTTCAA CCCATATACG TCGCAGAGCT TCAACCGCG	420
	GGGCGCGCA TCGCGCGCT CCTAGGGCG GCGGCGCGC CGGGACCAT TAGTTGACN	480
25	GAATCNCTAT GTCAAGACTG ACGTTGCTC GCATCGGGT TTATGTTTIA TTCCAGTT	538

(2) INFORMATION FOR SEQ ID NO:1057:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 560 base pairs
	(B) TYPE: nucleic acid
35	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40	(vi) ORIGINAL SOURCE:
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(A) ORGANISM: PAG1644RP

45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:
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50	GATCCTTTGC AAATTCGTCC ATAGGAATGT AAACGACCT GCGCTCCAC CTCCTGGTAT	60
	TGCAACAGG CATCTTGAGT TCGTTGGCC ATTCCATCTT TATATGCTGT TCTTCATGC	120

55

AAGGCACATT TTCGTCTTCT TCGGGCTTCT CAAAAACAAC CTTATGCACT CTCTCAGTAA 180
 5 TATACACAGG GTACGGGGTC GCCGTCCCTG AACATTAGGA AGAACCAGCC AAATGGGCGT 240
 GTGCCTGGCG ACTGGCCCGA CTTCTGCACK AAATCCACC TCAAGTATAT GACCATCAAG 300
 10 TCCCTGAACC GCGTGCTAAA CTGCTGGTAT GTGTGTGTOGA TATCTAGGG ACCGGGAGCT 360
 AGCGAATGG TATGCGGCAC TTCCAATAGG TAATGCCCCG GCGTTTGGA CCGATGGTAT 420
 15 ACCCTAGTAA CTTTGCCCTGC AAACCAATA TGGGGCTTGG GCTTTTTCOA GTGGGCGTGG 480
 TTGTAAATG GATCAATGT CTGCGGAGAT GAGATGGAGC TGTOGCTOGA AGATATGTCC 540
 20 TTAGCAGGT TATCGTCTTC 560

(2) INFORMATION FOR SEQ ID NO:1058:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 706 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1645RP

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

45 GATCTTGGA GAGGAGGACT ATTCAAGTAA AATGCCACGG CGGAAGATA AGATGAAGA 60
 GGAGTGATA CGAAAGTACG AGCGTGAGAA GAAGAAGAGA AAGAGAGGCG CATAATCCCC 120
 50 AGTGTAATAA ATCAATTCCG CCGGTTGGCT GCGCTGTAGC ATAATAATAT GTACGATAGT 180
 GGTCAGATAA GGTATTTCAA AAGTTAGGCA ACCCATGAAA CATCAAACCTT TTCAATGCAA 240
 55 TGATATGTAA GTTCATATA TTACGAGCTG TGAAATAGAG AAACCAAAAT GAATACTTTT 300

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ACCACACCAT AACAAACGCA CAATGTTACG AGAATGAAGA CGATAATGCA GCTTGAATAG 360
 5 TGCCACCATG GCGGCATATG GTACCTACTG AACAGCAGAA GCAAGCTAAA CGAGCTCAGC 420
 ATGAGGGACA CCACTAGAGA TACCAGGATC AACGCTGTGA TATAATTACT ACCTTCAAAC 480
 10 TCAGTCTGGT CATTTCOAAG AGCGCTGAAC AATGAAAACA TGATTCCCAC AGTGGTACCT 540
 GTGGTTATGC AAGATACGAG CAGGGTGGTC AGGTAAAACA ATGAGACCAC CTCATGGTGC 600
 15 TTGTATCCAT ATAGGACATC AAGTTCATCG TAACATACTA GCGCAGCCTC GTCATCCCAG 660
 TTTGGAACIT GCAGTTGGCT ACCACTCCCG GCAACGTGCT TTGCAC 706

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1645UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

GATCAGCGGC GGCTGGCGGC GCTGTTGCCG TAGCGCTGCA GCAAGCTGCG GCGCGCCGCG 60
 45 GCGCTCTGCG CCTGGCCCTC CCGCTGCCGC GCACCGCGCT CCGGCGTCTG CCGCCCAAGC 120
 TCCAGCCGCG TCGGGTTGCG ACTGATCAGC TGATCCACCG TGCTGCCGTC CCGGCCGCGC 180
 50 CTGTCCGGCG CCGCCGGCGC CTCGCCCGCC GCGCCATGCG CCGGTACAC ACGGCTCTTC 240
 GGATCGTACC GCGTCTCTTC GCGCGCACG TCGTCGAGGT ACGCGCGCGG GTCAITGCGC 300
 55 GCGCGGATCG CAGGCGCCCC CACGCCCGCC CCGCGCGGCC GCGGTCCAG TCCCAACTTG 360

TACCGTTCCA CTGCTGCGGC CGCGTCTCTT GCGCTGCGG GCGGCTCCG CGCGCGGGC 420

5 GCCACTGCGG GCGCCACCG CCCCTGAAC CCGTACCATC GGTCCCGCTT GGCTCAAAG 480

CTCAGCGCAT TCTGTCCCG GACCTGAAAC GCGGCTGCG CACCATGGC CGCGGCTGT 540

10 TTGCGCGGCC GGAGCAGGCA GTCGCGCGG TCATGATTGG CGCGCAGTT TCGTGCAACG 600

CCCGGTCCG CGCCCCCGC CGCGGCGGC TGCCCGCAC AAAACGGTCA CTTATTACG 660

15 AACCTGCTGA GCCACGAGA AGTCTGAGC GCGCTGCGG GGCTC 705

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1646RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

40 GATCGAGAAC CGCATGGACG ACAAGCCCAA CGTGGTGATC CTGGGGTCC GCTGGGGTGC 60

GATTTGGTTC CTGAAGCACA TCGACGCGG GAAGTACAAC GTGACGGTGG TGTGCGCAG 120

45 GAACTACTTC CTGTTACGCG CGCTGCTGCC CTGAAGGCC GTGGGCAAGG TGGACGAGAA 180

GTCGATCATC GAGCCGGTGG TGAACCTTGC GCTCAAGAAG AAGGGTAAAG TGTCTTACTA 240

50 CGAGGGGGAG GCGACGTGCA TCAACCGCA GCGCAACAG GTGACGATCA AGTCGGTGTG 300

GACGGTAGCA CAGCTGTGCG ACCCGGACAA CCACCTGGGG CTGACGCAGC AGGACTCCG 360

55 GGAGCTGAAG TAGACTACC TGGTGTCTGC GGTGGGCGCG GAGCCCAACA CGTTCGGCAT 420

TCOOGGOGTG GAGGAGCAOG GCAACTTTTT GAAGGAGATC CCACACTOGT TOGAGATCAG 480

5 AAAGCGCTTC CTGTGGAACG TOGAGAAGGC GAACCTGTTG CCCAAGGGOG ACCCOGAGAG 540

AAAGOGTCTG CTGACCATCG TGGTGTGGG CGGTGGTCTT ACCGGTGTGG AGACCGGGGG 600

10 TGAGTCCAGG ACTACGTGGA CCAGGACCTG AAGAGATTCA TGOOCTCCAT CGCTGAGGAG 660

GTGCAGATCC ACCTGGTGGG GGCCTTGCCC AACGTGCTGA ACATGT 706

15 (2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 657 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: PAG1646UP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

GATCAAATGG GTTAGCCCGT CTCGAACGAG CCTGCAACA TAGTGGCAGT AGGGGTGTA 60

40 GTCTGGATC GTCTCAAAC CGCTCAAAT AACTTCTCG TCCAGAATGT AGTCTGCCAT 120

GOOGTTGCC ATCTGTGTG TGATGTCTG AATCACTGC TGGTACTGG GCTTCAGCTT 180

45 GTGGAAGTGG GCTAGAATCG TGCTGAATC CACGAGCAG TCAGGTCTT TCTCGTCTT 240

CGGTTGCCG TCGAAACTCC AGGTATCCAG CTTCAGTTT TGGTGAAGT CCGGAGTAG 300

50 CGGCACTTT ACCTTGGGAC TGATGTTCAT ATCGTCTTCA ACAGTATCCA GCGCAGCAG 360

AATCAGGTAG AACAGCATCA CCGGTTGGG CAGCTCGGA TGTAGCTCA TTATCAGGC 420

55 CGCAAAGAC TCGAAGTCCG CTGTAGCAG TGGTAGCAC GCTTGAGCTC TGCAGAGCCC 480

TGCGTGTGTT CCGCAGGATA AAGCGGTTC CTCAGAAATT TGAGCTTCAG AGCTGCTTC 540
 5 AGCTCCAGTG GGTGTGTGAA TAATTGAACA ACGTTCCCA TGGTCAGAT TCGATTAAGT 600
 AATTGCCAAT TATGTCAAGC GCGTGTCACT TGGTGATGTC GCGCTGCTT GTACAGG 657

(2) INFORMATION FOR SEQ ID NO:1062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1647RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

GATCCAGCTA GATAGCGTGC CAATTGCTGA TAAATCCTGC CAGAATGCGA TAACGCTCT 60
 CTGAAACGGC CAACGCTCC GGAGCGCCAG GAGCTGTCC GAGATCGAG GCGTCTGGAC 120
 TCGATGCACA ACTAATATTG AATTCACTAT CCGCAGTAG GGGGTACAT AACTGCTTAC 180
 GTACTCCAC TACGACACTG CGCCCCGCAC GCTGCAAGTG CGATCGGCT TACAAAGACC 240
 AAGTCCTTG CAACACCTGG ATATGGTATC CATCGGGTC TCTGAGGACG GCGAGATTCT 300
 TGATAGACC CTTGTGTAG CGCAACTCC ACTCCAGGTC CGGTACGTC TCCTGATGT 360
 CAGCGCAAAG AGGCGCAGG TCACTGAGCG ACACACCCAT GTGGCTGTAC CCGTGGGCT 420
 CTGGTTCCG GTTGTGATAC GAGAAGTCG CGTCATCTC GTTCCCCAA TTGTGCTCA 480
 GCTCCAGAAT GCTCTCGGC TTCAACCGCT CGTCCGCTC CGGATACCC AGGAAGTAGA 540
 GGGTGAATTT CGCATTTGG TGCTCGCTCA CCTCCAGTAG CGACATACT AGCACATTCT 600

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GGTAGAACTC CAGCGACTTC GTTGGCTCCT TCACACGTAG CATGGTGTGG TTAAACTTGG 660
 5 GCCCCAGGTC CACTGGCTCC GGGTCCGACA AGTTGTACTG TATCAACTCA ATCCAGTATC 720
 CGTCGGG 727

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1647UP

(x) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

GATCCGAGCA CCGTGGGGT GCAACAGAGG AATATATGG CACTACAGAC AGTGCACAGA 60
 TGCAGGAGCT GCGCGGCTG GCGGGCAGC GCTATCTGGA CCGCGGGAG AGGGAAAAGC 120
 TAGACTGGGC AATACGGGAC CTTCATTGT TAGAAGAAGA CGTAAAGAAG TACCGATGGG 180
 ACAAGCTGAC GGAACGGGAG CGAAGAGAGA TTGGGACCAA GCGCAGCTC GTGCAAATTG 240
 TGCGGAGCG CGATGGGCG GCGGGGCGG CCGAGCGTC ATTCCATATG CCGGGGAGA 300
 CCGTGTGTGA GGCTACTGCG CCGCAGGAGA AGAGCTGGGA GGAGCAGCAG GTGCAAAAGG 360
 CCGTGGGCGC GGAGGGGCGC TCGACATAA TTGAGGTGA GGGCTCTGAA CAGTACGAGT 420
 TTGTCTGGA CTGGCGTCC GTTGTGCGCT TTACAGAGGA AGAGAGCTG GCTCCCGGCG 480
 AGCGTGTGA GAAGCAGCTC GAACAGAAGC TCGAGAAGGA AATTAAGCGC GTGGCGTGA 540
 TTCAAGAAAC TAGGAGGCAG CTTCCTGTGT ATGGGTACCG CGACGAGCTT CTGAAGGCGG 600

TGCGGACCA CCACT

615

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1648RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

GATCCAGCTC ATGCAGTGGC CGATTCCAGC CCTGCCCTGTC GTTTAAAGTC TTGAAGTAGT	60
TGGTGCTGAA ATGCTTGTCA AATTGTGACA GGTATGTTTT CGAAGATTTC GAGAATAGTC	120
CTTCCACCAC TTTCAATGGG TTCTCTCGA ACTTGTGGAG GAATGAATTC TCCAGCTTGG	180
AGAATGCATG CTGTGAAGAG TATATACGAG ACCCAGCTTT CGCCACGAAT TTGATGAGCT	240
GATTGAAGTC GTTGGCGCATG TCGCTCTCGG GTATGAATCG TGGCACAGTC AGGTCAAAG	300
CTCGCTGGGT CATAGGACGG TATGGTCCCG GTGGGTACTC GTGGACATCG AAGTTATCAA	360
GCAGATAGAA ATCCTTGATT TTGCCCTTGT CTGCGAGAGA CCGCAGGTAC GCCACGAAAA	420
GGTGGTACAG CGCGCTTCCC CGGTACGGT AGATCTTGTT CAGAATAAGT TCGTCGTGCT	480
TGCTTTCATC GTTGGCATCC TTGTACTCTT CTACCGCCTT GCAAGAGGGG AAACACACCT	540
GGCCCGCGGT GAATATTAAG TCCATCTGGC TCGTCTTCTC CACCAACAGG TCCGTACGCC	600
CAACGATCGT CACCAGGATT TCCAGAAAAG CGTAAGTCGT GCACATGT	648

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1648UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

GATCTAGCAG GTGTTGAACA GATAATGGAA TGGCTCTCCT ATATTCCAGC TAAAGTAAT 60
 ATGCCCGTAC CTATACTGCA GTCAGAGGAC AACTGGGATA GGGATGTTGA ATACACACCA 120
 ACACTTCACA GCCTTATGAT GTACGCTGGA TGATTGAAGG CCGCCAAGGA CCTGATGGAT 180
 TTGAATATGG TCTGTTTGAC AAGGGTTCCT TCCAGGAAAC ATTATCAGGC TGGGCGAGAG 240
 GCGTCGTGTG AGGCAGAGCT CGCATGGGTG GTATCCCGCT CCGTGTTATT GCGTTTGACA 300
 CTCGTACAAT TGAAACTGIG ATCCCTGCCG ATCCGGCAAA CCTGCATCC ACAGAAACTT 360
 TGATTCAGGA GGCAGGCTTA GTTTGGTATC CTAATCAGC ATTTAAAACT GGCAGGCCA 420
 TAGCTGATTT CAACCACGGA GAACAACTTC CACTCATGAT ATTAGCAAAC TGGAGAGGGT 480
 TTTCTGGTGG TCAAAGAGAT ATGTTCAATG AGGTCTTGAA ATATGGCTCC TTCATTGTTG 540
 ATGCTCTAGT GGATTATAAA CAGCTGTAT TCGTATACAT AACTCCAACA GGTGAGTTGA 600
 GAGGTGGTTC CTGGGTTGTG GTGGATCCTA CAATTAACTC TGACCAGATG GAGATGTATG 660
 CTGATTCCGA CTCGCGGGCA GGTGTGCTAG AACCTGCTGG TATGGTTGGT ATAAA 715

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 714 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1649RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

20	GATCAAAAGC AAAACTGTGA CGCAGAAAAA AGTTTCGCTG ACAGACGACA TGCTCGCAGG	60
	GCACCAGGG GTGGGCAAG GAGCGGTGCG GTTTCAGCG ATGGACCTCG GGGCGACCAC	120
25	GAATCTTTTG CTAAACAACA CTATCAACAA GACCAAGTTC AGTCAGCTAA AAAAAAGGT	180
	AGATAGTATC GAACTGCATA ACCAGCAGCT GCGCGCAGAG AACCAATAGTT TGAAAATCGA	240
30	ATTCCAAAAG ATGAGTTCCA GATATAACTC CATGGTGGAG AACCTGGTGT CTCTTAAAAA	300
	CTACAATAAT TCCTCGTTG AGAAGTTCAA TCTGCTGTA TCACGCTCG CGCAACAGGG	360
35	CCTGAAGGTT CCCCATOCAT TAAAGCTGG CAACTATGCA TCTTCACAGG TTGCCAAAAA	420
	TTCATCTGCT TCCGAGTTC AACCGCATGT ATCGCCGTTG GGTACTGTAG CACCTACGAA	480
40	CATACCCCTG GCGCAGGCTA CCCCCTCGAA AGAAGAGGCC AATCCTCCTA CAAGCCTGCG	540
	CCCAGGCTTC CATGTTCTGC TGGTAGAAGA ATGATTGGT TTGTATCCAA CTATGTTCCA	600
45	AATCTTGAG AAAATATGGC TGTTCGGTGG AAGTCGTAAC GGACGGCTA TCTGCTATTG	660
	AAACAGTAGA GAAATTCCAG TACGACCTCG TTCTGATGGA TATCGTATG CCA	714

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 663 base pairs
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1649UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

GATCGCTGGC GGGGGCAGCC ACATGCGGGG GCATTTCAGC TTCTACCACA TGCAATCTAT	60
GGGGCTGTG CGGGGTTC GCGGCAGGG GAAGTACGGG CTGGGGAGC CGCCAGCGGA	120
GGCACCACCG CGGGGTTC CCGAGTGA TGTGGTCTG ATGCGCGTC TAGGGTTCTG	180
CGCGATAAC GGGGGGCGC TCGGACGGG GGCAGTTAC TACGACAACT ATGTAAGCG	240
TACGCAGCAG CTGCACGCA GGAGACGCT GCTGGTGGG CTGGGGCTCA GGCAGCAGCT	300
GATGTTGCAC GTCCCGCTAG AGCGGCACGA CCAGTCTTG GACCGGTGG CCTGGGGGA	360
CGGACAGTTG AGGTGGGGC ANCGGGGCG CCGGGAGATA GTTGATATAT AAGTGTATCT	420
AGCCTGTAGT GAAGCTCCT TTCCACGCA CGAATGTCCG CGTCCCGCTC TGGTTGATGA	480
TCTGGCCTC CAGACGGAG TTGTTCCGT GGTCTCGAC GCGGGTGGT CGGACCACAA	540
CGAACTGGTT CGCCAGGTC GGGAAACAAT ACAAGATCTT GATGTGCTCG GTTACCTCCT	600
AATCGGTGCC GGTACGAAT GTGACTGCT CCCGCATCAG GTGCTCAGC ACGTGGCCA	660
GGA	663

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 706 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1650RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

GATGCTCTG CCGGACTCG ATTTTGTGC ACCGCCACG CAAGAAGGAC CTTGGTGCA	60
TCATGTACAC CTGGGCTCG ACAGGTGACC CGAAGGGTGT GTCGTTGACC CACGCTAACA	120
TGTTGGGGG CATTGGCGGT GTTTCGGTTG TGATCAACCG CGCGATTGTG AAGCCTGACG	180
ATCGTGTGTCAT CGCGTCTTTG CGCTTGCGC ATAFTTTTGA GCTTGTGTC GAGTTGACCT	240
GTCTCTACTG GGGGGCTTA ATTGGCTACG GCTCCGTCAA GACGTTGAGC GAGGCTTCGG	300
TCCGCAACTG TAAGGGCGAC ATGAAGGAGT TCCGGCCGTC CGTCATGGTC GGTGTGCGAG	360
CTGTCTGGGA GGGTGTGAGG AAGGCTATTG TTGCGCAGGT CACTAAGTTG CCTCCGTTC	420
AGCAAAAGAT ATTCTGGGGG GCTTACCACA CCAAGCTACG CATGAAGAAG TGCCACATTC	480
CAGGGGGCGA TCTAATAGGA AGCATGATCT TTAAGAAGGT GCGTGAGACC ACTGGTGGCA	540
ACCTTGGCTA CATCTTGAAT GGTGGCTCTC CATTGTGCGG GGATACGCAA GTTTTATT	600
CCAACTTGAT TTGCCCCGTG TTGATTGGTT ACGGCTTAAC GGAGACTGTG GCGAATGGCT	660
GTATAGTGCC TCCACACCAC TTCAAGTACG GGGTTGTGGG AGACAT	706

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 674 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1650UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

10	GATCCATTTC TCATGGAGAT TAACGCTATA TCGAGGGAAA GCAATAACAA GAAGCAAGCC	60
15	AAGAAGICTG TTAACCTTCTC TATGCTAGGG TTGACTGATT TTACCAAACCT CAAAAAAGCC	120
20	GATACTACAG ATGCTCTGGAG AGCGTTTAGG ATGTACGACG AAGTACAAAT GAAAAAGAGA	180
25	TTTAGTTATA AATGGGATTA TGATAAAGTG TCCAGGGAAT TGGATGAAGA GACATGGAAT	240
30	AAGATTATTA ATAGGGAAAC TTGAATTTA TTGCAATTAG TGGAAAGATA TACGGTAAAG	300
35	ATTGAAAACG ATGCCAATAT AACCTATTGG AGTTCTGTGG TTATGCGCAA CTCTGTGGC	360
40	AAGCATGAGG CTACAGGAGT GAGGCAATGT GCCAACTTCT TCTGTGGTAA ATGGGAAGAC	420
45	CACCGAAGC AGTTTCCCAA GTGCGCGCGT TGCAAGGCA CAAATATTG CAGTTGTGAG	480
50	TGCAACTAC AATCTTGGGC ATATCATCGG TACTGGTGCC ATGATGTTGG CTCTGTCTTC	540
55	ACGGGCACCT CCTCAACGGC AAACACCACT GGGACACATA CGCAAATGC TGTGGGTCAG	600
60	TGGGCTGGAA CCACGACCAC TACTACCAGG GGGCTACGG AGGTAGATCA ATCCATTTTG	660
65	ATGACAGCAA GGGG	674

(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 622 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1651RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

10 GATGGCGACG TTTACCGAAG AGCAAAAAGA AAAGTACGCG ATGGCGTTGA AGGACAAGGG 60

GAACGAGTGC TTTAAGGAOC AGCGGTACGA GGAGGCGATC AAGTTCTACG ACTGCGCGTT 120

15 GAAGCTAAAA GAAGACCCGG TGTTCTACTC GAATCGGTGG GGTGCTACG TGOOCTTGAA 180

CAAGCTGGAG AAGGTTGTGG AGGACAACCAC TGCTGCACTA AAGCTGAAAC CCGACTATTTC 240

20 TAAGTGTTTG CTTCGTCTGG CAACAGCTAA TGAATCGTTG GGTAATTATG CTGATGCTAT 300

GTTCGATTTA TCTGCCGTAT CTCTATACGG CCGGTACAGC TCGCAGACAA TTGAGCCCGT 360

25 GCTGGAGCGG AATATGAACA AGCAGGCTAT GCAAGTATTG AAACAGAAAC TCTCTGGTGG 420

AGAGAAACAC GAACTTCCTT CCAATACTTC CTTCAGGTCT TTCTTCGGCA TCTTCCTTC 480

30 GGAGACATCG TTGGAGAACT ACGATGAAAC TTCCGAGCA GACCGCATTTC TTCTCAAGGG 540

ATTGTGCGCC CTACACGGCC GGCAGGCAGG CTCCTATGAA ATTGCTGATG AAGCCTTTAC 600

35 CGATGCTGTA GAAAAGTTCA CC 622

(2) INFORMATION FOR SEQ ID NO:1071:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 679 base pairs

(B) TYPE: nucleic acid

45

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1651UP

55

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

5	GATCGTGATT TTCGCGGGCT GCATCCTGCA GGCTCCACAT CATGCCGTGC GCCAGGCTAT	60
	GCTGAACATC CCCAGCGGGG TCTACTGCAC GTTCGGTGGG CAGTCATCGC CTGOGATCCA	120
10	GTACGGTATC TCGTCTACAA ACTTCATCAC ACACGTGAAT GAGATCGAAA CCCAGACCT	180
	GGACCGCTTT CTCGAGGTGG TACGCAAGAT ACCAGACAAC ACCTACTGTA AAATCGGTCT	240
15	TGTGACCTTC GACAACGTGC CTTTGTCTAT CTCCTGAAG ACAAACTACC ACTACTTCCC	300
	CACCAGCGAG CTCTCCCGCA ACTCCGACAC CGGCGCTGG ATTGAGCACC TCTGCAACGC	360
20	TACCCCGCT AAAAAGTAGC AATAGACTGA TATCTTTAT AGAAGTATA AACTATTAC	420
	ATGTAACCCG ATCAGGTGAC GAGCGCTGCA CGCAGCTCGT GCAGCATGCT CAGTGGTATG	480
25	GCAGTAGGCG CCGCAGAGC TTCAGATGGG CACTCGCCGC CATGGTCCGC CCAGAGAGCT	540
	GCTTCAGCGC GCGCTGTCCC AGCCTGTGTT ACGTGGCTG CGGCCAGCCT TCGAAGCTT	600
30	GTACCTCTG CAGTCTTCG CCATCTCTTA GCTGCGCCTT TGTGGTCTT CATTAGTGT	660
	CGCACCATGA TCAGCGACG	679

35 (2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 692 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: single |
| | (D) TOPOLOGY: linear |

45 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- | | |
|----|-------------------------|
| 50 | (A) ORGANISM: PAG1652RP |
|----|-------------------------|

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

EP 0 866 129 A2

	GATCTTCGTT CGTGAAAACC TTGCACGTCT TCATGAGCTC AAGAATTGOC TCTGCATCTA	60
5	TTCTGTCCGG TTGGATTCTG CTTTCTTAT TGTCCTGAAT CATGCGGCA AAAGCGCGG	120
	GCGTCAGTC ATGACGGGAT CGGCCCTTAT AGGACTTCCC TGCAAGCGC ATGAGGCTOC	180
10	GCCAGCCATT TTCTTCAATA ATATTGACAA GTCTTCGTT TTCCAACAG ACCTTGTTTG	240
	CGAGACTGTG GAACGTGTT ACCTCTATCT GCTCAAGTAT TTCTACCTT TCCTCAGCAG	300
15	ACCATGCAA GTTGCAATCT GCTCTTGA ATGCTCCAT AAGCTTTTCA TTGATGTTAT	360
	CCACTGCTTT ATTTGTCAAG GAGAGGATTA GTATTTCAIT AGGAGCTACA ATCCCTTGT	420
20	AAACCAGGTT GTAGACTTTA TGCAGTAGTG TCACGGTCTT GCCAGACCA GGTCCCGCTA	480
	CCACATTGAC AGTTGTACAA GGCTCATATG GATGTGTTAC TACTGTGAT TGGGACGTG	540
25	TCAGTGCTTT CATTTCATGA TGATACATG TCAGCGTGC GCGAAGGAAA TAAATTGCTG	600
	AATTTCCGTT TTAAGATACT CAAAAGAAAT GAGATAACG CCGCAAGGG CCGAGTAGAA	660
30	TTACAGCAGC TATTGAATAT ATTTAGTTA TT	692

(2) INFORMATION FOR SEQ ID NO:1073:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 697 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
40	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1652UP

50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:
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55	GATCTCCCCA CCAATCTCTT CCAGCGCTT CTGTAAGCGT TCCCGCGTT GCTCTCTGC	60
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EP 0 866 129 A2

CTTTTGCTTC TTCTCCTTAC GGATTTTTCG ATACAGCGGC TTATTCAGTT CGAACTGTT 120
 5 CTCTTCCAC TGTTCCTTCC ATTGCGACTT CGACATGCOCT TCGGGAACGG GCGGCAAGGC 180
 AGCCCGTGGT TTTGGCCGAC TCAATGTTTC ATCATTATTA GTTTCAGGAG TCATTGCOCA 240
 10 GTTTCAGGAC TCTTAGCGCA AGGTCTTGTC ACTGAAGTAC AGTAAAATGG ATGCCCTTTC 300
 GCGGTGATGA GGCAATGACC TGGTGAAATT TTTCGCCCAT GGTGAGGCTG TATAGTGGTC 360
 15 ACGTGACAAC AGTTCAGCCC ATATATGGAG CCCCTAGGTC ATATAAAGGG TCAGGAGCCC 420
 GCTAAAGTCT TTGTATCTG ACCTTTTATT GGGGAGCTTT AGGGCGTGTG TCTCTATCCA 480
 20 GAGCCGTGTG GTGAAAAGCG TCTCAGCTCA GCGGTTCTA CTACACTGAG ATTTAAAAAC 540
 CAACAGCGAA GCAGCAGAGT ATGACGTCT TAGCAACTAA ACTCGAAGTT CCATGGGTTG 600
 25 AGAAGTACCG GCGGAGCTG CTGAAAGATG TGTGGGAAAC GAWGAAACGG TGGAGCGCCT 660
 GCAACAGATG CCAGGGATGG AAATATGCCA CACTTGA 697

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1653RP

(x) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

GATCTTTGAT GCTATTTTGT ACCTTAAGGG CTGTTCCGTG CTGGAGATGA TCTCCGGCTA 60
 55 TATAGGGGAG ACCGTCTTCC TGAAGGGTGT TGCTTATAT ATAAAGCGGA ATAAGTTTGG 120

EP 0 866 129 A2

CAATGCTACC ATGGAGGACC TGTTTGGGGC CATTAGTGAG GTAGCAGGCC TTGATCTCAT 180
5 GGCGAAGGCA AAAGATTGGA TTCTAAAGAT CGGGTACCG GTTCTGGACA TCACTGTTGT 240
TGATGGGAAG ATTCTACTGT CACAGAGAAG GTACCTTTTC AGGGACAAG CTGACGCCAA 300
10 TGACGACCTA ACCACCTGGT GGATTCOCCT GGAAGTGACA CAGGACTCAA CTGCACTAC 360
AACAGAAATG GTTTCTAAAT CCCAAGAAAC AGAGATCTCA GCTACCGATT TTGIGTTCTT 420
15 TAACAACGAT GCCCAGGCT TCTTCGGGT GCATTATGAG GATGAGACTA TTCTGGCTAA 480
CATCTGCAAG AACATAGGC AGCTGTCTC ACGCAGTAAA ATTGCGTTAA TTTCGGATGT 540
20 TGATGCCACT GGTACCTTCA CGCAACTCAT GGCTGTCTG TCTGCATTCT CTGCAACGCA 600
TTCCGAAGAC TACTATGTTA TGGAACTCTG CATTGTCCAT TTCCACTCG GCCTGCTCAA 660
25 TCATATATCG CGATGCGTCG CAGAGATCCG CAAGAAGCTT GCGGCGT 707

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1653UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

GATCTAATAC TGGGAGCGAC TGGGCGTTGT GCGGTGTCT ATCTGTATGC GAACGAGCGA 60
GGCTGTGATG GAGACANATT GTACTACGAT GGTTGCGCGC TCATTGCTGT GAACGGCGGA 120
55 GTTGTGGCCC AAGGCTCGCA GTTTTCGCTG AGGGATGTCT AAGTGGTTAC TGCAACTGTA 180

GACTTACAAG AAGTGAGAGA TTACCGGATG TCTGTGATGT CGCGAGGGTT GCAGGCAGTA 240
 5 TCGAATAACG TGACTTTTGA ACGTATTCAA GTACCTGTAG AACTGGCCGC GATGCAAGAT 300
 AGGTTCAATC CTACGATTAA CCTGACGAAG GCGAAAGCCC CATACTATCA CAGCCCAGAG 360
 10 GAAGAGATTG CGCTGGGCCC AGCTTGTGGG TTATGGGACT ACCTACGTGG TTGCAGAGGA 420
 ACAGGCTATT TTCTTCCACT ATCTGGGGGC ATTGACTCAT GTGCCACTGC TGTAAATTGTG 480
 15 CACTCTATGT GTGGGATGGT TGTCACGAA ACATCTGAGG GTAATCTGCA AGTAATTGCA 540
 GATGCGAGAA GATTGGCTGG TGCTAGGATG GACTGGATTG CAACCGATGC ACGTGAATTT 600
 20 GCAAATATGA TATTTACAC TTGTTTTATG GGAACAGCAA ACTCCACAAA TGAGACTCGC 660
 AGTCGGGCAA AGAACTTGC GGAACACCT 689

(2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1654RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

GATCTTATTA ATTTTGATGG TGCTATATTC TAAATTCAAG TAATGATAGC GCGTGATGCG 60
 50 GTACGTACCT ATACATATAA CGCACAGTTC TCCATCGTCT ATGCGTGTAT GAAAATCACT 120
 CCAGCCGTGC GACACGCCAC GTGTAATCTA GTGAGTTTCA AGTTCTTCTT CCTCATCGGC 180
 55 AGAAAGTTGG CCGCGGGGGG TGAGGTTCTT GAGCGGCTCC TTGAGCTGCG CGATAAGGCT 240

EP 0 866 129 A2

ATTCTCOCTT TGAGCATGCA TGGGATAACC CTCTAGAGAC ATATGAGCOG AATCTGCACC 300
 5 ATCTAAACCA TGTTCGCTGT TGCTGCCAGT GGCAGCTGCC AGTTTGGGAC TGGACAGACC 360
 TGTCTGTCCA TCTTTGTAAG AATCCTCGGT CGTTGCCGAG TTGGAATTCA TGGTTCCCAT 420
 10 AGTGTGCAAG ATTTTCTCCT CTCTCTGTAG TTCCAGATGG GTACCTGTCA GATTGATCAA 480
 GGACCTGCCG CTTTTCACGC GCGAGAGCTT GGCAGAAGA GAGTCCCCGG GTTGGCGTGG 540
 15 CTTACCAAG GTTTGTAATG GAGGTGTGAG ATCTGGGAGT CCTTGGTAGT CTCAGACA 598

(2) INFORMATION FOR SEQ ID NO:1077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1654UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

GATCGGGGC GGGTCGCSG CAACCAACGA TGTCAAGTGT GGATACCAGC GACCTGGTAG 60
 40 GCGTTACGGT GGGAGGAGCA GCGTTGGCG GAAAACCGGC AGCAGAGCAA GTACTGGCTG 120
 AAGTGGGGGC CGTATCTGTC GGAGCGGAGC TGGGCGACGG TCGGGAGGA CTACTGTTT 180
 45 GACGCGGACG CGTGGCGGCA CTTCOOGTTC GAGCAGGCGA ATGCGGGGT CTTCOOGTGG 240
 GCGAGGACG GGATCTTCGG CGTGAGCGAC AACCGGCAGC TGGTGTGCTT GAACGTGGGG 300
 50 ATGTGGAACG GCGGTGACGA GCTGCTCAAG GAAGCGGATG TTGGGCTGA CCGGGCGCA 360
 55 GGCAACCAC GGGGAGGACT GCAAGGAGCT GTACTACTAC CTGGACAACC TTCCGAGCCA 420

TGCGTACATG AAGGCGCTGT AYAAGTACCC GNTCAAGCGG GGGTTCCCGT ACCAGGAGCT 480
 5 TATTGCGGGC AACGACGGGC GCGGGTACGC GGAGCGCGAG CTCGAGGTGT ACGAACTTGA 540
 CCGGCTGTAC CGCGAGGCGG CGACCGGCGA C 571

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1655RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

GATCCACTTT CCACTCTGAC ATCGGTCAAT CAAOGCTGGG CACTCAGGTT CAGTTCIGAA 60
 35 GCAATTGCAG TCCCCGCACT TACCTTCAT TTATTTAGAG ACTTAGTGGT GTTATAAGTC 120
 AGTCCTATCG AACAGCTCTC GACAGTCATC GGAAACGAGA AGTTACCCGC CCTTGAGACA 180
 40 CAATCTGTTA CCGCACTTTG ATTTACATGC GTTACCCGCT CTGGGTCACG TGCCGGGAAG 240
 CACATGACAA AGGCGGAGAG CTAGTTAAGT GAGGCTCATT GGGGTATGCC GGAAACTCTA 300
 45 ATGACTAGAT CATCGAGAA GCACCGGTAT ATAAGACGCA TCACGGTGGT GCTCGAGAGA 360
 GTGTGTAAAA TGCCAATTGC TTAGCCACTG ATGCCAAATA CACTGGATAA GAGTTAAGTA 420
 50 CAAAACGGCC CTTGGAGGGA CCGGGTGTTC CAAGGGAAAG TGGTCTTGGT CACTGGGGGG 480
 GCCGGGACGA TCTGCAGGT GCAGGCGGAG GCAATGGTGC TACTTGGTGC CAAGGCTGCG 540
 55 ATCATTTGGC GCAATGTGGA GAAGACTAAG AAGGCGGCAG CGGAGATGCG GGAGTTGGGC 600

GACTCGGCTG ACTGCGTGCT CGGAATTGGC GCGGTGGACT TCCGGGAGGT CCGGACATG 660

5 AAAGCGCGCG GTGGAACAGA CGTTTGGCGC GTTT 694

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1655UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

GATCTCTCTG ACCGCCCCCA AAGCTGCTC CGGCGACATT GACTCTGGTG TTACCAOCCA 60

30 TTATGTGGC GCGGTTTCA TCCAGATGC CTTGGCCGT CGTCATGGTT TTGATCGTT 120

CCCGTACTCT GGCACCGATC AAATACTGG TATTTGAGTG CATATTGCTT TATCTATAG 180

35 TCTGGTACA TAAGCCGGG TTTGAGGG CGGGTAAOGA TGACGGGTAA CGTTCTTTT 240

40 TCGTATATG TAAAAAGAAA TGTGCAAACA TTTTTCATGA GATGAACGTT ATACTGGCTT 300

GTTTCTCTCT TGAAGTCAGC AATCTCTAAC CTTTGAAGGT GATTAAATAGG CTGTTGGTC 360

45 GTGTGGAAC ATTGACGGAG CTTTGTCTGT TGTAAGCGAT TAATCTGTGT TCGAGTTTC 420

ACTTTCTOGA ACTGGTAGCA GGTCTGACGG GTCTGCGAAG GCGTGGGAG ACTTGCAAAT 480

50 ATAGGCGCAA GACAACTGC GAGATACAGG GGAGCTGCTG CAGCGAACAG GTGGAGTGA 540

GGCGATCTT GAGGACTAGC TGCTCTGGGA CGAGATGGG AAGGAAAGCC TCGGATAGG 600

55 CGTAGCAAGC ACGGAGCCCA AGCGGTGAA GGTGTTTCATC CTGGAAGACA CGAGTGGAG 660

AGACACTGGG ACGGG

675

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 705 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic).

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1656RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

GATCTAGCGA TCAATCGCAG CTAACAGATG CTCTGACATT ATGCATGAGC GCAATCATGA 60
 TGGACACATC GAAGCTCAAG CATAAAGTAG AGGACTGGGA CATGCAAGCG TAGGCCATCT 120
 GCAAAAGCGT GTTGACCAAT ATGAACGAGG ATGCGTACTA CAAGCGCATG AAGGCAGCAA 180
 AGAATGACGT AGATGGCTTC TCACTCGATG AGATTCTTGG TAAGGACTAT AAAGAGTTGG 240
 TGTTCOCGAG CCGCAGTGCA GATCTACGTG TTGGCGTACC TACTGTGTG CCGTCTTTGG 300
 AATGGATGCG CGAGAAGTTC GCGACAATG GGAAGTACGAA GCTCTGGCAC AGTTTCCTTC 360
 TGGAGCATAA GTTAGATTTC CTCGTGGTGC TCACAATTAA GAAGGCCAAC GAGGGTTTGA 420
 AACGGGAGTT GGCTATCATG GCCAACTCCT GCGACCGTGC GCAGCAGGTC GAGTTCCTGA 480
 TCCAAAGCCT CACCCAGAG TTGCAGTTGA GCAAGACCTC TGTCTTCTCC CCGGCTCAC 540
 TCGTCATTGA GACGTGCGAC CAGAGAATGC TATCTGCCAG TCGCAAGCAA ATAGTACCTC 600
 TCCTCAAGAG AACCGTCGCC GAGTTATAGC ATGCTTATGT AACTAACGTT CCAGTTACCA 660
 TCTTCCACA TCTCAGCGGC AATGTGCGT TTGTGGTCTC CAACC 705

(2) INFORMATION FOR SEQ ID NO:1081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1656UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

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GATCTCTTCC TACCCGTGTAT TTCTACTTAG CAGGAACCTA AATATGTGGA AATCATGGCT    60
AGTAGGATGT TTTTCTTACA ACACAGACAT TTACGCCAAC CAGAAGCTA AGGCATGCAG    120
TATCTCGGGG AGTATCTGCC TAGGATGGC GTAATGCTAA TAGTGGTTGC GGGAGAGGCT    180
GGTGAGGTTG AACTGGGAAA ATTGGGTGGG CATAGGTTGA CTGTACAGT AAATGGAGCG    240
GCGAGGTGA TCGAATTGCC CTGTGAGGTT GATCCGCTAG CGCGGCGCG TATTAGACAC    300
TCGAAGGTG CATTGAGGT CCGGCTGAAG GCGGTGAATG GGACTGAGG CGGGGCGCG    360
GACTTCACTA TGCTGGCTGC AGAGGACGGG TGGGGCGGAA AAGACCTGGC GGTGCTGAA    420
CTGCGCTGCG CGCGGTGCGA CGGGCTGCTG GTTACGGGCG AACATGCAGG CGGTGAGCG    480
CGATGCCCTC CGAGTTTGG ACGGAGCTGA TGGACTACTG GCACTGCCAC AAGCCTGGCG    540
ACGAGTCTGC GGGCGCACAG CAGTACCTGA CGAATATATA CGCGCTGCTG CTTGGGAGCG    600
GGGAGCTGCT GGTGGGGGAC ACATTCGTCA CGGTGGGCGA GGTCTGCTG TCAGAGAAGC    660
TGGCGATGAG                                         670

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(2) INFORMATION FOR SEQ ID NO:1082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1657RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

GATCGATTTA GATTTCACCT TCAGGCACAC TAAGAGATGG ACTCCTTACA CTAAGGGTGG 60
 GCTGACGGGC GCGGTGAAC GTGTTTGTCT CGACGGACAG ACTGTGTGTG TAAGCGGTGA 120
 CCTAGTACCA TCTGCAGCTC TAGGTGAGGC CGTTGTACCT ACTTCAAACA ATTACACTTC 180
 GACTCCTCTA TTGAACGGG AGCCATTGCA CAGCTTGTGTT CCACCTTCTA GCTGGGTAA 240
 GAAGCGGTTC TCCTTCTCCC GCGAGCGGGG AACTCGTTT GCTTCAGCTG GTGACCACGA 300
 GGAAGCTGTT ATGACCAAC CGCTGGAACA AAGGTGATG TCTTCAAGGC CACCAAAGGA 360
 GCTGTGCCCC CCAAGTGGC TGAGAGAGCT AGTCGTGGG CACAATCAT TCAGAGGAAG 420
 GAATATCTTA TCTGTTAACC AATTCAAAG TTCGGACTTC CAGCCTTGT TCGTGTGGC 480
 CCAAGAGCTG CGTGCGGCTG TCGAGAGAGA GCGGTCTC GAATTGATGA AGGGCCGCT 540
 CTTGACGACC ATATTCTATG AGCATCAAC GGCACATCC TCCTCTTTTA TCGGGCAAT 600
 GGAGCGCTC GTGGTAGAA 620

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1657UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

GATCAAGTCC TTCCAGCCGA GCCAGTCTCG CACCGCATAC CAGAAATGCA TTGGCGCACC	60
TAGCGGGATA TTCTGCGGCG TGTACTGGT CCACGAAAAG GCGCAGCGT GTGCCAACGC	120
AAAGGCTACC ATCTCCAAAC AGAGCGCCAC ATTGTGTAC AGTAGCCCA TGTTCGTGCC	180
CSGCGAGTCC TGAATCACGT TCAGGTAGTG GAGAAGCGTG ATKACCATAC CCTGCCAGTA	240
GGATGCAAAA ATGATCAACT TAACACATAA GAATTTAGGC CATGGGTGT ACTTGGGCAA	300
CTCGTGTAC AAGCACTTC AGAAGAGCGC CAAGTTATAG AGCGACCATG ACGCGCTCGC	360
GTTGTATACA AGGTCAACC ACTTACATCC CAGATCCAC TCCAACACT GGAACGCAGA	420
CATCCCCAAG CAGTACACCG GCTTGAACCA CCGTACTGT AGAATGCCCC GCTTCACAGC	480
CAATAACGCC TTGGGGTCCG CCATATCGAC CATGGGCAAC ACCCAACGTC CCACAACGGG	540
AATCGGGTGC TGGATCCTTT TCTGCTCCGG CGCAAGGT	578

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1659RP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

5	GATCAAAAGT TGATTAAACT AATAAAAGAA TTATTTTATG TATATTGATT GTATAGTCAT	60
	TTTCAGACAA AAATCGTGGG AATTTTAGCG GCCAAACATA AAAGTCAGAC ATTAGAAACT	120
10	GACAGATACT TTATTTACTG CATAATTACA CTAAAAACAA CTGTTCTCAA AACTACGGA	180
	TTATTGACCG CCCCCTCACT AATAATGTAC TCCTTCTATC GGTTTCTTC GGTAGAAGC	240
15	ACGTAAAGAG ATCAGTTTCA CTTTGCAATT TGGGCACTTT TACGTTTCCA CTTAAGGATC	300
	ATTCTAGTGT ATTTTATGAC CAGGAAAGAA AAGGAGCCTA AAAACCTGAA GGCAGCCAGA	360
20	CCAGCGACTG ATCCCAAGAC AAAAACCAAA TATTTGTTAT TAGAGGTTTC TTCAGGTGAG	420
	TATATTTGGG TTATCATCAT GATCAAAATC AAATTGGAAA GCATCCATAA CATGACAATT	480
25	CTAGTCCGCA CATCAAGGTA GIGATCTGCT TGCTTTTGGG TAGGATCAAC TTTTATTTCT	540
	ACCACTTCAT CGATTTTAG ACGACCTTGA TTTCCTGGTA TTTATTATCG ATGTCTGTG	600
30	GCCATTCAGT ACCCTCAACT ATTTGTTTGC CACGGGGGCC TGGGTAAOCA TAGCTTCAGA	660
	CTTTGGCTTG GACCCCTGGG AAGGGCCTTT TGT	693

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1659UP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

5	GATCGAGTGG TCCACCAGGT AGTCCCTGGCC CGGCTTCACG TTGGGCGGGG TOGAGAAGTA	60
	GACCCGGTAC TGCTTCACG CCTTCTTCAC CTCTCTGTAG CTGCCCCGTC GCCCCACGAT	120
10	GTGGGGGTGG AACTGGGCCA GGTACTCCTT CAGCACCGCC GGCGGGTCCC GCGCAGGGTC	180
	GCACGTCACG AAGATCGGCT GCACGTCGAT GCCCCGTTGT TTCAGTCGCG GTAGCCACGC	240
15	CGCCAGCTTG TCCAGCTCCG CAGGGCAGAT GTCCGGGCAG TGCGTGAAAC CGAAGTACAC	300
	CAGCGAGAAC CGCCCGAGAA GGTTCCTTC TCCTGAACCTG TTGCGGTGTA AGTCCACCAG	360
20	CTGGAAAGGC CGCCCCACCG CGGCGCGGCC GTACCCCGGG TTGCGCTCCG CCTCCCGCTG	420
	CACCTCCAGC CGCCGCTTCT CGCGCGAAAA CACGTAGAAC AGCCCGCGCG CGAGCACAGC	480
25	AGCACCGCGG CGGCTTCCA CGTGTGAAC TCGATCGCCC CGCCCTCGAC CGCTGCGAGT	540
	GCGTTTCTTG CGCCCCCAGC GGGATCCGCG TCAACGGCGG CGGCTTGCCC GGCGCCTCTG	600
30	GCCCCCGGCG GCTCTCTGGG TCGCCAGCGG TGTTCGGGAG AACTCCCGCA CCCCCCAA	660
	CGCTGCTCTC TGCTTGCAA TTCCCGCAGC TTGCTGCAA ACAACGAGTC CTACTGATCA	720
35	TCCTTG	726

(2) INFORMATION FOR SEQ ID NO:1086:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 720 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50	(vi) ORIGINAL SOURCE:
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(A) ORGANISM: PAG1660RP

55

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

5	GATCAATTGG ATGCCAACCA AGATGAAGAC CATCTGGGTG AGTTAGCAGT GCACTCTGGG	60
	GATACATGGT CTGAGACCGA TAGGAATCTA ATTTTGAAAT TATTGGGCAA GTTCAAGAAT	120
10	ATCAAAGCTA TTTACAAATC CGAAGATGTC CGCCAAAGGT TGATGGAATT ATTGGGTAGT	180
	CGAACGCTGG AAGTGCAGAA ACTGGCCCTA GATGCGTGTG TAGCATACAA GGATCCAGTA	240
15	GCTGTGAAAT ATAGGGACAA TCTGAAGAAC TTATTAGATG ACACGTTATT CAACGACGAA	300
	GTAACAAAGT TATTTGCTCA GAATGAGTCA AGGGTTATTG TCAACACTGA TGAAGATTA	360
20	TTAATGCOCT TCATTTTGGG TATTTTATTT GGCCGTGTTT AGACACCTAA TACCACTGGG	420
	ATCAAAAAGA CAAGAAAAC TGCGGTCATA ACTGTCTGTC CAAATTTAGG TGAGAAGAAT	480
25	ATTACTGACT TCTTGGCTCT GGGTAGTAAT GGTATCAACT ACCAGTACTT CTTTGAAGAG	540
	AATGCGGTTA TTCTGACAG TGAGCTTACA GCGATAAATT TTAGGAGAAT GCTTGGCTTC	600
30	ATAAATGTCC TAAGTGCCCTC GTTGAATGTT TTAGGTTCOA ATTTCOCGA GGCGGTCAAG	660
	ACAACTATTA AACCTCTCGT TTACGCAATT CACATGTCAG GTCGTACTGG ACAGAATAAA	720

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1660UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

5 GATCTTATAG ATTTTCATCC CCAAGCTTAC AAAGAGAACG TTATCCACCT GTTTTAGCCA 60
 GGCTTGGATG TATTTTTCAA TGGTACCCAT GTTCTCCTGG CCCAAGTTCT TGAACAAGTT 120
 10 AGTTAGTAGC AGACTAGCCA TCTTCTGCA TTTAGGAGAG TGTTCATTTA CTGATAAGTT 180
 TGCTAGGAAC ACGAAGAATG AGGATGAAAG TTTCATTAGT AAAGCGGGCC CAGATTGTGT 240
 15 GATCAGAAGG TTAAGCAATT CCATAACAGA TTGAAGACCT TCTTGAGATG GATACTGCAA 300
 ATTGTTGACT AAAAATTCA ATTGTTTTTC CAGCCTGCCT TTACTTTGAT CATATTCCAT 360
 20 GAAGAACTGG TAATAGACAC TCCTGGCAAC ATCCCTGATT TCCTTAGCAT GATTGTTGAC 420
 CATGACTTCT GCAACGTTAT CAATAATATC GTACAGCTTC GGAAGAACA TATGTTTGA 480
 25 AACCAAGGAT TTCAAAAATC CAAAAGCCAG ACCTTGCTTA TTGGGCTCCA TCAAATCTGG 540
 TTCAATCCGA CCCAAAACAT ATTGAGGCGC AGAATCCTTT AATTCAATGT CTTTATAGCG 600
 30 GATAAGCGCA GATAAAAAC TACAGACGAC TTGACAAAGT TCACCAGAAG T 651

(2) INFORMATION FOR SEQ ID NO:1088:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1663RP

50
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

55 GATCGGGTT TCATCTCCCC ATACTTCATC ACCGATGCGA AGGCCAACAA GGTGGAATTC 60

GAGAAGCCAC TGTTGCTTTT GTCCGAGAAG AAGATC

96

5 (2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 583 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: PAG1664RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

GATCCTAGGG TGGTTCATGG CACTGAGCGG GACGTGTTCT TGGACCGGTC GAACCGCAGC 60
 AAGAGTCTGA AGTCCCTGAA CGGTCCTCTG GAGCGGCTGA AGCGCAATCG GCAGGCGGCG 120
 TGGATTTTCC CAGAGGGCAC GCGGTCTTAC ACAACGGAGA TGCAGCTGCT GCCATTCAAG 180
 AAGGGGGCGT TCCACCTGGC GCAACAGGCG CAGATTCCGG TGATTCCGGT TGTGATGTGC 240
 AACACGAGCA CGGTGTTCAA CCGCGGCTG GGCATCTTTA ACCGCGGCAC GATCAGGGCG 300
 AAAGTGCTGG AGCCGATCGA CACGGCTAAC ATGACCAAGG ATGACGTGGA CAAGCTTGTG 360
 AGCGACGTGC AGGCCAAAAT GCATGCCGAG TTGAGGGCGC TTGGCTACGC GCCTGCGATC 420
 GTGGACACGA GCCTACCCGA AGAGGCGCTG CGGCCGGAGT TTGTGGACTG CAAGGAAGAC 480
 ATCACGGAGG TAACGGCCT CTCGAAGTAA CCTTGGTTGG TATCATATAA ACGTTGCGAC 540
 GAGTTATGTA CATATAGCGC TGCTAAGTAG GCATTCAGTC CCC 583

50 (2) INFORMATION FOR SEQ ID NO:1090:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1664UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

GATCCGACTG	ACGGTGAATA	GGCCACCGTA	GCATGCGCGG	CTGAGCGCGC	TGGCGAACA	60
TAGCAGCGGT	CCTTCGAGG	CTCTGGTGGC	CAAGACAAAG	ATCCACTGGC	CCACCACGOC	120
CAGTAGGAGG	ACTGCCCACT	GGACTGACAT	CGTCGACACA	CGTTTGTTGA	TGCAGAGGTC	180
AATTATCAAG	CCCGACAGGA	AGCGCGAGCA	CGTCGAGGCA	ATGCAAAATT	CTGGCAGCAC	240
CGACGCTTGG	CCCAACAGGC	TGCACAGCGA	GCCCATGTTG	GTGAGGAACA	TCTCATOGG	300
GCCACGCGAC	AATAGCAACA	CAAGGGCCAT	GAAGTACGCC	GCTGGGTCTG	GGAAGAAGTT	360
GCGCAGCGCG	CGGGGATGTT	CCTGCGGCAG	CAGCGGCTGG	GTGGGGCTCT	GCATGCGCGC	420
GAAGGTCACT	GTGCGGGCT	TGACCTTGAG	CATAGTGAAG	ATGCTGCTGG	CAAACACAT	480
GCAGAAGCTG	ATCAGCGTAT	ATGCGACAGC	TAGAGTCTTG	AATACAGAG	AAAGGTCAAG	540
GTACGGCAGG	CCATTTCCAA	AACCATGGTA	TCTTCAGCAG	CTGGGACCTA	GCACAGAC	598

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1666RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

5			
10	GATCCTTGCG TACTAAGAGT TAGACTTTAA TTAATAATAT TATTTGTAGA AGATAGAAAC	60	
	CATACTGACT CACGTGTTAT TTAACCCATC TCACGTAAAC TTTTAATTGA CGAACAGTCA	120	
15	AACCCCTACTT AGCTGTTACA ACCAAGAGGA TAGGTTGAGT CGACATCGAG GTGGCAAACA	180	
	TAACCTACAA TAGCTACTCT ATCGTTATAT TACCTGTTC AATTTTGTTA TCATAATAAC	240	
20	ATTTAATTAT TATTICAATA ATTCTCATTA TTGTCAGAC TATTICATTA TGTATTATTT	300	
	ATTAATTAAT ACATATTGGG CTTTGTGGA TATAATTATT GTTAATCCTA CTCATATATC	360	
25	TAGTGTGTA ACGTCTTAT AACTTTATAA AAAGGATTGT TATAAGCTTC GCTGCAGATT	420	
	GTCCTTTATT ATTATAAAAT AATATTAGGA GTTCTTTGCA ATTAACCCAA TTTACTCAAT	480	
30	ATATTTAAAT ATTGATAATT AAATTTCACA ATTTAATGGG ACTATTAAAT AATCCCTAGC	540	
	GTAACCTTTA TTGTTATCA AATACCATTA CAATATGAT ATTTTGTTC ATTATGCCAA	600	
35	ACTTAAGTGA TTGTCTACT TGTAGGTAAT ACAATTATAG CACAGTTATA CCATTATATT	660	
	TATTTAATAT ATTATCCCTA TATTATGTTT TATTACATA TAAACTGTA CAT	713	
40			

(2) INFORMATION FOR SEQ ID NO:1092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1666UP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

5	GATCCTTATA AAATGGGCAA TAGACGTGTT ATAATATAAT ATACAAAATT ATAAATAAAT	60
	ATTTAATAAA ATATAAAATT AATAATTAAA GTATTATAAT AATTAAATAA ATTATTTTAT	120
10	AATAAGTATG GATTTTAAAC TGAAATTGT TAAATGAAA TAAGAATTGC TAGTAATCTA	180
	TTAATAAGAA AGTAATGGTG AATACTCTAA CTGTTTGGCA CTAATCACTC ATCAAGGTT	240
15	GAAACATATA ATTAAATAAA GAATATTAAT TAATTTATTA ATTATTAATT ATTATTAATA	300
	TTATTTAATA AATATAATAA ATATTTTAAT TTAAATTATG AATTAAATGCG AAGTTGAAAT	360
20	ACAGTTACTG TAGGGGAACC TGCAGTGGGC TTATAAATAT CTTTAATATT CCATTTTTAT	420
	AAAATAAATA TATTTTTTAA TATATTTTAT AATAACTATA ATTAAATAGT TAAAATTTAA	480
25	ATTATAATTT AATAATTTAA TAACTTATTA ATTAGAGAGT TAGGGTACAT CCCCCCTAAT	540
	GCTATGCATT ATGGTTGGTA CCACTCTAAT TAATAAACTA TAATAAATAA ATACTAATAT	600
30	TTTATATCAA TTAAATTATA ATTATTTTTT ATTAATATTT TAATATTATT TAATGAAATA	660
	TATAAATAAA GTATTAT	677

(2) INFORMATION FOR SEQ ID NO:1093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1667RP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

5	GATCCATCGT GGTGTGTTT ATTACCTGTA ATTCCATTGA TATCCTGGCT ATGCAGTGCT	60
	GGAAACGCTC CTCCAGGGCC TCTATTTTGT TATTGAGCTC CAAGTACTCC GCGAGCTTAA	120
10	AGGTCAACGA GAGCGACCCCT GGATTGCACC TGACGGGAT CTCAAGGACC TTCTCGTGCT	180
	CGTTCTGCTC CACAAACATG GCGTAGTTGT ACCATATCTC CGGCGCAAAG CACATGTGCT	240
15	GCACAGCCTG GCGGTGCAG TATTCCAGCC GCTGGGCGAG CAGCACTTCG GGCAGGTGGA	300
	GCTGTGTGTC CAGCTCCAC TGGATCCACT TCGTCAGAT CTGCAGCTGG TACTCATGCT	360
20	ACTGACGGG GCGAGGCAGG TTCTGCTGIG TGGCTGGIT TAGCTTCGTG GGCAGCGAGC	420
	GCGCAGGCC CTTCGTCAGG TTGCACCACT CCTGGTACAG CGAGCGGCA TTCATGTAGC	480
25	TGCGGAGAG CTCTCGATG AACTTCGGG CGTCAACTG GTTGACCTCC TGCTCCACT	540
	GCGTGTATTT CTCCAGTAC CGTCCAGG ACTCCACTGG CAGGCACAGC AAGGCGCTTG	600
30	TACAGCTTGC GCAGAATCTC GACCGGCTC TGCTCTCC ACTTGCTCAC CGGCTTCCAC	660
	TGCTCCAGAA ACTGCAGGTA GTCTGCCAG AACTGCATCG ACCGGG	707

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1667UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

EP 0 866 129 A2

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GATCTAAGGG ATGGGTGACT GCTGCCGGTG CTCACAGCAG TGGCAOGTAG CTAGTAATGG 60
 TGGGAAATCG ATCAAAGAGG GTGCGTCTGG CGGTACAGGC AGAAAGCAGC CCGGCCGATA 120
 CAAGTCCAG TTCTACAAGC AACTGCAGTT CCAGGGTACG AGGTACCAGG TGGTGACTION 180
 GCGGCCGTAT CTGATAGAGC GGTACGGGGA GCGCAAGGCG GCGACGATCA GGTGTTTGT 240
 CAAGTGCATC CATCGGAAA TCAACGAAGA TGTGACAAGG ATCAGCGAGC AGCGGGTGAC 300
 GCACGGGGTG TCGAAGTGGG AGAAGTOGAA GCTGTTCCTG CTGCTGGTGA CGCTGTGCA 360
 GCGGGGGGGG CCGGAGTACT GGCTGGACAA GACGAACGGG TGCCAGAGCC GCGGGGGGG 420
 AGACGGGGCG CGGAGAGCG ACGAGGTGGA GGAGGGGGGG AGCGGGGGGG GCGAGAGGCT 480
 CGTCTGCACA CTGGTGGAGC AGATCATGCG CGAGAACATC ACGGAGGACT ACGACGAGAG 540
 CGTGCAAGAC GAGAACTACG TGTCTCGTC GATATGGGCG AACTTCATGG AGGGGTTGAT 600
 AAACCACTAC CTAGAGAAGG TCATCATAAC CAAGTCGAG CTGAAGGTGT GCCAGCAGCT 660
 GTACCAAGCC GATGATGAAG ATCATCTCAC TCTATAACGA ATACAACGAG CTCATGGACA 720
 AGA 723

35 (2) INFORMATION FOR SEQ ID NO:1095:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 722 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1669RP

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

EP 0 866 129 A2

	GATCAACAGC ACCTCCACCT GCGACAGGTC GAACTCATCG TAAAAAGGCA GCGACGGGAT	60
5	ACCCTGGTGG GCGGGATGCA CACCGGCATC CAGCATGACC GTCTTGCCCT TATACTGCAA	120
	TATATGGCAT GAGCGTCCAA CCTCATTGCT GCGCCCAAGC CCGAAGAATC GGAACGAATT	180
10	CGTATCTAAC TTCTCTCCG TCATCCGCAA TTGTGTTATG TCTGCCTGCT GCGAGGTGCT	240
	GTGCTCTCTA CCCAATGGCT GCGACACTGG CTACTGAGAC AATTCCACGT AGCTGCTGCT	300
15	GCAACTTTTT TGCAGCTATG GAAATACCGT GGTTCGGTAG ATTTGATTCT GTGGAGATGA	360
	ACGATCAAAC GCGAACACTG GTTATCGGTG ATGGGTGTG TTAGTACCCA ATCAACCGCA	420
20	GAGACAAGTG CCACTATTAA TTGTAGTACT TACAGGAACA CCGATCGCAA GAACTCTTAA	480
	CGGCTCGGTT TACCAACGAT CAACACTTTT CTCTCGAAC GTTATGCTGT GCGGCGGTGG	540
25	CGATTGCGAA TGATTGTTGA ATTGAACCAG AGAGCGGAAA ATTTTGGTTC TCAAGTGACC	600
	GTATCTTACA TAAGCTACTG AACTATATGA AATACCGACG TTGCTCGAGG ACGCTAGCG	660
30	CAGTGTCTCA AGCAGTGATC ATGAGATTGA GTTGTCTGA TGTGTACATT GAGAGTACTG	720
	GG	722

35 (2) INFORMATION FOR SEQ ID NO:1096:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 675 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: PAG1669UP

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

EP 0 866 129 A2

	GATCAACAAG TGCAACAGCA AGGTGCAGTT GGGCATGTG CCCTCGGGGA TGGTGATTGA	60
5	GTGCCAGGCA ACCCGCAGCC GCGAACAGAA CCGCAAGCTG GCGCGGAGA AGCTAGCCGC	120
	CGGCTGGGG CAGCCCCCGG GTAGGGCCAG CGAACGGGAG CTGGCGTTGC GCACGTGGGC	180
10	GCGGCAGGGT AAGCAAGGCG AGGCGGGCAA GAGCGGGAG AAACAAGAGC GCGCGCGGC	240
	CGAACGGGAG GAGCTGGGCG GCGCGCGGA CGCGGAGGAC GCGAACTTC TGGTCAGCT	300
15	GCTCGGGAAG CCGCGCGGA CCTCTAGTG CCGCGGGGG CCGCGGGGG AGCGAGGGC	360
	GTCTTTTTCG GCAATTCCAA ATAGACACC TAGTGGCTC TGCTGCGGC GAGCGCAGAG	420
20	CAGGCAGCTA GCACACCACC GTCCAGGCG AGCGCTTTTG CTGGGAGTC GTGCGCAGT	480
	CCGCTGGCTC TGGTGTGCAC ATGCGCTCC GCGTGGCAC CGCAGTGCAG AGCTACCTAC	540
25	GTACGTTTGC AGGCTTCGCA GTAGGCTGA TACTGGCTCT GGTGAACTT CCGACAAGA	600
	GTAAATCTC ACCAAGAAC AAAAGATAT GTTAGTGAGG ATATCTCACA TTCTGTACT	660
30	GGAAGTACAC AAAGT	675

(2) INFORMATION FOR SEQ ID NO:1097:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 697 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1670RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:	
55	GATCCGGCAA GATCGTCGTT CAGTTGACCG GCAGATTGAA CAAGTGCGGT GTCATCTCTC	60

EP 0 866 129 A2

CAAGATTCAA CGTCAAGATC AACGACGTCG AGAAGTGGAC TGCCAACTTA TTGCCAGCCA 120
 5 GACAGTTGGG CTACGTCATC TTGACCACCT CCGCCGGCAT TATGGACCAC GAGGAGGCC 180
 ACAGAAAGCA CGTTGCTGGT AAGATTTTGG GTTTTGCTTA CTAAGGGGCT GCTATATAGC 240
 10 GTATCTAGCT CTAATGTACG ATACTCAGTG TCTATTACGA CGCCCGGAG CTCCACGGGC 300
 CACATACGAG GGCAGCCGGC GACGGCAAGC GGGAAATCAG ATCGGTTAAT TAGCAGTAGA 360
 15 TTAGTAGTAT ATATGTACAA ACAGCATACA CATGAACGGC GTGCCCGATC ATAATCTTCT 420
 AACTCTTCTA CCACCCCTCT TTCTGGTAGA GTGGGATGG ATAGGAGTGA CGTCCTCGAT 480
 20 ACGGCGGATT CTCAAGCCGG ATCTGGCCAA AGCTCTCAA GCAGCCTGAC CACCTGGACC 540
 TGGGGTCTTG GTCTTGGTAC CACCGGTAGC TCTGATCTTG ACGTGCACAG CAGTGATGCC 600
 25 GACCTCTTA CACTTGGCAG CGACGTCTG AGCAGCCAAC ATGGCAGCGT ATGGAGAGGA 660
 CTGCTCTCTG TGGGCTTGA ACTTCATACC ACOGGTA 697

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1670UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

GATCTATTTG TGCCGTCCG CATTAAGCAA GCGGCAAGCA TCGATCCAAA TCATGAGAGT 60
 55 ACCCTGGGGC TTTCACTTTC CAAGCCTTTA TCAACAAATC TGGTACACGA TACATCCATC 120

EP 0 866 129 A2

GCGACAGCAC ATATACCAGA ACGGGAAAGC CGACAAGATG GCACTAGACT CTGGTAGGTA 180
 5 ATCTGAGTTC GACCATATCC ACTTCGTTAA TGGTGATAGT TGATAAAAAG AAACGATACT 240
 GAAAATTTTA ATGGTTACCA ATCTCATCTC ATCGCCATAC TGAAAGAATA TTGTAGGTCT 300
 10 CGCAGTGGAA CAAGGATCAA GCGCAGGCTA AGACAATAAT GGTTCGAGCG GAGGCAGTAC 360
 AGGAACTACC CCCAGATGAA GAAGAACTGG CCTTGGCTAA GCTAGTGTTT GGCGACACAG 420
 15 CAGACTTCCA TGAAGCGCTG CGAAATGCAG ACCTTAATTA TGTTTCTTCA GATGAAGACG 480
 TATATGGCCA GGAGTCGTCC AGTGATGACG AAGAAGGGAC TGAAATTGGT CAOCTGAATG 540
 20 ATGACCAATT GTTTTTTGTG GACGAAGGTG CAGATACCGA GGAAGAGCA GATGGAGAAC 600
 CGGAGGCCAT GGAGGTGGAC CAGGTTAGCG AGGAAAGCGA CTCGGAGAG GAAAGCGGTA 660
 25 GCAGCGCTGC ATGGTCAGAT TCGGATGACG AACACTTAAA CGTTACAATA GGG 713

(2) INFORMATION FOR SEQ ID NO:1099:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 743 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1671RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

50 GATCGCTTTC AAACCATCCT GTAACCTACG TGAACACAC TTTACAAGAC AACGGCATAT 60
 CGACAATCAC AAGACTTCCT CGAGACATGC CGGCCACCA TCTTCATCGT GTACTGACGG 120
 55 ACTATAATCC AAGTGGCCAT TTGAATTGCG AGCATGATGC CACGCTTTCC AACCTGAGCT 180

CGAAACTGG AGATGTACAT CGGCCTTCCA ATTCTCTTC GAGTTTAAAT GGAGCACAAA 240
 5 AAAGGGCTAG CATCCCAAAT ATCTTAGGCT CTGCTOACT TAGTAATCAA TCAAGAACTC 300
 CAGACAACCG TTTAACACAT GGTACATCGA TCCATGAGAA CCGCGGTTA GAATTAAACG 360
 10 GTGATCAGTC TTTACTCTTT GCGGTAATA CAGGCGAGC ATCGGGTAAC TTGGGGGTG 420
 TTTCACCGC CGAAACTCC CGAAGGAGCA ATTGCGATGA TCAGAGCAA TATAGATTAC 480
 15 ATTCCAAGC TTTCATTG ACTGCCCCC CAAAGGAAC TTCTAAGAAC ACTAGTCCAG 540
 GTACAACGT TGCACCTGCG AGCGTTGTTG GTACAAACAC AAGGAACACA CAACGTGGAC 600
 20 CCACGGGAGA TGCTCCCAA GAATCAGTCG AACAGCCGA ATCAGCTTCG CGGCAATCG 660
 ATGAATCTAG CGCAAGAATT ATGTCGCTA GTCATCATAC GGAGCCAGTA GGTCTGTTT 720
 25 CGACAATCTC TTCTAACACA CGC 743

(2) INFORMATION FOR SEQ ID NO:1100:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 661 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1671UP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

50 GATCAGGGAT GCGGAGGACA TTCCGCGAGC TTATCGGCGA GCACGACCTA CGGTCCTGGA 60
 ACTATGTCAA GTACGGCAAG AAAGCTATTA AGGCCTTCGG CTTCTGCGCA GACGCATATA 120
 55 TTCAACAGAT CATCCAGCTA GCCATCTACA AGTATGTGGG CAGACAATTG CCAACCTACG 180

AGGCTGGGTC GAACAGAAAG TTCTTCAAGG GTAGGACCGA AGCGGGCCGC GCGTTTCTC 240
CGGCCTCCGC CAAGTTTGTG AAGACTTGGC AGTCGCCGA AGCATCTCCA AGTGAGAAGA 300
TTGCTGCTCT ACGTGAGTCT GCTAAGAACC ATTGCTCGCT GCTAAAGATG GCGCGGACG 360
GCCAGGGTGT TGACCGCCAC TTCTTCGGTA TGAAGAACAT GTTGCGTGAT GCGAGGAGC 420
ATCCTGCACT CTTCGGGAC CCGCTGTTCC AGCACTCCTG CACGTGGTAT GTGTCTACCA 480
GTCAGCTATC TTCGGAGTAC TTCGAGGGAT ACGCTGGTC GCAGGTGAAC GAAAATGGCT 540
TTGGTCTGGC GTACATGATC AACAATGACT GGTACACAT CAACATTGTT ACMAAGCCTA 600
AGAAGTCGGG CTATAGTGTG CACGAGCTTT CACTACTACT TGACCGAAGC AGCAAACGAG 660
A 661

(2) INFORMATION FOR SEQ ID NO:1101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1672RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

GATCGTGTAT TTGTCAGGCC CATCCAAGCC CTCCCCCGCA CCCAAACCCA CTATGATGGG 60
CAAGAAGTGC TOCAACGTCG GATGGGCAGC CTGCAACAGT TCTGTCOCCT CCGCGCTOGA 120
GAAGAGACGA AGTAGTCTGC CGAATTTACA GCGTTGGGC GCGGTGGTTA GCAGGAAGTT 180
GGACAGTCCC CAGTGAAAGG CAGATGAGCG CGAGTGGCTT TTTGCGATGG CAGATCCGCA 240

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GAAGAGATCT CTCAGGTTGT GCACAGCCAT GCCAGACGTT ATTATCAACC CGCAGAGGTC 300
 5 GCGGTACCTG GACAGGAGGC GCGCGAGCGC ATACTGGTCC CGCAGGTGGT TTCCCGCCGC 360
 CAGTGATATT TGGACCAGCG GTACCGGGAC ATCCCAATCG TCATCCACGC ACTTCGAAGC 420
 10 GGAGAAGCCA ACTTTTtaggg GGACCCAAAC GCCATGGTCT ATGCCGGGTT CTGTGAGCAC 480
 AGGCGATAGC GGGCTGCGTA TGTGGTTGAT GGTGTCCGCG ATGTGGGTAA CTAAAGCCAT 540
 15 GCTTGATTTC CTATGGAAct CCTCCTCGTA CATCCGGGTC GAGAAGCCAT AAAAATCGTA 600
 TATCAATTCC TTCTCCAACG GGT 623

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1672UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

GATCCAGAT TAGATATTAC TTAAACGTC CACAGCTTTT TGATGGCTA GTTCTGCTGC 60
 45 ACGTCTATAA TGGTCCATCG CCTGTGCAT GTCCGGATGA CAGCCGACCG CGTCTCCGT 120
 ATAGAAGCCC AAGGCATACT CGCTTTTCGG TAGCCGGCCT TCGGAAGCAA TGGATGCTTT 180
 50 ATACGCCCAT TTGTAAGATT CTGAAGCGTT GGGTTCAGC ACGCCCTTGA CACCACTTAG 240
 GTACCAACCA CTCAAAGCGA GCATAGCCAT GGCATTTCCC TTTGGTCTG CGTTTCAGC 300

CTTCAAGTAC CACACGATGG ATTTCTCAGG GCTATACGGC AAGTGTAAAT CAGCGTACTC 360
 5 GTAGCAGTGT CCCAGCTTCC ACTGAGCAAG CGGATAATTA AATTTAATGG CACATCTGAT 420
 GTAAAGGTCT AGAGCCTTTA GGGTATCTTG TGGAACTGTC TGCAACTTGA CAGCCTGCTG 480
 10 CAGCTGTGGA TGCAACAAT CAAATTCATA GATCTTTGCG AGTTCTGTATA ACGCCTGGGG 540
 AGAGACGGTC TTGTCTGTG CAGCAGCCCG CTCGAACCAT CGTATAGCAG AAATGACATC 600
 15 CTGTTCACA ATAATTCAC CTGTGTCATC ATCCACCAGG CCATTCAGTT GGGAACATAC 660
 CCAACTTATA CATGCTACTG CTCTGTCCGG AAGA 694

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1673RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

GATCCAGCT CTTACGCTCG CTCAATTGAA AACCTTTTCT AACTAGCTT TCTTATCAAG 60
 45 GAAGGACGGC TAGTCCTAGA AGATGACGAT GAGGGCTTCC CGGCATCCG ACCCAAGGAA 120
 CCCCTCCCGC AGGATCCCGC CGAAAAGGAA CTGGAACGGC AGGACGGAA TGAOGGOGC 180
 50 CAGAAGCATA TCATCTTCCA AATGGACATG GCCACGTGGA GGAAGCTTAT AGACAAGTTC 240
 CACATCACAG AGTCATTTT ACCGTGATCA TGTATAAATA GCGGCATCT ACGTATCACC 300
 55 CGCTGGCCCG GCGCTGACC AACCAGGCAC TGCTAGCAGC TCATCTATCG GCCACTTCG 360

AATGGTCAGC GCGCAACGT CTGTGTCAG GCGGTGTCC TGTAGAGCT CGATGCCCC 420
 5 CCAGCGATC ATCACCOCAT TGTCTGTACA TAGATCTGGA GCTGGATAGT GAAAGGAGTC 480
 GAACGGTCTG AATAGTTCAG TCTCGAGTCT GGCAOCGAGG CGOOGGTGG CGCATACGCC 540
 10 GCGGAACAC ACAAACTGTG CCACATCAGC AACCTTATCA GCATTGAGC CGCAGCACCA 600
 GGTTAATCTT GGTAATCAA TGGTCGAAAT ATGGCCTCCT GAATCTGAAW TGCTGCTACC 660
 15 CGCGGTCCG CCTC 674

(2) INFORMATION FOR SEQ ID NO:1104:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 726 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1673UP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

40 GATCGCTCTA CCGACGTACT GCATGCCTGT CTGGTCTTA AGTTAAAAAC CACAGCACCC 60
 AATCGTTTAC ACCGCAATCT TAGACCAGGA GCTAGTGCTT GCGAGCCOCT GTCGTTCAAA 120
 45 TGGCAGGACT GTTGTGTTGT TGTGAACCTC GCGACTGAG GAAAGGGGGC GGAAGATCTA 180
 TTTTGCACCT ATTGCAACC GTTTAGATAT TGAAAGCAGG GCAACACTAG TAAAACTCGA 240
 50 AATTAGGACA TTOGTGAACA GATGTGAGCA GAGGATTCCG GATGCGCTTC GAAATGATGA 300
 GGGCGCATGC TGCATACCOCT GGCCGTCCGG CGTAGTGTAG ACCGTGCAGC GCATGCTGCA 360
 55 AAACAACGGC GCGGTGGCGT CGGCATGCAG GTAGCACAGC ACCTGCAGCA GCGCAGGGGT 420

GCATCCAAGA GTAAAGCCAC ATGTGGGGG CGTTGCTCCG TATGTACAAG TTATGTCATT 480
 ATTTCTACAG ATATCATGTT GAATATTAGC CCGGATCAT CTAACAATG GTATCGTTTG 540
 GTCTATCTCG CTACGTCAA GATGCAGGCT CCGCCGGGG ACTACGGCC AGGGTGGCA 600
 GAGCAGTTTG GTATAGGAGA AGCATGATAC TGCTTTGGAT GCTGGTCCAG ATGAACCTGG 660
 GGGCCACACC GCTGAAGGG CCACCCAGTC CCTGTAGCG AAGTACGACT AACAAAGCTGC 720
 GGAAGA 726

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1674RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

GATCTCATTG AGGTACACAG ACACAGCTGG CAGCGAGCC CAGGCTGGA TGGACGAGTT 60
 GGCGAAGCAA TCAATCCGGT TGTTGCCAG CCTGTGCTG TGTTTGCTT TCCTGTGGA 120
 GCTCTGGAAC ATAGCAGAAC TACCAGGGG ATAGCCAGT GTAGATGTC GGACCTAGA 180
 TATAGTATGA AAGTGCAAGT GTGCCACAA GAAGAAGTCT TTGTGGTATG TTGTCCGTTT 240
 CGTAGAGAAA GCTTCCGACC TTATTAATAG AGAGTGTAAC GTGTAAACA GAAGAGGGGT 300
 ATGTCACCTT GTGCAGCATG TAGATGGACT TGGGTATCTA GTCAGCCGTT GTGCTTGAAG 360
 GTGGACCAAA CTAATCCTTA GTGCATAGTA TTATGTGGG GGGGCTTTG AACCAAGCTT 420

TTGGGATGCT CGAAGGCGGA ATAATACTOC ACGTGACAAT AATATACGTC AACTATTAAC 480
5 GGCTAAATTA TCCCTTGCGA GGAGAACATC CCGTAAATTA CAATTATCAT TCTATATTAT 540
AAACATATTA TAAAACGTCC ATCTTGCTAA TATAAAAACA ATCTAGGTCG GCTTACCAAC 600
10 CATATTACAT CAGTAGGCAG CGCGATCTGC ATCCGTCATG GCGTGGAGTA TCCAGTT 657

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 695 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1674UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

35 GATCATCATC AACTATATCG AGAAGGAGTG TGACCGGGC GTTGCTATGG GTAAATACCC 60
GTCTACCCCTT GACCGGGAAG CGGTCCGAAA GCTGGTGGCA AAAGATTGG AGAACTTCOG 120
40 CGTAACCAAC AGCCTCAGC TGAACAGTCT CTCCTATAC TTTCGCAACC TAACACGGGA 180
GCAGCGGGA ATATGCATAT ACAACAACTT CACCGACTGG AGCTTGCTAA TCCTTCOGGA 240
45 AGAGGAGAAA ACCAAGTACT GCAAAAGAAA GCAGGGTCTT TCGTCAGAAT AACAGTAATT 300
GTAATATAT AATCTGGAGC TTCTCCAGC GGTAGAAGGT CCAATTGT AATGTACTAC 360
50 TACCTGAGCA CTGTGTCCG CTCATCGCT CCTTAGAAAC TGTGTTCAG GAGCTCGGAT 420
GGCATCTGAC ACAAAGGTTG CAGACGCAGG AGAGTATATC TCCAAAGCCT TGGGTAACT 480
55 TTCTAACCTA ATATTTTGA AATAAAGCCG AGTCGCAGTG TATCACTGCT CCAGTCAGTA 540

GATTCTGACT TCGTAAAATA TGTGTTCTAT GGGTGAACA TTITAAGTCA TAGTTTGTCT 600
 5 TTTTCCCTG ATATACTTCC AAATACATAT ATCACTGAAG TTCCATCGGA AGCACCTCCA 660
 CAGTACGGCC TAAGAAGAGC AGAATAATTG CTCCA 695

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1675RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

GATCOGTGCA ATAAACCGCT TGAATGCACT GTGGAAGTAG TTGCGGGTCT CGATATCAAA 60
 GTCGACAAAG AATATCTGCA GGTGTGTAGC CAAAATGTCA AGCACATATC CAAGCACTGG 120
 ACGGAGGCC TTATGCGAGT AAGTTAGCAC TTCAAATGCA CCGAGCTTGT ACTTGTGGAT 180
 TCGCAGAAGG CTTTCCAACG TCGACAGCAT GATCAGCTTG TCTTGTGGA ACGGCTCCTC 240
 CTCTATCCCG AGCTCCTGGC CAATTTTGAG AAGCGGTAGA AGGAGAGCAG GGTGCCCTCG 300
 CATGTTCCGC AAGATAAACA GATCGAAGAC CTTOGGCGGA ACGGTCCGAA AGAGGGCTC 360
 CAGCACTAT AGTTGCACTC GTTTCGGCA GGTGCCCTCA AGAAGATGCT GAACCACTG 420
 CTGCTCCAC AACTGCAGC ACATCTCCAG TTTATCTCT GTATAGTGT GCACATATAT 480
 ATTGGCCAGC AACTGTGCA CACTCTTGCC AACGCGCTC GCAAGAGAGT CCGACCACAT 540
 GTATCCAGA GCGTGGCAA TGAACTCCG CCGACCTCT AGAACAATTC CCAGGTCAAT 600

CCGCTCCGAT AGCACGTCCA CCATGAAGTA CACGAACCTC TTTGAAGGAC TCAG

654

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 715 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1675UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

GGATCCGCTT CCACACCGAA AACGCAGAGG ACCAGGACCG TGTCTCGAAT GTGGTTGGCG 60
ACGCCATCAC GCAAGTCAAC AGGCTCTTTG GCGACAAAGG CATTCACGCC TAGGTTGATA 120
AGAACATCGT GTTGTGTCAG CAGTCCGGCC TGTCCGTGCA GGCCCTCAGG TTCTGTCTCA 180
ACCACTACAA CTGGGTGAC GACACCCCTG GCTCCACCCC CGGGCACTCC CCGGCTGTCT 240
CGCCCGTCAT GACCCCGGTC AATTCCTGCG TGGCCATGTC TCCAAGCACC GCGCATCTA 300
AAACCCCTC GCGCGGACC GCAACAGCCA GCTACTTTAG CAATGGCGGT TCCACCAGTC 360
GGTCGAGTT TGTCTGTGTC ACTGGGACTT CATCGCCGGT CCTGGAGCCG CTGTTCCAGT 420
CTATCAATGA ACTGGCCAAA AAGGGGACC TGGCCTACGG ATCACTGTG GCCTACGGCG 480
ACGCTATTAC CACATACGCT AAAGAGCAG TCGAAGGTT CAACGAATTA TTTGGCATTC 540
TAGACAACT GAACTTCATT GGCTGCTGAG CGCCCTGTT ACATAGGTTA TTAATCAATT 600
AAATCCTTTC TCTGGAACCT TATAGAGCCC TGCACCTTGC GCTCCGACG CATATCCTTG 660
CTGACTAGTT GTCAGCGGTA GCCTTTAATA AATTACGTAA TATGTGGTAT TATCA 715

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1676RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

GATCCCGACA CCAGCATGCG CTCGTGGAAC GGGTGAAGT CTGTGTCCAG CACCTGTGCC	60
GTGTGCCCCG CGAACAGAGG AATTTGGTCT GGGGCTTGC CCACTCTCTC CACGGGCACT	120
ACCGCGAAGC CCGCTCCGCC CGACGAATTC CAGTAACCG AATGAACTT GCGTTAGTC	180
TTGATGAGAT TGAATCCCA AGCATTGATT GTCACCTTGA GGTCTCTGTA GAAGAGTTC	240
TTCTTTGTTG ATTGTCCGAA GACGTGTCTA TACTTGGAAG CCGGCACAAA CTTCCCACTG	300
CAGTGCCGTT AGTTTGCGT CCGCACAAAG TCCAGTCTG GAGAGTATGA CATACTCAT	360
CCTTGCAATT CTTTGGGGTT TAGCAGCTCT ATATGCGTGT ACACCGTAAA CATCCGTAAC	420
TAAATATGTA ACGTGGAAGT GAAGGGTACT GGAATCTAAA GGGGAAAGAA GTACCCGTTG	480
ATGGTGATGG TACTGTCAAG ATGGCTAAAG CGAACCTCTG GCTTGGTTGG AACTCAGAAA	540
GGTCACCAGA CTCCTCTTAT TCTTGTTT	568

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1676UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

GATCGGCGG	CTCGTGCTC	GCTGTATTA	CTAGGCCAG	AAGCAATTGT	ATAACCCACA	60
TATTGTAAAG	TTTGTACTAT	CCTCCATGGC	CTGCCCCAC	CGACAGCGCG	CCTTTCTGTC	120
ATTGGGGTGC	CGGTGGCGC	CGGTTTCAA	CCTCGGCCA	TGGCTCGCGC	ATTAGCTGCC	180
AGTAGCGATG	CAACCGAAT	GGGAAGATG	GAGCGGCGAT	TGGTGGGTAC	GAAAAAGCTT	240
TTTACGGGTA	CTGTTTGCTG	GTCTAACGCA	TCCAGGCCAC	GAGGCTAACC	AGTATGAATA	300
CCGACCTCTT	TGGCAGCTG	GTACTTGTC	CGATCCTCG	GTCCCCCATA	GCGTTTGTG	360
TGCTTCTATC	ACGGTATGCA	ATGTTATGAT	GCGTGTGTC	GCGAACATGT	WCTAACAGGC	420
GACAGCGTGC	TGATACGCC	GTGCCCCGG	CTGGCAGCG	CACTGAAGGT	GTACACAGTA	480
GTGTGAATG	CGTGCTAAG	CGCAACCGG	CGGCGCAAG	TGGCAGGCG	TGGACGCCAC	540
TGGAGCAGAT	GCCGACGCG	ACTTGCGT				568

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 653 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1677RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

5	GATCTGCAAT TAGGGCATAT AAAGTGTGGG TACTGTGTCA TCACTAGTGG GCGTATGCAC	60
	TGGTAGTGCC AACTATGCGA ACAAGGGGAT ATGAAGATGG CCTGGCAGGG CTTAATTTTA	120
10	CATAGGCAGA TTGAGCAATC TTCTCTCTCA AGGCTGCGG TTAGCTTTTG TAGGTTCGGT	180
	AGGCGGGCTA GTGCTCTTTT GTTGAACGGG TTGGCCCTTC GCTTCCAGGA TTGTTCAC	240
15	TGACTCTCA TTTTGACGCA TCTATATATC TTCTCTGTGC CGCCACGGAA ATCCATTGCC	300
	AGCTGCAATA TGTCGCGTC TTTCAAGGGG TAGTCTTTTG ACATAACGGA TGCTGTGCA	360
20	AGCCGCATCT GATTAAAGGA CGTCCCGGAC GAGGACTTGA CGTCGGGCAC ATACCAATTG	420
	CCCTGCTCAT CCACCTTAAA CACCCCGTGT GTGCGGACA CAACCTTGCT CTGAATACC	480
25	ACGGGGTGGA AATGATCCGG GAGCGAGCG ATCGCTGCG GAACCCGTTT TGTTAAAGC	540
	CCGATAACCA ACTGCGAGCT GGGGCTGGG GTCGCGACA TGGGATCAA AAAGAGCCCC	600
30	GGATTATTGG TGGTGGAGTG GTCAATGAAC GCGGTAAAC GGAGCGAGAA GAA	653

(2) INFORMATION FOR SEQ ID NO:1112:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 625 base pairs

(B) TYPE: nucleic acid

40

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1677UP

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

55

GATGTGGCC TTAAGCCCCCT CGCCGCTGC GCCTGCGCAG CCTCAATGC ACTCGTCCG 60
 5 CGTCGGCTAC ATCCAGAGC ACTTCAGGC GCGCTGCTG TTTGGGCAGA CGCTGGCTT 120
 CTTTGGCAG CGCGCGTCA CGCCAAGCT CGTGCCCTTC CCTAGCGGT CTGGCCACT 180
 10 GATCCAGGG CTGACGCGG GCGAGCTGA CTTGGGCTC GGCTCACC AGGOSTTGT 240
 GCGCGCATC GCAGACAGC CAGCGGCGC CGCGCGGC TACCAGATTG CCGCACTA 300
 15 CGTGGCTCG CCACTCAACT GGGCGTCTC CGTGGGCGC GGTGGCCC TGGAGCAGT 360
 GGACAGCTG GACGGGCGC GGTGGGGT GTCAGGCTC GGCAGCGGT CGTACGTCAT 420
 20 GAGCTATGTG CTGCGCTGC AGCGGCTT CGCGCGGC TTTGGGCGC ATCGGTGTG 480
 CCACACTTT GCGGCTGC GGGCGGCT CACGACCG CGCGCGGAC GCTTTCTGT 540
 25 GGGAGCACTT TACCTCCAAG CGCTACAG AGCGGGGA GATCGGCTG CTGGCAACA 600
 TCCCCCCCC CTGGGCTCG TGGGT 625

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1678RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

GATCGCTGT CGGCATCATC GGAGACATG CCTCCATGTT CCGGATGGT AGGATAAAGC 60
 55 AATTGTACG CCAGACTTGG GTCACAGAT TTATCAAGAA AACAGAAGT AACCCCACT 120

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TTAGTCAGGC AACTAAGGAT ACTGCTAGAT GGGCTAGAGA ACAACAAAAG CATCAACTAA 180
 5 CCCTATAGCC TTACTATCCA GAATAATTTA TCTTATTACT CATTTTCTTC TGGTTATCT 240
 CGCTCTCTC CTGTTATCTT ATAATACTTC CCTGCAATG TCTTCATTAT TGTGTCTGCC 300
 10 TGGCGACAGA CCGCTTCGTT GTCTCTTCTT TTGTTGACC CTGCACTGAC CTGGCCATGC 360
 TGCTCTTCTT AGTGGTTTGG TACAGGTGCG GGGTCTTTT ACACAACCTT TCTACTAGT 420
 15 CTTCTATCTA ATCCATCTA CTTTCTACT TTCTCTCTT ACTTTATCCG TGGACCCGC 480
 TGCTGTCTT ACGTGGCAGC TTGTAGCATC TATATAATTG TATATATOGT GGTGGCAACT 540
 20 ATCTACGGCT GCTATACATC TGCTGCCCGG TCTGATGGC CGAGCGGTC ACCAATGCAG 600
 TAAAACCACA TAACTTTTA AGAGTTACAA GCTCAAAAAC GTT 643

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1678UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

GATCCGGGTT CGAGTCCCGG GAGGGGCTGC AGGCAACCAG CGCTTCTTTT TGGGCTGGT 60
 50 AGTCGAGGAT TGTTGACTGC TAAACCCATA CAACCACATA TTGCACTGGT GGCTTGCCCG
 CCTAGGCCGC CTTGCCGCTC CCGGTAGCC CGCCGGGGG ACCACGCA CGAGACCGTG 180
 55 CGGGCCCGGC ACGCGATCA CCAGCGCAG CCGGTGCAG GTAGGGGGA CAGCTGAAAA 240

GTTACTACAA TTTGAGGTCT CGCATACTGA CACAGAGGGT CTTACACAGC ACCAGACGAA 300
 5 TCAGCAATGG CTAAGCAATC TCTAGGTATG TGACAGAAAG ATGTGGGCTC CGAAACATTG 360
 GGAATGAGCG TCTCTGGCGC TGCGATCCGT GGTAACCTGG GCATACGGCC CAGCGCGCAG 420
 10 GCGGACCTAG CATAATCCAG TCGGTGGAAC AAGTTGGTGG CCGGCACAG TACTAACATG 480
 TCTGCAGAG TTTCTCTCGA CAGAAGAAAG GCCAGAAAG CGTACTTCAA CGCGCCATCT 540
 15 TCCGAGCGCC GCGTGATCAT GTCTGCTCT CTATCCAAG AGTTGAGAGA GCAGTACAAC 600
 ATCAAGTCTC TACCAATCAG AAAGGACAAC GAGATTATGG TTGTGGGTGG CTCCAAGAAG 660
 20 GCCCAAGAGG GCAAGGTCT TCTGTCTACA GATTGAAGTA CGCTGTCCGC GTGACAAGG 720
 G 721

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1180RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

GATCGTCTG ACGGTGGTGG AGTTCTGGAC AAACGCGGTG CTCTTTGACG AGATCGTGCA 60
 50 GCCACTGGGC GAGATCATCG ACCTCTACAC CCAGTTGAGC GCGTCCACG AGATAGACCG 120
 CGCTGTGGCG AAGACATTG AGGAGGCGAG GGAGGTATTT TTGTGCGCGG CGATGATTAA 180
 55 CGAGAACAGC ATACTGATTG GCCACGGCCT GGAAAACGAC CTGAACGTAT TACCGATTAT 240

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ACATGATAAA ATTATTGATA CAGCTATATT ATACCCGAAT GGTAAGTTCA AGTCTCCCT 300
 5 CCGGAATCTA GCCTTTCAGG AGCTCAGTAG ACGGATCCAG ACGGGGAGC ACGACAGCTC 360
 AGAGGACGCC ATTGCAGCAA TGGACGTGCT CAAGCATAAG CTGGGCATCC CGCTCGAOCG 420
 10 CAAGACGTGG TAGCCCTACG GCTGCTCCTC CAGCCGGGTG AGCCTGTCTT CAAGCTGGTC 480
 CTGCCTCTCA ATTAGCGTGT GTATAAGCTG CTTAAGGTTC TGTAAGTCAA TCGGATCAT 540
 15 CCTATCTTCT GGAAGCTCGA ACTTGACGTT CTTGCTGCGG GTCACGATCT GGTCTTTGCC 600
 CACCTTGATC CTCGATGCTT CCGGAATTTT GCC 633

20 (2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 706 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 35 (A) ORGANISM: PAG1680UP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

GATCGGGGCG CGCGGTGGCC GGCATTTCCG GAAGCGGCCA CGGAGCAGAG GTGGCGCATT 60
 45 CGAATGCGAT ACGTCTTCGC CACGCCGGAA AAAAAATTTT CGGCTATATA AGGAGAGGCG 120
 GCGTCTTGC TGCAGGCAGT TTCACTTTCT CTAAAACCAA AGAACATCGA TTTCTTTAGT 180
 50 CACTCGCTTC CTTACACCGA AATGCAATTC TCACCGTGG CTTCATCGC AGCCGCTGCC 240
 GCGTGGCTT CCGTCAAGC CAACGTGACC ACGGCCACG CCACAGAAA CCAGACCACC 300
 55 TTGGTCAACA TCACCCACTG TGAGGACAAG ACCGCATGCA CTGCCACGT CTCTCCAGCT 360

5 TTGGTCTCCA CCGCCACCGT CACCATCGAC AACGTTGTGA CCTTGAGCGA GAACCTGGTGC 420
 CCACTATCCA CCACTGAGGC TCCTAAGCCA CCAGTTTCCA CCGCCAAGCC ACCTGCTTCC 480
 10 TCCAACGCGA CTGTTCTCTC AACTGAGACC CAGTGTCTC CTCCTTCACT GGTGCCGCTG 540
 CCAAGGCCCT ACCAGCTGCT GGTGCTTGT TCGGGGGCCG TGCTGCTTTG TTGTTGTAAG 600
 15 TTTAGTTCCG CCGGTGAGC CCTCGTTTCG TTTAGAGATA TATAGGAAC TATGTGACTG 660
 ATTCTAAGCT TTTACACCAG CATGATTGG TTCTGGGGCG CACCGA 706

(2) INFORMATION FOR SEQ ID NO:1117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1681RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

40 GATCATTTCTA AACAGATTAA CCTTCTCTCCA AATTACTTTA TTTCCTTAAT CTCGATAAA 60
 TGGTTACATT GCGACAATAA GGTGCCCGTG GTGCTTACAG ATATACATCT ACCGAGAAAA 120
 45 TTTCGGCCAC ACACTCGTAT AGAAGAAAGA AATTGATTG AAACCTCTGA GCTAGATCCG 180
 ACGTTCAGTG GACTCTTCCC ATTTAAGGTT TTCAACAAAT TCCAACTCA TGTGTTTAAT 240
 50 GCCTTGTACC ATACCGATGA AAATGTATTT ATTGGAGCTT GTAAGGGCTC GGGTAAAACT 300
 GCAATGGCAG AATTAGCTTT ATTGAGTCAC TGGAGAGATG GTAAGGGACG TGCCGTCTAT 360
 55 ATATGTCCAT CTCAGGAGAA AATTGATTTT CTGGTGAAGG ATTGGCGAAA CAGATTTTTA 420

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AATGTGGCAG GTGGAAAGGT TATTAATAAA CTCACATTGG AATTAACTAA CAATCTTGA 480
 5 ACGCTAGCCC AGTCGCATTT AATCTTAGCG ACCCAGAGCA GTTTGACCTG CTTTCTGTC 540
 GCTGGAAAAG AGAAAAAAC ATCCAGACAT TAGAGCTGTT GATTCTAGAT GATCTTCATA 600
 10 TGATCAGTAG TGACTTGCTT GGGCAAGGT ATGAAAATAT AATATCCAGA ATGCTGTICA 660
 TTCGGGTCA ACTTGAAAAC GGCTTGCGT ATAGTC 696

15 (2) INFORMATION FOR SEQ ID NO:1118:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 659 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: PAG1681UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

35 GATCAGGAAT GATCCTCAA TTGTCAGGAA TTATGGTTC ATATTGGTTG AATTGCCAA 60
 GATTACTCCT GATGGTATGG TANTGTCTT CCCCTCATAT TTATATATGG AATCATTAT 120
 40 TTCAACTTGG CAGACAATGG GGATTCTAGA CGAGGTTTGG AAATACAAGC TCATCCTCGT 180
 GGAAACACCA GACGCACAGG AACTTCTCT AGCTTTAGAG ACTTACCGAA AGGCTGCTC 240
 45 GAATGGGCGC GGGCAATAT TACTTTCTGT GGGCGTGGG AAGATTTCTG AGGGAATTGA 300
 TTTTGACCAC CATTACGGTA GGACTGTATT GATGATTGGA ATTCTTTTC AGTACACTGA 360
 50 ATCGGTATT CTAAAGGCGA GGTAGAGTT CCTAAGAGAA AACTATCAGA TACGGGAAA 420
 TGACTTTTTA TCCTTTGATG CAATGAGACA CGCGCTCAA TGTTTGGGAA GAGTCTTGAG 480
 55

GGGTAAGGAT GATTATGGCG TGATGGTGCT CGCGATCGG CGATCTCAAG AAAGAAAAAC 540

CAACTTCCAA AATGGATCGC ACAAGGGCTC TCTGATGCTG AACTGAACCT TTCTACTGAT 600

ATGGCGATAG CTAATACAAA ACAATTCTTA AGGACGATGG CACAAGCAAC TGATCCGAA 659

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 707 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1682RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

GATCGTAAAA TTTGCTATAC AATGGTTTGG GTAGGTCTTT TAAAAGGTGG TCAATCTCAT 60

AGTGGCTCAC ATCAAGGGGA ATGTTTAAAA AAGCACTCT CTGATGTGTA GGCGGAGGAG 120

GCCTTGCGTC TCGCGGTCC CTGAAAGGTG AGCGGCGGA GGGGCGGTAC TCTCGGCCCC 180

GATACGTGCT TTCCCCAGA CCCATGGGTG AAGCTAGTCC ATTACGTAAG TCTCGAGGCG 240

GATATTGCTA TAATAACAAT GTAATCGTTA ATACTCAGC TCAAGTAACC TTGCGGTGGG 300

TCATGTATCA CTTAAGGTAG TAGTGGGTG TGTCTTTTG CCGTTAGTAT CGATGAAGT 360

TTGGTATCGA GGAGAAAAAG ATGTCATAC TTTCTACCA GTACCTGGT TCAAGTGTTT 420

GTCAACAGAC ATTGTCCCTT CCAACTATC CTGTTTGAAG GGCAAAGGCT GTGTGTCAAG 480

AACGAAGTTT TCACCATTTT TCCGAAGGC TCGGACAGC GATCGAAAGA AATAGGATAT 540

ATACGTACAC CTTTCTTAA ATATCATTTA AAATATCCTG GAATTTGGAT ATGTGGCCAT 600

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ACTGGCTCTT CAGCTTCCTT ATCCATGAGA TAGAAGGAGC AACTGTGCG AAGGTGCCCTT 660

5 CCACAGTTAC TTAAGTTTCC GTAAGCAACA AGGAGTCTGT ATGCGGC 707

(2) INFORMATION FOR SEQ ID NO:1120:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 700 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1682UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

30 GATCCAGTGT GTACGGCCAG AGTGGGCTG GGGCACCAGC AGTACCTGCT CCGTCTGTT 60
 GAAGTTGCA ACATTCCCGT CCGCATCAGC ACCGGGCTG AAGTATCTTG TACCGGCGCT 120
 35 GAATCTGCTC CCGCGGTGA TCAGACCCAC ACTAACTGGC GTACTCTGCA ACACAGTGTC 180
 TACCACTTIG ACGTAGCCGT AGATTAGGG CAGAAGAAC TCGTTGGCCA GAGCGTTTTC 240
 40 CTCGGCCAGG TTTCGCAGCG GCTCTGTGGC ATAGTAGTTC CAGAAGAAC GCGTGTCTGC 300
 AGTGGGCCAC GAGGCTGGCC CCAACCTTC GTTCGGCTGC ACAGAGTGGC TCAAGTCATA 360
 45 CGTGTACGAA TAGTACAGCG TTGCTTTCG GAGGTGGTGG CCGAGTAGCG CAAGATACTG 420
 GTTGTCTCTT GCAGATGGCC GGATACTGGT GTTGACCAGC ACCAAAGAGT GCGCGTTCAC 480
 50 TTGTGAAAGA GAATGGGCAC CCAGGTTTCC CACCACCTCC ACGCGGTCCG CCGTTAGCAC 540
 CACGCGACTA TTGGGCAAAT GTAATATCCC GATCAGGCCT GCGATCTTGC GAGTTTCTCC 600
 55 ATCTTTAGGG AAATTGCTGG GGTCTACGAG TGTCAAGCCC GAATCGTGAT GCGAGATAGA 660

CAACACCGCT TCACTCTGGG AAGTATTAGA TGGCTTGAAA

700

(2) INFORMATION FOR SEQ ID NO:1121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 652 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1683RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

GATCTATATC ACCAATCATC ATGGTITTTGA AACATTGGT GCTTAAAAAG GGACACAGCA 60
AACTACAAGC AGGCAGCAGC AAGCACTCTG CAGACTAAGG GCAGGCTCA TCATAAGATG 120
CTTAGGGCTG AGCTAGTAAA TGCCATTCOG TGCCAAGGTG CTCAGTGIGT CGCTGTGGTT 180
GATGGGGTTC GACAACITGT GGTGGTGCGA AATAATAGGG ACTTCTTGGT GTACTCCAGT 240
ATGGACGAGA GAGGCTCGC TCTAGTTCAG ACATATACAG AATTGCTTGG CCCGAATTAT 300
GGTGTAGAAG AGCTGCTGTA CTCGGAACGG CTGCGGACAA TATTGCTCG CACGACCAAG 360
TGCTTACTGC TACTTCATTC GAGCAACTTA CAACATTACG ACAAGATAGT TGACAAACGA 420
GGCATTGACC ATGCTGGCT GTTGAACAT CCATGTGGGA AGGCTGAGAC GTGGATGACG 480
GTGCTTGTTT ACTCGGTCAC AGGGTCGAGC AAGATAAAGA TGCTGACATG GGTGGGGCGG 540
CAGTTCCAAG CGGTGCATGA GGTCCACTA GGCACGGAT CGGAAGTCAT CCAGCTCAGT 600
AAGTGGCGGC CGCATGCTG TGTGGTGTCT TACCTCGAC GACTGTATAC CA 652

(2) INFORMATION FOR SEQ ID NO:1122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1683UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

GATCTGTGCA AATTCTGCTC TAGCATTATC AACTTTGTGA CCACAACCTTA GAATTCCCCC	60
ATCATGCATT ATGTTTATAG ATGTACAGTT CTAAAAAATT CGGTAATATA ATGAGACCTA	120
TCTCTTTTTC TCATCCTTAT AGTCACCCAA AGTTTAAACA TGIGACATGC TGCCAGATTT	180
ACAGTCATCT GCGGCTATGA TTTCTTGCG AGAOCCTGCCA CAATTATAAT GTGTTAATAT	240
ATTGCTTCCT CTGAGGTGA AGAGCGAGAA AAGTTCACCTG CTCCTAATG TTAAATTCCT	300
CTGGCAAACG TAGCAGCGGT TATCTTCATC TACCACCAA AATTCAGATA TGATCTGGGA	360
TAAGCGATAG GTGCTTCGA TGAGGTGAC TTTCAAAGA TTGTTCTGTA TAOCGATTG	420
GTTTTCTTC ATGGACGCAC TTTTAATCCT TCTACTTAGG AATTCGTTAA GCGTGTATAT	480
CGAATATIG GCGGCAGTT TCTCAAACAA TGTATCGCA TCTAGCTTCG AACCATTCTC	540
TAGCAGAAAC AGATGAACGT TTCTCCATCC GCTAAATCT ACCTTCGCA GCAGCTTTTC	600
AAACAAGTTC ATGAGAGCTG CTGTGCTGC ATTTTGTGTT GTGGCATAGA GCTCATAC	660
ATATAGAGAA GCTTGTTAT AATTCCTAG ATCATCACT AGGATCCCTA ACGCTGTT	718

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 577 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1684RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

GATCTGTACA	CTTCAATATC	GAACGAAGTG	TCACCGGCAT	ATTCTGCAGA	GATTTGAAAA	60
AGCCACCAAA	GCAATATGAC	ATCAGGGTAG	AGCTTGGAGC	GAGTAATCTC	CGGTGATTGG	120
TCGATCTCCT	TTAACCAAGC	AGCAAACCGT	GTCTCATGTT	GCTTTTCCCA	GCTAATAATC	180
TCATGCACCA	CAGCCATAGA	TTCAAGCATAA	TGAAGGTATG	TTGCGGCGGC	CTCAATTACAC	240
CATTTGATAT	ATATTTTCCC	CAGGCCATCG	ATGAAGTTCC	CTTTGGTCTG	CAGCTTCCCA	300
AAAATAGGTG	TCAAAAGCAG	TTCTTTGTGC	AAGTCAATCA	GCGGATAAAA	GATGTCAAAG	360
GCAAGAGAGG	CGAAGTTTTC	GTCGGTGGGC	AGCAACGCGG	GCGAGAATTG	TGCGCGGTAG	420
ATTTCTACGG	CAGCATGGGC	CAGGTTGAGA	CTTTTCTCTT	CGAGCACAAT	AAGGTCAAAT	480
ATGTAGCTCT	GCGCTTTTAC	TTCTCTAGGA	TTAATCTCTG	AAAGCTCCTC	GTCGGTCAGT	540
TTCCAGTACT	CGGTCCAAAG	TCCACCGGG	CGGCTGA			577

(2) INFORMATION FOR SEQ ID NO:1124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 707 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1684UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

10

GATCCATGAC GAGCAGCTGG ACCTGCTGCG CGCTCTGGGC CTGGGCGCAG AGAACAAGGA 60

AACGCTGCAG AACCTCCCGC TGGGCGCGGT CAGGTCACG TTCAAGGACG TGGTGAAGGA 120

15

CTACTGCGAG GCGCAGGGCC TGCTGCTCGA AAAGACGGGC GAGTGGCCA CCTCCGGGT 180

CTACCAGCAT GCAAGTACTG TCCGGTCTT CACGTCACA CAGTACACC GCGCGCGCG 240

20

TGTAGCTCTG TGGAGGACG TGCTTTGGGT TCAGGAAGGG ATAGGCTTCA AACCTAAGTA 300

CTTATACGAA CTAGAACTC TTCTAAAGAG CGCTTAGTCG TCTCATATAT ACAGGACCTA 360

25

GTACTCTTGG CGCACTCAGT GCGCCTGCTC GCTTTTCGGG CTCTGGGCGG CGGCTCCGT 420

CTCGGCACG GCTGCTCCT CGCTCTCAG CTGCTCGCG TAGTGCTGG GGTCCTGCG 480

30

GAAGCATCCT GCATCACTG GAATCTCCA CGCAGTCAAT CCGCTTAGC TGGGCTCTG 540

AGTACACGAA GCAAGGGAAC GCAGCCTTGA ACTCTCGCC GCAAGGCGCG TGCGCATGC 600

35

CGCCAGGCA TGGGAGTCC CAGTGAATCT CGCCGCTGTC GCGATTGTAT GCTCTGCTG 660

CCCTGGGCAG CCTCAGCGC GCTAGCTTTG TCTCCGCGG CGCTCGG 707

40

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 666 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PAG1685RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

10 GATCAACTTC GCCTAATCCC TTAATCATTG TCACTGCTAA CTTGAACTTA GTCGTGTGIGT 60
ATGCCCTATAG TGAACGTTTA ATGTGATGGT TTTATAGTAA TCGATGGAAC TTTATCOGCG 120
15 AAGCCTCAAG CTGATCATCA CGTGAGTAAC CGTCGATATG CAGAACAGAG GATACCATAA 180
ATTGCTATTTA GTAATCAATT AATAGACTTA CATATAGCTC AAAGCTGATC ATTGATGCGT 240
20 CTCAAACTCT TTTCATCGTC TGAACCTTTC GGATTTTCAC TTCTGTATC ATTATACCAT 300
GTATAATCCT CTAGTACGCT AGTAGTCTAG TATCTGGAT AACCCCCCTA TATTACATAT 360
25 AATATGAGTA AAATACAGAA TGAAGTTAGC GGATAATCTA AGGCTAAGGT TGCCTACACT 420
AAGTTAACGG GGGGCTCTTT ATCTTGACG TTGTCTTCT AATCAATAGA ATTGTTTTC 480
30 TTTTTCACCT ATTTGGTCCC TGCCAACTG CGAGCCACC CGGTATCCT TAGCCTCTGA 540
GGTGTCTCT TCGACATCAC CTTCGTCTC CGGATCTCT CGGAGCTGG TTCAACTGTA 600
35 CGCTCGGTGC ATATTTAGTG TGCTCAAGGT TGCTGAAAAT AGATGCGAGC ACCTTGTCOA 660
GATATT 666

40

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: PAG1686RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

5	GATCCTCTCC GAGGTCAAGA GTTGTGTCAT GAATTAACTT CATTTTAGGA ACAAACCTGT	60
	CTAGGGTTCC CGCTACTAAT TCCTGCTCGA CTTTGAAATC CCAAATTTG ACAGTCTTGT	120
10	CTGGGAGGC AGTCACTAGC CTCTTCCCAT CACTAGTTAG GTCTAAAGAC CAGATTGCAG	180
	CGGTGTGTGC CTCTTCAATA TTTTCTAGCA TAGTAGAAGA TCGAGATCA AATAGCTGAA	240
15	GTGGCCCCG TCCTGTACCC AGAATAACCA AGGCGCACCC TGGTAAAAAC TTACAGCATA	300
	AAGCATAGCC ACAGTCAAGA TTGGGATAC AAGTTTTAGT CTTGATGTTT CAGACCTTTA	360
20	GGTTCCATT TGAAGCAGTT GCTAGTAGCT TATCATGGCT ACTGATGTCT GCAGCAOGTA	420
	GATCAGTCTT ATGGCCCCG GATTCGATAC TATGCAATTT GATCGCAGTA GGCTGGAGCG	480
25	GTTCCTTCTT TTTGTATGGG ATTGAGTAGT ACTCTATAGT GTTGTTTGCA GTCGTGATCA	540
	CCAGTTCCAA TTTAGATGGG GTACAGACCG TCCATGAAGA TGCTTTTAGC TTAAATAGGG	600
30	ACCTTACGAG TTGAAAAGG ATGCAAAAGT AAGTTGGCAT AC	642

(2) INFORMATION FOR SEQ ID NO:1127:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 675 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1687RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

55

GATCAGGACA GTAGCAGCTT GACTGAGTAT CAGCAGGAAA AGCCTAGCTA ATTGGGOGGA 60
 5 GTACAATTAC AAGTACCTGT CTGACTACTT CTTTTTGTGG GATGCCATAT TTTTTAGGAT 120
 GGCTGCAAC GGCCCGGTGG GGGGCCCATC CAAATTTTATG GAGTTGAAGA GCTGTTCAAT 180
 10 GGCCTTTATC CCATCTGCAC CGTCCTTATC GCGAACATG GCATGCAACT CTTCAAGCAT 240
 GATATCTTCT TCCTCGTCT CTGATCCGGC GTGTGTGTGG TTTGGGCACT CTTGTAGGC 300
 15 GCCATTCTG TAATGTTGAA GCTGTTCTTT GTTCATCTTC AGACCTCCG TCAGGAAATA 360
 TTCAAAGAAA TCGTCTTAC TAATATCTAC GCTTCACTC TCGAAAAATG TCCGAGCCTC 420
 20 TTCATCCCCA GCTGAAGACC CCGACCAGA AACATGCTCA TTGCTACCTT CATGTCATC 480
 TTTAATATCT GTCAGGAAAG TCTCCAGGA CAGGGCCAAG GCATCCATAG ACGCCTCTTT 540
 25 GTCCGCAGTC GGTACCTCCG TAGTTAATTC AGTCGTAGAG AACTCCACCG GCGCTCTAG 600
 CTGTTTGTGA TGTACCAGAG CGCTTACTAG GTCACCTCT AACTTTCTT TGGGTCAGC 660
 30 TGTCGTTAAC TGGCC 675

(2) INFORMATION FOR SEQ ID NO:1128:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 655 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1687UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

55 GATCCGTTCC AGTTTGGCCA GCGGAAGCTG GCGGACGAGG CGGACATCTG GGCTCATAAC 60

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GGGTGGGATA ACGTAGACTG GGGTGACGAA CAGATCCGGC TCGCAAAGGA GAAGATAGAA 120
5 GAGCAGAAAG AATACCCGGT GCAGGAGTTT GACAAAAAGC TGTATCATAG CAACCCCGCA 180
AGGTACTGGG ATATATTTCTA TAAAAATAAC AAAGAAAAC TCTTCAAAGA CAGGAAGTGG 240
10 TTGCAGATTG AGTTTCCCTC TCTATACGAA GCTACCAAGA AAGATGCTGG TTCAGTGA CT 300
ATCTTCGAGA TTGGGTGTGG TGCGGGCAAT ACCATGTTCC CGATCTTATC TGCAAACGAA 360
15 AACGAACACT TACGCGTTGT GGGTGCGGAC TTCTCCCGA AGGCCGTGGA ATTGGTAAAG 420
ACGTCCAAA ACTTTAAOC CGGAATGCC CACGCGACG TATGGGACTT AGCCAAOCT 480
20 GATGGTCTTT TGCCCGATGG TGTCGAGCG CATTCGGTGG ACATCGCAGT AATGATTTTT 540
GTTTTTAGTG CCTTGGCGCC CTCACAGTGG GCCCAGGCTA TGGATAATTT GCACAAAGTT 600
25 CTAAAACCAG GCGGTAAGAT CCTCTTTAGA GACTATGGCA GGTATGACTT GGCTC 655

(2) INFORMATION FOR SEQ ID NO:1129:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 716 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1688RP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

50 GATCTTGTG AGAACA CTCA ACATCGGCGT AATTGCAGAG CCCCCGGTGA CCATACCGAT 60
TTTCTGTGAC GCATTGCTCA CATAGCTGAA CCGTCTTACA GGACCTTTGA ATTCCACAGT 120
55 TTGGCCTGGC TGTAGCCAG CAAACCATTT GGATACCTTA CCGTGCACAT AAGATTTGAC 180

AATGATATCG AAATGGCCCT CGGCAAATTT GTTGGAGATA GGCGTGTAGT AACGCCTTC 240
5 TTCTACACCA TCCAGCATCA CCTTCGCAGC TAAATGAAAG CCAGTAGGTA TATCAAGAGT 300
TTCCACGCTT GAACGGAGCT TGAATCTGTA TATCGCAGCA TTTTTCCTTA GAACGATCCG 360
10 TTCTTCCAAT TCTAATGGCG TCCACTCAIT TGAAGAATT GAAGTCTGTC TTCGTATGC 420
TAGTAGCAGG CGTGCACTTA CAAACATTGC CAAAGCTAGA ATGCCTAGAA GGTACCATGC 480
15 GTTCCCGGCT GACCAGGCGA TAACAAGAAC GCCCAATGTA AAGATGCGGC TGGGGATGAA 540
GATCCCATGA ATGGGATCAT CCAATATCTC CATACTCTG CGTTCGGTCA TACTAATATT 600
20 TTGAAAGCTC GTCGTAGCTA TCGTCTAGTA AGGATGAGAA CGGTTAATAT ATGCTTCTC 660
CTAGTTCTAT AAGCACGGAC TCCTTTGCAA CTGGTGAAGT ATCGTCTAAC GGTCAAT 716

25 (2) INFORMATION FOR SEQ ID NO:1130:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: PAG1688UP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

GATCAGGCGG GACGGTACT TGCAGGAAGG CCTCAAGAAA CCCAAGGGGG GCGAGGAGGG 60
50 CTTCTCGAGG TTTTTCACG AGACGGGCTC GGGCAAGTTC GTGCCGCGCG CGGTGTAGCT 120
GGAATTGGAG CGAACGTGA TCGACGAGGT GCGCAAGGCG GCGTACCGCG AGTTGTTCOA 180
55 CCGGAGCAG TTGATCAGG GAAAGGAGGA CGGGGGAAC AACTACGCGC GTGGGCACTA 240

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CACGGTGGGG CGCGAGCTCT TGGACGATAT CCTAGACCGC ATCOGCAAGA TCTGGACCA 300
 5 GTGCGACGGG CTCCAGGGCT TCTCTTCAC GCACTGCTT GGCGTGGTA CGGCTCOGG 360
 CTGCGGTCT CTGCTTTTGG AGCAGCTTTC TATCGACTAC GGCAAGAAAT CGAAGTTGGA 420
 10 GTTTGCCGTG TATCCCGCGC CACAGGTGTC CACCTCGGTC GTGGAGCCAT ACAACACCGT 480
 GTTGACCACC CACACCACAT TGGAGCATGC CGACTGTACG TTCATGGTGG ACAACGAGGC 540
 15 CATCTACGAG ATGTGCAAGA AGAACTTGGG CATCTCGAGA CCTAGCTTTG CGAACTTGAA 600
 CAACTTGATC GCCACGTCG TCTCTCGGT GACCGGTCA TTGGTTTGG ACGCTCCTT 660
 20 GAACGTGGAC TTGAAC 676

(2) INFORMATION FOR SEQ ID NO:1131:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 700 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1689RP

40
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

45 GATCGTCAC AAGTTTGACG AGCTAAAGCT AAAGGAGGTG TTGTTGAGAG GTATCTACGG 60
 TTATGGTTTC GTTGACCCAT CTGCCATCCA GCAGGTGGC ATCTTGCTA TCATTGAGG 120
 50 CCACGACGTT TTGGGCGAGG CCCAGTCCGG TACCGTAAG ACTGGTACCT TCTCGATTGC 180
 TGGTGTGCAG AGAATCGAG AGAGCATCAA GGGCCACAG GCGTTGATC TAGCTCTAC 240
 55 CAGAGAGTTG GCGCTACAGA TCCAGAAGGT TGTGATGGC CTTGGCTGC ACATGGACGT 300

TAAGGTCCAC GCTTGTATCG GTGGTACGGA CCTGTGTGAG GACGCGAGG CCTTGAGAGC 360
 5 CGGTGGCAG ATTGTGTGTC GTACCCCCGG CGTGTGTTC GACATGATTG AGAGACGTWA 420
 CTTCAGACT GACCACATCA AGATGTTCAT CCTGGAAGAA GCGAAGAGA TGTGTCTCTC 480
 10 CGCTTCCAG GAGCAAATTT ACAAGATTTT CACCATGTTG CCACCAACCA CCCAGGTGCT 540
 GCTATTGTCT GCCACCATGC CAAAGGAGGT GTTGGACGTG ACCGACAAGT TCATGAACAA 600
 15 GCGGTCCAG AATCTTGGTC AAGAAAGGAT GCCTTGACCT TGGGAGGTA TCCAGCAGTA 660
 CTATATTAC GTGAGAGCG AAGAGTACAA GTACGACTGT 700

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 657 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1689UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

GATCGCGCTG AACCTCAGCG AGGCAAGGCT GGTGATCAAG GAGGCGCTGC AGCACCGGCG 60
 45 GCGGTGTTC GGCAGTGGC GGGACGGCT GGAGGAGGAC GAGGCGGAG GGGGAACACA 120
 ATATGACGCA GGAGAAGGAG CTGGCGATGC TGGACAAGCT GCTGGAGAAG ACGACGGGGG 180
 50 GACAGAACCA GCGCTGAAG CAGACGATGG TGTACCTGAC GAACTTGCG CGGTTCGGG 240
 ACCAGGAGAC GGTGACGGCG GTGACGCAGC TGCTGGGCTC GACGGGACTG CACCGGTTCG 300
 55 AGATTGGCA GCTGGGGTTC CTGGGCTGC AGGACGGGA CGAAGCCAAG ACGCTGGTGC 360

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CGAGCCTGGG GAACAAGATC TOGGAAGAGG ACCTGGAGCG GATCCTGAAG GAGCTGTGGA 420

5 ACCTGGAGAC GCTGTACTAG ATAGCTACAT AGACAGGAAG AACTTGCCGC CGCCGCCCGC 480

CCACCAGTGG TOGAGACAGG AGTGCGATGT GTGCTCGATG TCGACGGCCT CGCGGCCGAA 540

10 GTTGCAGACG CAGCGCTCGG CGAGACGGCG GACGTGCGCG GACGGGCACG TCGCGTAGGG 600

CACGTGGAAG TTACCGATCT CCTGAAGTG GTGCACTCG TCGCGCGCA GGAACAC 657

15 (2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 base pairs

20 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1690RP

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

GATCTGAAC TAATGTCATC CGCGGAAGAA CATACTAAGA GCTCATGTT ACATCGAGAT 60

40 GAGACAAAGT ACCTGATGTA TAAGAGTTT ATTGACATAT GCGCTGGAG GCAAACGGCA 120

GGCTACCGCC TGCCCCGTT TCGTCTACA CATGACAACA TAATTGTGGC AATGTCAGGC 180

45 GCGGTGGACT CTTCAATATG TGCTGCTTTA TACGCTCACT TCCAAAAGT CCGTGGGCTC 240

TACATGCAGA ACTGGTCGCA GACGTGGGGC TCAGGGCCTG TAGAGGGTAA GCGCGAACCT 300

50 TGTACGAGC AAGATTGGAA GGATATTGAG AAAGTGGCG CGTACCTTAA TATTCCCGTC 360

GAGAGAGTCA ATTTOGAAC GGACTIONG CTGGATGTTT TOGAGCCTAT GTTACAACGG 420

55 TATCAACAGG GTTATACTCC GAACCCAGAT ATTGGCTGCA ACAGGTTTGT AAAGTTTGA 480

GGTTGCGGG AGCACCTGGA CAAGGAGTAT GGACGGGCA ACTACTGGCT GGTAACAGGC 540
 5 CACTATGCGC GAATCCTATC CCCCAGACT CGCAGAGAGA CCCAAGTCT GCGGAGCCAT 600
 TATGCGCCAA AGGACCAAAG TTACTACTTA TCCCAAGTCC GGCGGGAGGC CCTCGGGAC 660
 10 CTCTTTAATG CCCATGGGAT TTCTAACAAA ACCGGAAGTC CGACAATGGG CCGCAGAA 718

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 696 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1690UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

GATCAGAAAC ATCACCATAT GGIGTCTGAA GACCTTACGG CGACGGTCCA TACAGCTAC 60
 35 CATCTCCAAG CCGATGATGC CGGCTATAT GGACACGGCC GAGCGCGTGA TTGCCAGGAT 120
 TCGCAGCTTC AGCAGCTGGC TCGAGGTGAA CGTCGAGAAC ATCCCCGGCA GTCCGAGCAC 180
 40 GAGGTTCAAC GTGGTGTGT TGTAGGACCC GAATACACAT GTGTAGTTGC TGTCCATGCA 240
 CTGTATCTGA GACGGCCCT CCATCTTGCA CGTGCGTGG CTACAGTCT AGCTCCCGCT 300
 45 CGCACCTATA CTTTGTATCT GTTTCGCCCT TGCTGGGGC TAGCCCCCTC GCGCTTGCT 360
 CTTATCCCTT CTGAAGTCG TCTCCCTAA GTTGATCC AGCGACCTCC TAGTCGAAAA 420
 50 CTGCTGTCTA CGTTGGCCAG GCACTAGTTG CCTCCACTG CAGGTTATCG ATAAGTCTA 480
 AAATACCACC AAGCAGGGT TGTACTGCTT CTATACGCA ACCCTCGCTT TTGTTGGGC 540
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TGACACACTC AAGTGACTGC AAGAAGACTA CCTACTCAC AGATACCGTC GTCCGTTGTA 600
 CGCACGCTAA AAGACAAGTT AAATCTACGA CACATATAGT GCCTGCAAG CTCACCGCAT 660
 CCGGAAGGAA CAAGCTATTA GAAACTGAGA CACCTC 696

(2) INFORMATION FOR SEQ ID NO:1135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1691RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

GATCTTCTTT GTATTCTGG TCTTACCTGC CCCAGACTCC CCTGTACTA ACACCGACTG 60
 GTCCGCTC TGTTCAACA AGTTGGGTA TGCTGCTCC GCTACGCAA AGATATGCGG 120
 CTGTTGCTT TCCTGGGTG ACCCATGGTA CAAGTTCACA TAGTCTGGG TGTACACCTT 180
 GATGTTGCTG TACGGATTCA ACGGACGAG GAATAGCCCA GAATAAGTAT ATATCATATC 240
 GTCTTGTAT CGGTCTCCA AGTTGTACAA CACAGACGCC TGTTCAGT GGTCAACTC 300
 GGACATATCG TCTATCTTGT CAAAGTTGA CGGATTCACC GCGGGTCT CCACCTCCAG 360
 CACTTCTCGT TCCTTGCCAT TCACTCTCAC AAGACAGACC TTCTCATCT TGTCTGTTT 420
 GTTTTAATT GTCTTTGTTG AAACCAACTG TCCTTTCACA AACACCTCT CAGCATCTGG 480
 AACCCTAATC ATTTGACATT GTTCACTCAT CGGGACAGAT GCTCTTGAAC TTATCTAATA 540
 TGCAATAACC AAATTCAACT TTACTTTAAT CACCTGCTG TTACACAGA AGCAATGTTG 600

GATCTCATAT TCACACGACC TACTTTTTCG AAACACTTAT TTGTTTATGT CGGCTCGAG 660

5 CATACACGTC GGTCACGTGA CAAGCGCATG TAC 693

(2) INFORMATION FOR SEQ ID NO:1136:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 705 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PAG1691UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

30 GATCATTATG CAACCGAATC TGGTATCTCA GAAGATTACC GTAGGACTGT GCCTGTCCGA 60
 TCGATTACGT TAGTGGGGTA GAGAATGAAG TAAGAAGCAG CTCTGCGATT ATTGTGCTTT 120
 35 TGCGCCTCAT GTGAGGTAAA GGCCTATCCC GCAGGGTGGC GGCTTTCTGC AAGAAAATCT 180
 GGGCATCAG CCCCCGAAAC GAAATGCGAT AGTCACCTGT GCCATGGCGA CGAGTCATTT 240
 40 CCCCATTCGT ACAGAAATGA ACGGGCAGAA TCGGGTAATG GATTTTCTGT GCGTTCTGTG 300
 CCAAAAGGTG ATCTCCACCT GGTGCTGCC CTGGGGCGT GGTGAGCAG AGCACCTGGA 360
 45 AAAAGAACAG CACAGAAGGC CAATGCAGTT GGCCAATTGA GGCAATAGCC GAGCAGGAAC 420
 AGTCGAAAGT GGGTGTCTG GCGCTGTTGG ATCTGAAAAA TGCAGGAAGT TACAAAAAAC 480
 50 AGTGGGGCAA TACATAGAAA CCGGCGACCC GGCGATCGCC TAATCATCTG CCATGGAGAC 540
 GCGGGTCCG CGCTGAACC AGCGGTGAA ACCITGAGG CATGGTGATA CCGGCCCGTC 600
 55 GCGGGGCAC TCAACAGGC ACGTGTAAAT CCGACAAA CGCAGCGGG TAATTCCTTT 660

CCGCAAGCCG GACGGGTATA TGAATOGTAC GATACCAATT GTCGA

705

(2) INFORMATION FOR SEQ ID NO:1137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1692RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

GATCTAAATA TATATAATTT AATTTATAAA GATTAATATA AACTTTTTTA TTATAATATT 60
TAAGTATTAA ATTATTTAAA CTATTATTAT CATTATTTAA TAAATTAATT ATTGATTAT 120
TAATACTTAT TATATAATTA TTATATAATT TACTTAATTC ATCATTATTA ATATTTATAT 180
AATTATAAAA ATAATATTTA ATATGAATAC TATTTAGTCT ATGTTCAAAT TTAAATTAG 240
TTATTAAAAT ATTATTAGAT ATTATTATTT TCTTAAATAA ATTATTAAAT AGATTATCAA 300
TAATTAATAT ATTATTTTAT AATTGTTTAT TAAAATAATA TATTTTATTA TTATAAAGAT 360
TTAATTTATT TAAATATTGT AAATTATTAT TTTTATTATA ATATCTATTT TTATAAATAT 420
TATGTTGATT TATATTATTT AATCTTTTTA TAAGAATTAT TATTAAAATT AATTTTAACT 480
TTAATTTCTT ATTATTAAAT TTTATATTAT TTAATAAATT ATATTCATTT TATTTATTTA 540
TTTATTTAAT TAAATTAATT ATTTAATTAA TATTTTATCA TTATTTAATT AATTAATAAA 600
ATATTATAAA GAATGTAGTT AAAAATACTT ATAAAA 636

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1692UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

GATCTTGATA CTAGAGCTTA TTTTACTTCA GCTACTATAA TTATCTTAT TCCTACTAGT 60
ATTAAAGTAT TTAGTTGATT ACTAACTATT TATGGTGGTT CATTAAGATT ACTAACACCA 120
ATATTATATC TATTATCATT TTTATTTTAA TTTACTGTAG GTGGTTTAACT TGGTGTAGTA 180
TTAGCTAATC TATCATTAGA TGTAGCATTG CATGATACIT ATTATGTAGT ACTACATTTT 240
CATTATGTAT TAAGTTTAGG TGCTGTATTC TCTATGTTTG CTGGTTATTA TTATGAAGT 300
CCTCTTGTTT TAGGTTTAAA TTATAATGAA AAATTATCAC AAATTCAATT CTGATTAAAT 360
TTCTTAGGTC TTAATATTAT TTTCTTCCTT ATGCATTTCT TAGGTATTAA TGGTATACCA 420
AGAAGAATTC CTGATTATCC TGATCTATTC CTAGGTGAA ATTTAGTATC TTCATTTGGT 480
TCTATAATAA CTATTATATC ATTAAATGTA TTCTTTTATA TTATTTATGA TCAATTAATA 540
AATGGTTTAA CTAATAAAGT TAATAATAAA TCTATTAATT ATATAAACT AACTGATTTT 600
ATTGAATCAA ATAATATTTT CTTAATGAAT ACTACTAAAT CATCATCTAT TGAGTTTATA 660
TTAAATTCAC CACCTCTTAT TCATTCATTT AATACTCCTC TAATCAATC TTAAAATAT 719

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 714 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1693RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

GATCCCTTAG CGACTCTCTC CACCGCTCGA CGAGGOCATT GAGCTCTTAC GAACTGCACA	60
AACCTACTCG AACTCTGTTT CCAGACTTCT TTCTGTTTGT CTTCAACTGC TTTCGCATGA	120
AGTACCCOCC AGGCTATTTT TCTTACCCGC CTGGTGTTTG TCTATATACC OGGTTGTATT	180
TTTGATAAAA AACTCAGCTC TTCTCTAAG GCAGAAATAT ATATOCAGTC CTTAGOGCCA	240
TGCGAAAATC TGCTTTTITA CCGCTGTTTC TCCCAGTCTT AGCACTGGCA GAAAAAGAT	300
GTATGGCGTA TAGGCGCTGG CCCCOCGGAA AAAAAAAAAA AATAGAAAAA TAGAAAAATA	360
AAAAGACGTG GCGCGCCCCG CCGGCAGACG AAGAAAAAAT AGCGCGCCAC CCTTCCAAGC	420
AGACGACAGG CGAGACATAA TAAATCCCA CACCAAGGGA AGAAAGTCTT GTGCACGCTC	480
CCGGCTTCAT ACGCTGCCAT TCTGTTCAT CCGGCTTGCA AACCCAGTAG TGGCATGTCA	540
AAGCATTGCT CCGACGCTCC GCTGCCTTGC AGTCGACATC CTCTTCTTAA CCCCAGCCAG	600
ACTTCCATA CTTTGGCACT TCACATAGCA TATCACTTTT CAGATCACTT ACGTGACATT	660
CCGGTACGGA ATGGCACTCC AATGCOGACA AACCTCTTCC TACCCCGTGA CTTA	714

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 692 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

TCGCCAGGCG GGTGTGTC ACCCGCAGCA ACAGGACGAG AACTCTCCGC TTTCGGCCTC 180
 5 GTGAGATTTT GGATTCAGTC ACGTGATTCG CGTAGAGGTT ACCCGGAAAG AGCGGCTTGG 240
 ATGCCAGTAA TCACCGCCGT TATCCCGGCG CTTCCTTAAGC ATTCAGTCTG AGCGGCTTCT 300
 10 CCGCGCTTCC TTGTCTCTCT GGAATTTCAA AGGGGGGGCG GTATATAGGC GCGGAGAAAA 360
 ACACGGTGGC GAACGTTGTT GCGGCCAAGC GTTATCGTGA AGAACAAGCA TAATGGTTTC 420
 15 CCTTCGGTT ATTAAACAGG TGCAGGCGCT AATCCAGCAG AACCGGTGT TCATTGCATC 480
 CAAGACGTAC TGTCGGTATT GCCAGGCGGC AAAGCGTAGG TTGCTGGAGG AGAAGCGCGT 540
 20 CCGGCAAGC GCGTAAAC TGTGGAGCT TGACCCATG GCGAGGAGG GCGGGTGAT 600
 CCAAGCGCGG TTGCAGGAGC TGAGCGGCA GCGACCGTG CCCAACATCT ACATCAACGG 660
 25 GCGCATGTG GGTGGCAACA A 681

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1698RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

50 GATCTGGTGC TTTTCAACGC GCGCCCCAG ACAATTTCCG GAAGCATACA TATCGCCATT 60
 ACATAACAG ATTTTATGAC TAGTACAGTT AGGTATGTGG GAGATCACCG GAATAACTCC 120
 55 TATATCTEAT TTCTGTATTC TCAGGTACTG ATCGCTGTTG ATGAACGGGC AACCTGTGA 180

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CTTGGGGATT AACACTGTAT GAAGCCGGAC GGGGGGGTAG CACATTGGTA CTAGGCTGGC 240
 TGAATTCATA ATTGGAATAA GGTGCTGCTT GCCCCGATGG CTGGTATGTC CGGTGCTGGG 300
 TTGAAGGCAT AAAATTGCTC GAGCTGTAGC ATGTTGCCCTT CTCTAGCATC ATGTTGTATG 360
 TAACCTCCGC ATTGGCCAGA ACCTGGGCA ATGATGCAAG ATCTTCTTC TTCTGGGCAT 420
 ATTTACCGAT GAGTTTGTG ACATGTGGTC TAAGCGGTGT GACGGTAGAG TAAAGTTCTG 480
 ATATCTGTC TTGTTGTG ACATCCACAT TCTGGGAGAC OCTTAGTTTC TGGAGCAAGT 540
 TCTGACATT GCGGCTTGC GCAAAGACAG CATGCTCTG AGCAGCTOC TTAGCTAOC 600
 CCTCTGCAST TGGCTCAGG CATACGCCGA CATAATTCAC TGGGAAAAT ACCAACCTTG 660
 CCGCGCA 667

(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1698UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

GATCAGCAAG CTGGCCGCG CAGGTGTGCA TCTGGGCAG TCTAGTGT TGTGGGCTC 60
 CTCCACTCAA CCATACATCT ACGGCTCTTA CAAGGGCATC CACATCATTG ATCTAAACCA 120
 GACGCTGTTT CACCTGAAGA GAGCTGCGAA GGTGTTGAG GGTGTTGGG AGAATGGTGG 180
 CCTGATCTTG TTTTGGGTA CCAGAGAAGG GCAGAAACCA CCTTTACGGC GGGCTGCAGA 240

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GAGGGTGGGT GGCTGTTATG TGGCTCGAA ATGGATACG GGGACCTTGA CAAACCCAAT 300
 5 TGAAATATCC ACTGTCTGGG GCAGGCATGA AGTTGACTTC GAGGGCAATC CAACTGGCAG 360
 GGAATTGACA GAAGAAGAGA ACATCCGCAT CATAAAGCCG GACTTAATTA TTGTTTIGAA 420
 10 CCCAACAGAA AACATGAACG CGTTGAGAGA GGCTATGCAG GCTAGAGTGC CACCTATTGG 480
 GATCAITGAC ACCGACTCAG AGCCTTCAAT GGTACATAAC CCGGTCCCTG GTAACSAACG 540
 15 ATTGCTACG TTCTGTAAGT TTAATTGTAA AC 572

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1699RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

GATCTGGGTG TATATTTTGA TGTATATGGA CTTCACACTT TCGGAAGCAA TGGAACCTGA 60
 40 AAGCTGGTTG ACCACTCTGC TGTATCTCTG TAGTCTTTCT GAAACGACCG TAAGAAAATT 120
 AACCTTGAGC GGCGATAGGG AAGATGCAAC TTAAATTTC TCTACTTGGT TACTCAAATA 180
 CTGATATAAT AATGCAGCCT CAAATATGCT GTGGAAAACA CCACTTTTGC CGTTCCGAAC 240
 50 ATTGGGTGGG ATTTGATAA CCTGATTGGA GATCGGGAAC AAACCTGACG TAGTAGOCAG 300
 TAACGTGTAG GAAATATACT TTAAACGTC GGCCTCGGGC ACCATGTTGC TGTAGTATGG 360
 55 GTTAGACAGA TATGCCAATG GAGTATCGTG CTGCTCGGGC CGCTTGGGGA CCGGGCCGGC 420

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1693UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

GATCCGTAAC TTCGGGATAA GGATTGGCTC TAAGGATCGG GTAGTGAGGG CCTTGGTCAG	60
ACGGGGCAAG TGTGCTTGTG GTCTGTCTC GGGGGCTTGC TCTGGGGAC GGACTGCTTG	120
CGTGCTCTGT CGTAGACGGC CTGGGTAGAC CATCTCTGGT CGTGGCTTGC TACAATTAAAC	180
GATCAACTTA GAACTGGTAC GGACAAGGG AATCTGACTG TCTAATTAAA ACATAGCAAT	240
GCGATGGTCA GAAAGTGATG TTGAGCCAAT GTGATTCTTG CCCAGTGCTC TGAATGTCAA	300
AGTGAAGAAA TTCAACCAAG CGGGGTAAA CGGGGGAGT AACTATGACT CTCTTAAGGT	360
AGCCAAATGC CTCGTCATCT AATTAGTGAC GGCATGAAT GGATTACGA GATTCCCACT	420
GTCCCTATCT ACTATCTAGC GAAACCACAG CCAAGGGAAC GGGCTTGGCA GAATCAGGG	480
GGAAAGAAGA CCTGTGTGAG CTTGACTCTA GTTTGACATT GTGAAGAGAC ATAGAGGGTG	540
TAGAATAAGT GGGAGCTTCG GCGCCAGTGA AATACCACTA CCTTTATAGT TTCTTTACTT	600
ATTCAATTAA GCGGAGCTGG AATTCATTTT CCACTTCTA GCATTTAAAG TCCTATACGG	660
GCTGATCOGG GTTGAAGACA TTGTCAGGTG GG	692

(2) INFORMATION FOR SEQ ID NO:1141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 673 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1694RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

GATCCGTTCC TTGAGAAGCA CCTAAAGCCT GAACTCCTGG CAGAAGCGAT CAAGGGAACC	60
TCTTGGGAGG GTAAAGTTAG TATTAACCTG GTAGACGGAT TCGACCACTC GTATTACTTC	120
GTCAGCACGT TCGTGCCGGA ACACGCAAAG TACCATGCAG AAAAGTTGGG TCTAGTTTGA	180
GATTTGACGT TCGGCTGTT AATTTGGTATA TACTTACATA TTTAGTCATA TGACGGCTTC	240
AAGTACTCTG ATTCTGCATT ATAAGTGCAG CGAATGCCA GCTCCGGCA GTAATGGCAA	300
CGCAAACCTGA ATTTGCCGGT AGTCAACCT TGGCCGGTTG CAGCAGCGT ATGCTCCGAG	360
CAGACTCAA CGTCGCTATT TGGCGGGTAT CTACAGCCTC GTGGGATCT CCTGCCCAA	420
GACAGCCACA GATATCACTC TCCAGCCCC AGGAGTAGAG TTCACCTTTG TCGTTAGAG	480
CTAGGTTGTG GTAGTCTCCC GCAGATACAG CAATAAACTT CTGGCCTTGT TCCAAATTCA	540
TCTTCATGAA TGAGTCTCG ACGATATCAC CATTATTCAC CTCAGGGTG TATGTGCTAT	600
TCTCGGTACA TAAAACCAGT GTCATGCAAG ATGCTCAAT CTTCGTTAAC CGTCCATCAA	660
ATGGCAAAT CAA	673

(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 676 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1694UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

10	GATCAGCCCC CGACCGAAGA ACACTGGCTT CCCTCTGGCG AGCGCGAAA TTCTTGACC	60
	GAGTATCAAC AAATOCAGTT AGATAACGAT CACATGATTG CAACACTGCG GGAATTCATT	120
15	AGTTACCAGA CTGTTTCCCA ACTCCAGAG CCCCAAATA TCATCGATTC GGTAGGTGT	180
	GCGAACTTC TCAAAATCT CTTCACTAAG CTGGTGCTA ACCATGTGG GCTTATACT	240
20	GTCAGTACAG GCAGCAACCC GGTGGTCTC GGCAGTICA AGGCAATGC AGCGCGGCC	300
	AAACGCATAC TATGGTATGG CCACTACGAT GTGATATCG CGGACACCC GTGCACTGG	360
25	GACAACGACC CCTTCAGCT CACTTGGAA AATGGGTATC TTAAGGAAG AGCGGTGTCT	420
	GATAACAAAG GCGCGTCTG TCGCGCATC TTCAGTGTAG CCGAGCTTTT CCAGAAAGGA	480
30	TACCTGAACA ACGACATCAT CTTTCTAGT GAGGGGAGG AAGAAAATG CTCTGGGGC	540
	TTCAGGAAA TTTTGCTTC CTCGAAGG CTCTCAATC AGCGGTGGGA CTGGATCTG	600
35	TTCAGCAATT CCTACTGGCT GGATCAGAAG GTGCCCTGCC TCACTATGG CCTCGAGGC	660
	GTCATAAAG CGAAA	676

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1695RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

5 GATCTGCCCC CAAAGATTTC CGTGCCGGC TACCCCAAAA GATTTTCGGT GCGGCTACC 60
CCATCAGGAG ATGGCACTGG CTCATGGCG AGCTCCTGGG CATTTGCCTA TGACAGAGGA 120
10 ATGAGTCAGC TTTACTCCGC CACACCATAC TCCCGGGCCT TCAACAAGCT TCTGTTTGCC 180
ATCGGCATCG TGGCCAGTTC TTACACTGGG GCGCCACCTG CATCGGCGGT CATCGCAGCC 240
15 GTTTTGTCAC AGTTCTCCCT CCGCAGGTAT CGTCTCCGA CCGGTAAAGG ACGGACTAC 300
GCAGGGGCTG CCGCACTCAC GTGCGGGCGG GTCTTCTCTC CCACCGTGAT AGTCACTTTT 360
20 CAGTAGTGIG TGCTGCTTG AATTGGCAGG GCAATGGTTC AAGCTGCTCT GGCGCGAAG 420
ACGACCCCAT CTCGCAACG GCGTTGGCG AGAAAGGGTG TTTGGGACCA GACATCGGCC 480
25 ATCTGCCGA GTCAGCAGCT GCCTTGGTAC GGAGCTACCT GTCTATATTA TCCCTTAAT 540
AAACATGGA TATGCTGTT ATTGTATGCC AACGGTTC CCGGTACAAC GGGGTAGTCC 600
30 CCGCCCTCC TGAGCTATCC TGGCCGATGT GAAGTGCTT TGGTTAAGTG GTCTGCTTTC 660
CCGGGCCACT TGTAAACACT ATGGCGGATC ATACAGCCAG GACTCAAATA C 711

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1695UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

5	GATCTGAAAA GCAGGAAGTC GCAGTGGGAG GCGCTGCGG GCACGTGCTG GCCAGCGAAG	60
	GGTGCGCGG ACGCGCCACC GCGTACGAC ACGGCGCTCG CACGCGCGC CGCGCAAGGC	120
10	GCGCAGGCGG TTGCGCCCA GCGGACTAC GGCACACAGG CCGGATAGC GCGCCAGGGG	180
	TACGCGCGC GCGCGGGTA CACGCCCCAG CCGGCTAGG GCGCACAGC CGGCTAGGC	240
15	ACACAGCGCG GCTACGGTGC ACAGCGCGC TACGCGCAC AGCGCGGCTA CGGCGCACAG	300
	CCCGGCTATG CCGCGCAACC CGGTTAGGA TACGCGCGC AGCGCGGCTA TGGTGCGCG	360
20	CCCGCGCGT ACGCGCAGCA GCGCGGCAC GGTACCGCG CCGCGCAGC CGCGCGCGG	420
	CAGAACGCG GCGCAACAA CATGATGATG GCGGCGCTGA TGGGTGCGG CGTGGGGTTG	480
25	ATGCGCGGGT CACTAATGAC CACAGCCATG TATAACCAAG ACAAGGAGT GCGCGATGCT	540
	GCGTACGACC GCGGCTATGA AGAGCGTCA TCGAGGCGA CTTCTAGGCC GCACCGCGTC	600
30	ACGTGCCAGA CCGGTAGAGA GCTAGGACAA CTTAGGTAAC GGTGCGAGT ACGC	654

(2) INFORMATION FOR SEQ ID NO:1145:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 711 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
40	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1696RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

55	GATCTTGTTT TCATTGACA TCGAGGCGTT TGAGAGCAAC ACATCTGTG TCACAGAGGT	60
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GGGAATCTCG GTCTACGATC CCCGOGAGAA CGAGGACACG CTGCTGCCCC ACTTCGCGAC 120

GTACCACCTC TGTCTGAGG AGTCTCTGG GTTGATAAAC AAGCGGTTTG TTCCGAATCA 180

CAAATGCGAG TTCTCCATG GTGAAACCAT GGTAAATGCG CTCTCCGAGT GCGTTGAGTT 240

CATTACGGG CTTATCGAGT ACTACTGTG CCCACCCAGG GGCGTGGACG ACAAGTACTC 300

GCGGGCAATT GTGGGTCATG GTGTCTCTGG TGATCTGCAA TGGCTTAGGA GTCTGCTCAT 360

CGACCTGCCC ACGATCGCTG GCCCAGGCAA CTCCCATCG CGCGACCATG TTCTGTCTCT 420

AGATACCGCG CATTATACC AGTACTTCTA TGGTCAGAAG GGTTCAATCC TAGGTAAGAG 480

CTTAAGATTG CACGGTGTCC CACATAGCTA TCTGCACAAT GCAGGCAACG ATGCATATTA 540

CACATTACAA CTGCTCATGA AGATGGGCGA TGTGCAGCAA CGCATCCGGC ACCAATGGGA 600

CGATCTATAT GCTGTCTTCC ACACGTTGAA GCAATGGGAA GAGTATGAGA ACTCCACGCC 660

CTCCACTCAG CACGCAGAAT CGTCCATAA CAGCACCGCG GCTACCGGGA A 711

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1696UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

GATCGTTCAG AAACCCATCG CCTCGCTGCG TGTCTGCTA ACGCCAGAA CGCCACTGT 60

GGTCTTTTCA CTGCGCTGG TTCTTATTC CGCAGGGGG CCTCGTGGG CCGCCAGCGC 120

TGGCCAGGCG GGTGTGTGTC ACGCCAGCA ACAGGAGGAG AACTCTGCGC TTTCGGGCTC 180
 GTGAGATTTT GGATTCAGTC ACGTGATTC CGTAGAGGTT ACGCGGAAG AGCGGCTTGG 240
 ATGCCAGTAA TCACGGGCGT TATCGCGGCG CTTCCTAAGC ATTCACTCTG AGCGGCTTCT 300
 CCGCGCTTCC TTGTCTCTCT GGAATTTCAA AGGGGCGGCG GTATATAGGC GCGCAGAAAA 360
 ACACGGTGGC GAACTGTGTT GCGGCAGGC GTTATCTGTA AGACAAACA TATGGTTTTC 420
 CCTTGGGTT ATTAAACAGG TGCAGGCGCT AATCCAGCAG AACCGGCTGT TATTGCATC 480
 CAGAGGTAC TGTGGTATT GCGAGGCGC AAGCGTAGC TTCTGGAGC AGAGCGGCT 540
 CCGGCAAGC GCGTAAAC TGTGGAGCT TCACCATG GCGAGGAGG GCGGGTGAT 600
 CCAAGCGCG TTGCAGGAGC TGAGCGGCA GCGCACGTG CCGACATCT ACATCAAGG 660
 GCGCATGTG GTTGGCAACA A 681

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1698RP

(x) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

GATCTGGTGC TTTTCAAGC GCGGCGGCG ACAAATTCGC GAGCAACA TATGGCAAT 60
 ACAATAACAG ATTATATGAC TAGTACATT AGCTATGTG CAGATCAGC GAATTAATCC 120
 TATATCTTAT TTCTGATTC TCAGGTACTG ATGCTGTG ATGAAGGCG AACCTGTGA 180

CTGGGGATT AACACTGTAT GAAGGCGGAC GGGGGGGTAG CACATTGGTA CTAGGCTGGC 240
 5 TGAATTCATA ATTGGAATAA GGTGCTGCTT GGGGGGATGG CTGGATATGC GGCTGCTGGG 300
 TTGAAGGCAT AAAATTGCTC GAGCTGTAGC ATGTTGCTT CTCTAGCATC ATGTTGTATG 360
 10 TAACTGCGC ATTGGGCGA AACTGCGCA ATGATGCAAG ATCTTCTTC TTCTGGCAT 420
 ATTTACCAT GAGTTTGGT ACATGTGTC TAAGGGTGT GAGGTAGAG TAAGTCTG 480
 15 ATATCTGTC TTGTTGTG ACATCCAT TCTGGGAGC OCTTAGTTC TGGACCAAT 540
 TCTGACAT GGGGCTTC GCAAGACAG CATGCTCTG AGCAGCTTC TTAGCTACT 600
 20 OCTCTGCAAT TGCTCAGG CATAGCGCA CATATTCAC TGGGAAAT ACCAAGCTG 660
 CCGGCA 667

(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1698UP

(x) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

GATCAGCAAG CTGGGGGCG CAGGTGTGCA TCTGGGCGAG TCTAGTGTG TTGCGGCTC 60
 CTGACTCAA OCATACATCT AGGGCTCTTA CAAGGCATC CACATCATG ATCTAAACA 120
 50 GAGCTGTCTT CAGCTAAGA GAGCTGGAA GTGCTTCAG GTGTTGGG AGAATGGTG 180
 OCTGATCTG TTTTGGTA CCAGAGAAG GCAGAAACA OCTTAGGCG GGGCTCAGA 240

GAGGGTGGCT GGCCTGTATG TOGCTOGAA ATGATACCG GGGACCTTGA CAACCCANT 300
 5 TGAAATATCC ACTGTCTGGG GCAGGCATGA AGTTGACTTC GAGGCAATC CAACTGGCAG 360
 GGAATTCACA GAAGAAGAGA ACATGCCCAT CATAAGCGG GACTTAATTA TTGTTTGA 420
 10 OCCAACAGAA AACATGAAG CGTTGACAGA GCTATGCCAG GCTAGAGTGC CACTATTCG 480
 GATCATTCAC ACGGACTCAG AGCCTTCAT GTTCACATC CCGGTCCCTG GTACCAAG 540
 15 ATTOGCTAGG TTCTGTAACT TCACTTGTA AC 572

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: P461699RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

GATCTGGGTG TATATTGGA TGATATGGA CTCACACTT TOGAGGCA TGGAACTGA 60
 40 AAGCTGGTTG ACCACTCTGC TGTATCTCG TAGTCTTCT GAAAGGAGG TAGAAATTT 120
 AACCTTGAGC GCGATAGGG AAGATGCAAC TTAAATTTC TCTACTTGT TACTCAATA 180
 45 CTGATATAT AATGAGCCT CAAATATCT GTGAAACA CCACTTTCG CGTTGGAAC 240
 ATTGGGTGG ATTGATATA CCGATTGGA GATCGGGAAC AAAGTGGAG TAGTAGGAG 300
 50 TACGTGTAG GAAATATCT TTAAAGTTC GCGCTGGGC ACCATGTTG TGTAGTATG 360
 GTTAGACAGA TATGCCAATG GATATGTG CTCTGGGC GCGTGGGA CCGGCGGCG 420

GTAGGCAGAG GTTACCGCCG ACCGGCGCTC TGAAAGCCGC TTCACATTCT CGAACGACTC 480
 5 TGCATAGACA CTAACCGCCC TCGACGGCGT CATCAGCGAG TTGTGCGGTT GCAGCGTGGC 540
 GTTGTGAAGA TATCCAGACG CCGTGCGCCT GTGTGGGAAG GCGGTGCTCT CCTGCGGCAC 600
 10 GCTGTTCAAC ACCGTCAGGT ACTTCAGCAC CTGCTCCTTG CTACCGAAAC TCTCCAGCAC 660
 TTTC 664

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1699UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

GATCTCCACC GCGTCCAGCA CCACGATCCG GTCACCGTCC CACCGGTCA TOGCCACTGT 60
 40 CCGCGCGACG CTTTCGAAAA CCGCCCGTCC CTCGCGGTC GCAGCCCCTC CCCCCTGTTC 120
 GTGCGTCCGG TGCTCGGCTT CCGCGACCG CAGCGTCGCC ACCACCCGCT CTATATTCAC 180
 45 GCCCCGGGGC TTCAGGTGT CCGCTTGAT GGCAGGGCTG GTGGGTTTCT CTCCCACCAC 240
 CTCACGGCTC TTGATAAAGC TGTCTTAAT CACCTTAAAG CTCGAGTAT GGCCCTTGCG 300
 50 CCCACATAGT AGCGTCAGCG TATGGTTTCC CGAATCGTAC GCGTATATCT TGCCCTGTGT 360
 TACACCGTCG AGGACGTTGG TCACCCGCAC CTTGAATCCA AGGATATGTT CCAAGTTGAT 420
 55 GCTCATTTCTG CTCACTTCCA AGCCACACA GCTATCCTGG CCACCTTAGA ATGCCACGCC 480

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TGCTCCCCGT CCACTGGCTG ACTCCCAATC GTTCAGTTTG CCGTGIGGST ATTTTTTTGA 540
 5 AGTGGCGCTC TAACGATGAA GTAGGATTTT CTATGTATTA CTATGTGCA CAAAGGTTAG 600
 TTCCAATAGT GCTTGCAACT ATCAGGTGCT GTGGAATTCC AA 642

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1700RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

GATCAGCAAC CGCAGGGAT GAGGGAGTCC GCTCAGCAC GGTCTTGTTT TCAGGGCTTG 60
 GCTTGCTTTT CTCCTTTATG CGTGTACTA CTTCTGTGAT GTGCTGGCA TCCAGGCCCC 120
 TTTTCTTAG CCTGCTTGT AACCTGGCA GGCGCGGT GCTACGAACA CGCAACTTGG 180
 CTTCTGGATC AGCAAGCTC GCTCGGTGTT TGGCAGCCG TTGGCATGCT CGCGGATCCT 240
 CGCGTCAAT ATACCAGAAT GCATCATGCT TCGCTGGCTC TATATTGACC TGGTGGCCAT 300
 ATATGAAAAG GCGTCTTIG AAGTTTGTG AAAACTCGTC TGCTGAGAT GCGTAGCGA 360
 ACCCAAGGAA GCATTTATTG CGGCATTAC GAGGCTGGA AACACTAACT ACCCGTACT 420
 TCTCATCTAC CAGTGAAGG GGCAGTCTG CGGAAGGAAG CGGCTCTGGC AACGTTTCT 480
 CGCCGATAG AGCATATGGG TTATCTTGT TGATGGACTT CAACAGTTGT CGAGCATATT 540
 CTATCTTGA GGCATTGAC GCTGGCAAAT TTGACAGGTA GACACTGGAT GGCGGGGTTA 600

GTATCGAATC GACAGCAGTA TAGC

624

(2) INFORMATION FOR SEQ ID NO:1152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1700UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

```
GATCACTGGG CCTGGAGGGG CGCGCTTTT TCGGCTGTT GTAGAACAGC ATGCCGCGGC      60
GGACCTTGTC ATAGAAGTGT TTAGACTGTA GGGTTCCCAT CGAATGGGAG CGGCGGTAGC      120
TGTGACTTTT CATGATAATG GGGGTGCANA GCTTGAGGTG GTCGTGTAC GGGGAGGAAA      180
TGAGGTTGCG GCCGAGACGG AGGTGCTGG CGCGCGGAG CGACGAGCG CGGATGGGC      240
ACTTCCAGGA CTTGCGCGAC GACGGCGGT GCGCGAGGA GTAGGAGCG ATGGGGAAGT      300
CGCCGCCAAG CTGCGAGCG CGGAGCCAG ACGTGAGCG CTTCAANAAA CGGCGACGGC      360
GGTTGGCGGG CTGGAGCTGG CCGCGACAA ACCGAGAGC GCTGTGGCG AGACCGGTG      420
GCGCGCTGC GCTGCTGGTA AGCCAGTGG CGGACTCAG CAAGCGGAC ATGCCCGGA      480
AGTAGCGGC GCTGTTGGCG CTGAGCTTCG GAAACATCTT GGAGAAGAAG CCGGCTCCG      540
TGGAGCGCAA CACGCGGTCC GCCTGGAGA TGTGCTCTG CGTGGAGTGC GCCAACTGCT      600
CCA                                                                                   603
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Claims

1. An isolated DNA molecule comprising a sequence selected from the Sequence Listing.
- 5 2. A method of sequencing the termini of randomly picked *A. gossypii* shotgun clones to obtain linked pairs of genomic sequences
3. A method for characterization and validation of an *Ashbya* gene comprising
 - 10 (a) inserting into *Ashbya* sequences of genomic pAG clones as provided herein in the attached Sequence Listing a chimeric gene construct comprising a selectable marker plus adjacent multiple cloning regions from a suitable cloning vector;
 - (b) selecting clones carrying *Ashbya* sequences disrupted by the selection marker gene in a suitable host system;
 - 15 (c) transforming *Ashbya* with a disruption cassette according to (a);
 - (d) revealing the disrupted open reading frame by DNA sequence analysis around the site of integration of the selection marker module and determining the orientation of the selection marker module;
 - (e) determining whether deletion/insertion at the disruption site results in any phenotypic alterations.
- 20 4. A method for characterization and validation of an *Ashbya* gene comprising
 - (a) designing cassette for gene targeting comprising terminal Short Flanking Homology regions encompassing a selectable marker module;
 - (b) transfecting the gene targeting cassette of (a) into *A. gossypii* and selecting transformants;
 - 25 (c) verifying correct gene targeting by applying suitable testing procedures;
 - (e) determining whether deletion/insertion at the disruption site results in any phenotypic alterations.
5. A method for characterization and validation of an *Ashbya* gene involving a triple selection marker module which method comprises
 - 30 (a) inserting of a reporter, a selectable marker and a strong promoter, which is preferably a regulatable promoter, in front of the start codon of a coding sequence of interest (promoter exchange mutant) within the *Ashbya* genome
 - (b) applying potential antifungal agents for growth to the promoter exchange mutant of (a) and to a wild-type strain, respectively;
 - 35 (c) identifying a growth or non-growth phenotype of the strong promoter exchange mutant.
6. Use of a DNA molecule according to claim 1 to identify *Ashbya gossypii* promoters and terminators.
- 40 7. Use according to claim 6, wherein a putative promoter region is identified by sequence alignments and the ORF of a genetic selection marker plus start codon and terminator is placed downstream of said putative promoter region.
8. Use of an isolated DNA molecule according to claim 1 and variants thereof in a screening method for identifying compounds capable of inducing broad spectrum disease resistance in plants.
- 45 9. Use according to claim 8, wherein the suitability of the DNA sequence to be used in a screening assay is determined in gene disruptions in the *Ashbya* genome.
10. Use according to claim 9, wherein a disruption cassette is used comprising a selectable marker plus adjacent multiple cloning regions from a suitable cloning vector.
- 50 11. Use according to claim 9 which is based on a gene targeting procedure involving short target sequence homologies added to both ends of a DNA molecule encoding a selectable marker.
- 55 12. Use of a DNA sequence according to claim 1 for distinguishing among different species of plant pathogenic fungi and for distinguishing fungal pathogens from other pathogens such as bacteria.
13. A DNA molecule comprising a DNA sequence selected from the Sequence Listing which molecule is validated as

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a potential target in a pesticide screen based on the use of said molecule in a gene disruption method according to any one of claims 3 to 5.

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